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:	***2008.002-005F***	(to be completed by ICTV officers)

Short title: A new species in new genus Cryspovirus, family Partitiviridae
(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:

Max L. Nibert: mnibert@hms.harvard.edu
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ICTV-EC or Study Group comments and response of the proposer:

Proposer Max Nibert is a member of the Study Group on family *Partitiviridae*, and proposer Said Ghabrial is the chair of that Study Group. Proposers Keith Woods and Steve Upton have been involved in most of the characterizations of *Cryptosporidium parvum virus 1* to date.

Comments of the Study Group as to why the genus name "Gammacryptovirus" was not used. Historically, the genera *Alphacryptovirus* and *Betacryptovirus* were created under the old family *Cryptoviridae* of plant viruses. Because of similarities between members of these two genera and the fungal viruses classified under the genus *Partitivirus* in the family *Partitiviridae*, the three genera were combined under the family *Partitiviridae* and the family name *Cryptoviridae* was dropped. The Study Group did not consider the name "Gammacryptovirus" for the new monotypic genus in this proposal (with a protozoan virus as the type species) because it implies that the virus being considered is a plant virus. Furthermore, there are at least three new reports of partially characterized plant partitiviruses (plant cryptoviruses) that are distinct from members of the genera *Alphacryptovirus* and *Betacryptovirus*. These would be more appropriately grouped under the genus name "Gammacryptovirus" in a future proposal. The Study Group did consider the name "Cryptosporidiumvirus" as the genus name but opted for "Cryspovirus" for brevity.

MODULE 4: **NEW GENUS**

(if more than one genus is to be created, please complete additional copies of this section)

Code	***2008.002F***	(assigned by ICTV officers)

To create a new genus assigned as follows:

Subfamily:	
Family:	***Partitiviridae***
Order:	

Fill in all that apply. Ideally, a genus should be placed within a higher taxon, but if not put "unassigned" here.

Code	***2008.003F***	(assigned by ICTV officers)

To name the new genus: *Cryspovirus*

Code	***2008.004F***	(assigned by ICTV officers)

To assign the following as species in the new genus:

You may list several species here. For each species, please state whether it is new or existing.

- If the species is new, please complete Module 5 to create it.
- If the species already exists, please state whether it is unassigned or is to be removed from another genus and, if the latter, complete module 6(a) to 'REMOVE' it from that genus.

Cryptosporidium parvum virus 1 (new species, see Module 5)

Code	***2008.005F***	(assigned by ICTV officers)

Note: every genus must have a type species

To designate the following as the type species in the new genus:
Cryptosporidium parvum virus 1

Argument to justify the creation of a new genus:

The following are some of the key shared features that argue for placing Cryptosporidium parvum virus 1 in family *Partitiviridae*. (1) Bisegmented dsRNA genome. (2) Each genome segment is packaged in a separate virus particle. (3) Total genome size, 3.0–4.5 kbp. (4) Each segment includes a single long ORF, one for the RdRp in one segment and one for the coat protein in the other segment (Fig. 1). (5) The RdRp clusters phylogenetically with those from other members of this family (Fig. 2). (6) Isometric nonenveloped particles with a diameter near 30 Å. (7) Semiconservative transcription.

Although multiple features identify Cryptosporidium parvum virus 1 as a member of family *Partitiviridae*, no other recognized members of this family infect a protozoan host; all others infect plants or fungi. Moreover the RdRp of this virus is phylogenetically distinguishable from that of other members of this family (Fig. 2). Lastly, the coat protein of Cryptosporidium parvum virus 1 is only 319 aa in length, shorter than that of other recognized members of this family (next closest, 413 aa, Fusarium solani virus 1). These facts justify creating a new genus in family *Partitiviridae* to harbor the new species *Cryptosporidium parvum virus 1*.

Argument to justify the creation of a new genus:

Continued …

Why should Cryptosporidium parvum virus 1 (CSpV-1) not be placed in a newly created family? Even though CSpV-1 is the first bisegmented dsRNA virus to be isolated from a protozoan host, its features are consistently similar enough to those of other recognized species of family *Partitiviridae* (see first paragraph) to warrant inclusion in that family.

The family *Picobirnaviridae* of bisegmented dsRNA viruses was recently recognized by the ICTV. The following are some of the key distinguishing features of recognized members of that family that argue against placing *Cryptosporidium parvum virus 1* in family *Picobirnaviridae*. (1) Vertebrate hosts. (2) Two ORFs in one genome segment (unknown protein and major coat protein) separated by an AUGA stop/start signal. (3) Phylogenetically distinct RdRp.

Origin of the new genus name:

Cryspo: a sigla from the host genus name, *Cryptosporidium*.

Argument to justify the choice of type species:

Cryptosporidium parvum virus 1 is the only member of the new genus that has been characterized to date.

Species demarcation criteria in the 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.

Not yet applicable: *Cryptosporidium parvum virus 1* is the only member of the new genus that has been characterized to date.

References:

Khramtsov NV, Woods KM, Nesterenko MV, Dykstra CC, Upton SJ (1997). Virus-like, double-stranded RNAs in the parasitic protozoan *Cryptosporidium parvum*. Mol Microbiol 26:289-300.

Khramtsov NV, Upton SJ (1998). High-temperature inducible cell-free transcription and replication of double-stranded RNAs within the parasitic protozoan *Cryptosporidium parvum*. Virology 245:331-337.

Khramtsov NV, Chung PA, Dykstra CC, Griffiths JK, Morgan UM, Arrowood MJ, Upton SJ (2000). Presence of double-stranded RNAs in human and calf isolates of *Cryptosporidium parvum*. J Parasitol 86:275-282.

Khramtsov NV, Upton SJ (2000). Association of RNA polymerase complexes of the parasitic protozoan *Cryptosporidium parvum* with virus-like particles: heterogeneous system. J Virol 74:5788-5795.

Khramtsov NV, Upton SJ (2003). dsRNAs of *Cryptosporidium*. J Parasitol 89 (suppl): 165s-168s.

Kniel KE, Higgins JA, Trout JM, Fayer R, Jenkins MC (2004). Characterization and potential use of a Cryptosporidium parvum virus (CPV) antigen for detecting *C. parvum* oocysts. J Microbiol Methods 58:189-195.

Jenkins MC, O'Brien CN, Trout JM (2008). Detection of *Cryptosporidium parvum* oocysts by dot-blotting using monoclonal antibodies to Cryptosporidium parvum virus 40-kDa capsid protein. J Parasitol 94:94-98.

Annexes:

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

Fig. 1. Genome organization shared by (A) *Cryptosporidium parvum virus 1* and (B) *Atkinsonella hypxylon virus*, the type species of genus *Partitivirus*, family *Partitiviridae*.

Fig. 2 Neighbor-joining phylogenetic trees (phylograms) based on the complete RdRp (left) and CP (right) sequences of each analyzed virus. Sequences were multiply aligned using M-Coffee version 6.0.7 as implemented at http://www.tcoffee.org [Moretti et al., 2007; Wallace et al., 2006]. Trees were then generated using PAUP* (version 4.0b10) and plotted using FigTree (version 1.1.2). Abbreviations and accession numbers for members of family *Partitiviridae* included in the trees are: CSpV1 (U95995 and U95996); AoV, Aspergillus ochraceous virus (EU118277 and EU118278); PsV-S, Penicillium stoloniferm virus S (AY156521 and AY156522); GaRV-MS1, Gremmeniella abietina RNA virus MS1 (AY089993 and AY089994); DdV1, Discula destructiva virus 1 (AF316992 and AF316993); DdV2, Discula destructiva virus 2 (AY033436 and AY033437); OPV1, Ophiostoma partitivirus 1 (AM087202 and AM087203); FsV1, Fusarium solani virus 1 (D55668 and D55669); PsV-F, Penicillium stoloniferum virus F (AY738336 and AY738337); AhV, Atkinsonella hypoxylon virus (L39125 and L39126); CrV1, Ceratocystis resinifera virus 1

(AY603051 and AY603052); FpV1, Fusarium poae virus 1 (AF015924 and AF047013); PoV1, Pleurotus ostreatus virus 1 (AY533036 and AY533038); RnV1, Rosellinia necatrix virus 1 (AB113347 and AB113348); RsV717, Rhizoctonia solani virus 717 (AF133290 and AF133291); BCV1, Beet cryptic virus 1 (EU489061 and EU489062); VCV, Vicia cryptic virus (AY751737 and AY751738); and WCCV1, white clover cryptic virus 1 (AY705784 and AY705785). Each tree was rooted by designating human picobirnavirus (hPBV, AB186897 and AB186898) as outgroup. Respective consensus trees obtained from 2,000 bootstrap replicates showed identical topologies to the displayed phylograms, and the bootstrap percentage values are indicated at the nodes. Scale bars indicate distance in units of 0.1 substitutions per aa position. Colors: orange, genus *Cryspovirus*; cyan, genus *Partitivirus*; and magenta, genus *Alphacryptovirus*.

MODULE 5: **NEW SPECIES**

code	***2008.006F***	(assigned by ICTV officers)

To create 1 new species assigned as follows:

Genus:	***Cryspovirus* (new)**
Subfamily:	
Family:	***Partitiviridae***
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:

Cryptosporidium parvum virus 1

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.

The following are some of the key distinguishing features of Cryptosporidium parvum virus 1 (CSpV-1) that argue for recognizing it as a new species in family *Partitiviridae*. (1) No other recognized members of this family infect a protozoan host; all others infect plants or fungi. (2) The RdRp of CSpV-1 is phylogenetically distinguishable from that of other members of this family (Fig. 2). (3) The coat protein of CSpV-1 is only 319 aa in length, shorter than that of other recognized members of this family (next closest, 413 aa, Fusarium solani virus 1).

References:

Khramtsov NV, Woods KM, Nesterenko MV, Dykstra CC, Upton SJ (1997). Virus-like, double-stranded RNAs in the parasitic protozoan *Cryptosporidium parvum*. Mol Microbiol 26:289-300.

Khramtsov NV, Upton SJ (1998). High-temperature inducible cell-free transcription and replication of double-stranded RNAs within the parasitic protozoan *Cryptosporidium parvum*. Virology 245:331-337.

Khramtsov NV, Chung PA, Dykstra CC, Griffiths JK, Morgan UM, Arrowood MJ, Upton SJ (2000). Presence of double-stranded RNAs in human and calf isolates of *Cryptosporidium parvum*. J Parasitol 86:275-282.

Khramtsov NV, Upton SJ (2000). Association of RNA polymerase complexes of the parasitic protozoan *Cryptosporidium parvum* with virus-like particles: heterogeneous system. J Virol 74:5788-5795.

Khramtsov NV, Upton SJ (2003). dsRNAs of *Cryptosporidium*. J Parasitol 89 (suppl): 165s-168s.

Kniel KE, Higgins JA, Trout JM, Fayer R, Jenkins MC (2004). Characterization and potential use of a Cryptosporidium parvum virus (CPV) antigen for detecting *C. parvum* oocysts. J Microbiol Methods 58:189-195.

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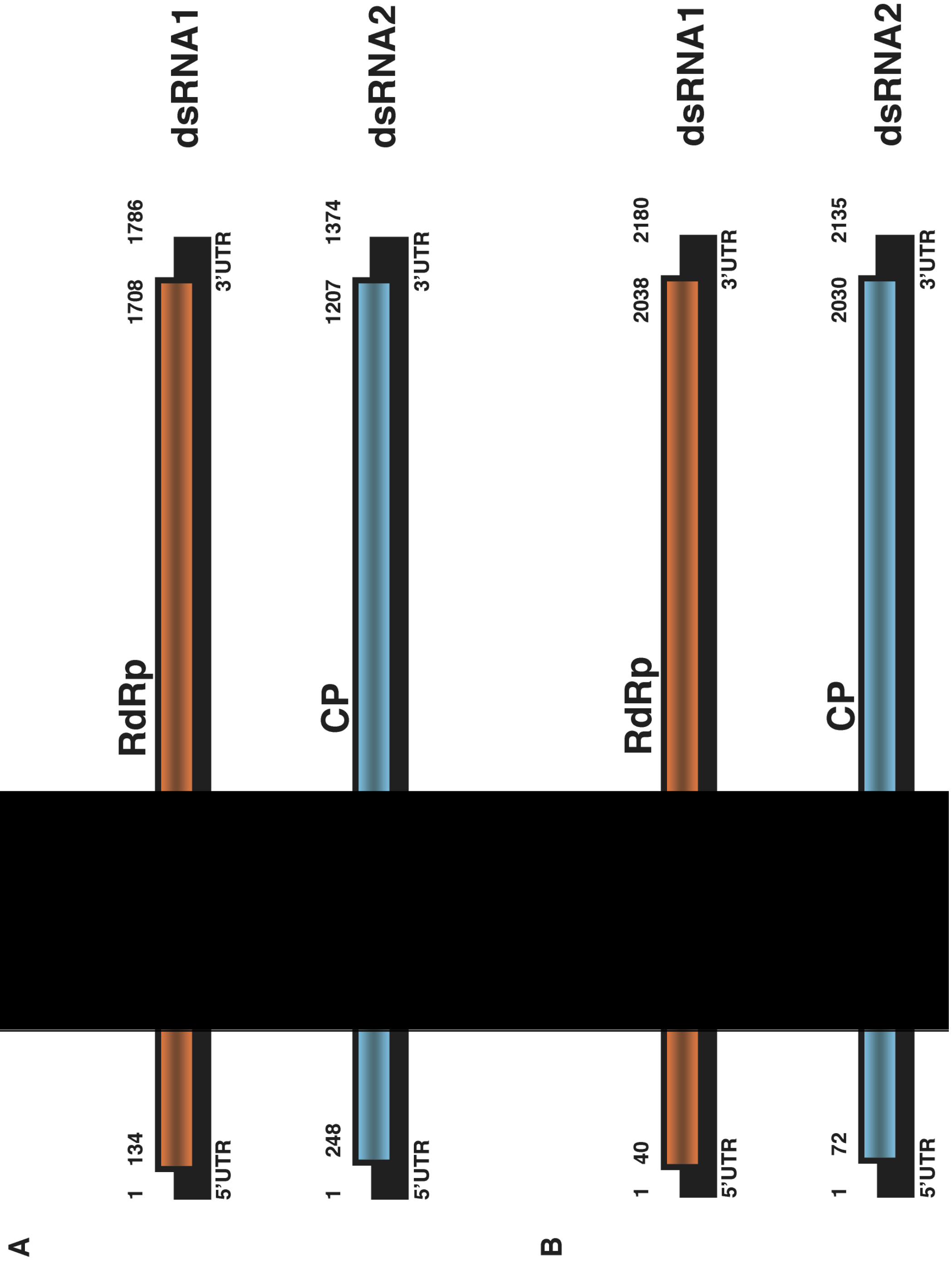
Annexes:

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

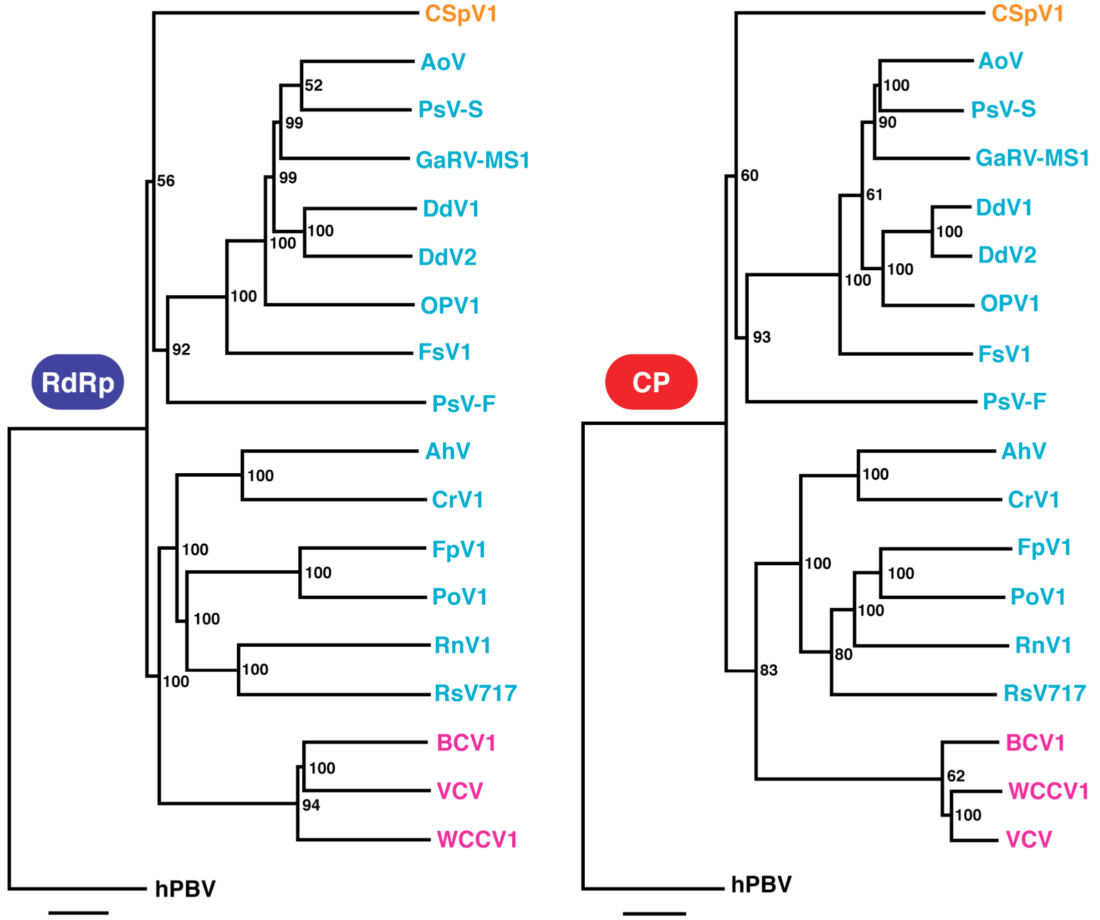
See figures for Module 4.

Fig. 1



[redacted]

Fig. 2


RdRp
CSpV1
AoV
PsV-S
GaRV-MS1
DdV1
DdV2
OPV1
FsV1
PsV-F
AhV
CrV1
FpV1
PoV1
RnV1
RsV717
BCV1
VCV
WCCV1
hPBV
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AoV
PsV-S
GaRV-MS1
DdV1
DdV2
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PsV-F
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