



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:	2008.001F	<small>(to be completed by ICTV officers)</small>
Short title: Five new species in the genus <i>Partitivirus</i> <small>(e.g. 6 new species in the genus <i>Zetavirus</i>; re-classification of the family <i>Zetaviridae</i> etc.)</small>		
Modules attached <small>(please check all that apply):</small>	1 <input type="checkbox"/>	2 <input type="checkbox"/>
	3 <input type="checkbox"/>	4 <input type="checkbox"/>
	5 <input checked="" type="checkbox"/>	6 <input type="checkbox"/>
	7 <input type="checkbox"/>	

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

Said Ghabrial: saghab00@uky.edu Max Nibert: mnibert@hms.harvard.edu
--

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

The proposers : Said Ghabrial is the chair of the study group (SG) on the family <i>Partitiviridae</i> Max Nibert is a member of the SG on the family <i>Partitiviridae</i>

MODULE 5: NEW SPECIES

Code	2008.001F	<small>(assigned by ICTV officers)</small>
To create 5 new species assigned as follows:		
Genus:	<i>Partitivirus</i>	<small>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)</small>
Subfamily:		
Family:	<i>Partitiviridae</i>	
Order:		

Name(s) of proposed new species:

<i>Ceratocystis resinifera virus 1</i> <i>Ophiostoma partitivirus 1</i> <i>Penicillium stoloniferum virus F</i> <i>Pleurotus ostreatus virus 1</i> <i>Rosellinia necatrix virus 1</i>

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

Argument to justify the creation of the new species:

explain how the proposed members meet these criteria.

The criteria to differentiate species in the genus *Partitivirus* (as listed in the eighth Report of ICTV are :

- Host species in which the viruses naturally occur; partitiviruses lack natural vectors and they are confined to the fungal host species from which they were first isolated.
- Size of dsRNA segments.
- Protein sequence similarity. Amino acid sequence similarity >40% between RdRps of viruses from different species in the same phylogenetic cluster and <40% between members of species in different clusters (see Fig. 2).
- Serological relationships.

The five newly proposed species meet the outlined criteria for species demarcation (see below)

Virions of members of the genus *Partitivirus* contain two unrelated segments of dsRNA, in the size range of 1.4 to 2.3 kbp, one encoding the capsid protein (CP) and the other encoding the RdRp. The two segments are usually of similar size and are encapsidated separately. The genomes of at least 15 members of the genus *Partitivirus* have recently been completely sequenced (Table 1). The genomic structure of *Atkinsonella hypoxylon virus* (AhV), the type species of the genus *Partitivirus*, comprising segment 1 (2180 bp, encoding the RdRp) and segment 2 (2135 bp, encoding the CP), is schematically represented in Fig. 1. The presence of one or more satellite dsRNA segments is common among members of the genus *Partitivirus*. For example, in addition to the two genomic segments, preparations of AhV contain a third dsRNA segment of 1790 bp (Table 1).

In addition to the genus *Partitivirus*, whose members infect fungi, the family *Partitiviridae* contains two other genera, namely *Alphacryptovirus* and *Betacryptovirus*. Members of the latter two genera infect plants. The genomes of only a very few members of the genus *Alphacryptovirus* have been sequenced to date and no sequencing information is available for members of the genus *Betacryptovirus*. Recent phylogenetic analyses based on amino acid sequences of RdRps (conserved motifs) of members of the family *Partitiviridae* led to the identification of two large clusters within the genus *Partitivirus* (Fig. 2). One large cluster with strong bootstrap support includes the partitiviruses DdV1, DdV2, FsV, GaV-MS1, OPV1, PsV-S and PsV-F (see Table 1 for virus abbreviations). The CPs of these viruses share significant amino acid sequence identities (34-62%) but less so than the RdRps (55-70% identity). The second large partitivirus RdRp cluster consists of AhV, CrV1, FpV, PoV1, RhsV-717 and RnV1. These two large clusters were proposed to comprise two subgroups (subgroups 1 and 2) of the genus *Partitivirus* (Fig. 2). Interestingly, the CPs of these two subgroups differ significantly in size with average sizes of 47 and 74 kDa for subgroup 1 and 2, respectively (Table 1). Thus the newly proposed species OPV1 (Crawford et al., 2006) and PsV-F (Kim et al., 2005) belong to subgroup 1, whereas CrV1 (Deng and Boland, unpublished), PoV1 (Lim et al., 2005) and RnV1 (Sasaki et al., 2006) belong to subgroup 2. These two subgroups may well warrant future ICTV recognition as separate genera, but that is not the goal of the current proposal.

References:

- Crawford, L.J., Osman, T.A., Booy, F.P., Coutts, R.H., Brasier, C.M., and Buck, K.W. (2006). Molecular characterization of a partitivirus from *Ophiostoma himal-ulmi*. *Virus Genes* 33, 33-39.
- Kim, J.W., Choi, E.Y., and Lee, J.I. (2005). Genome organization and expression of the *Penicillium stoloniferum* virus F. *Virus Genes* 31, 175-183.
- Lim, W-S., Jeong, J. H., Jeong, R-D., Yoo, Y. B., Yie, S. W., and Kim, K-H. (2005). Complete nucleotide sequence and genome organization of a dsRNA partitivirus infecting *Pleurotus ostreatus*. *Virus Res.* 108, 111-119.
- Sasaki, A., Kanematsu, S., Onoue, M., Oyama, Y., and Yoshida, K. (2006). Infection of *Rosellinia necatrix* with purified viral particles of a member of *Partitiviridae* (RnPV1-W8). *Arch. Virol.* 151: 697-707

Annexes:

Table 1 (attached)

Figures 1 and 2 (attached)

Figure legends

Figure 1. Genome organization of *Atkinsonella hypxylon* virus (AhV), the type species of the genus *Partitivirus*. dsRNA1 contains the RdRp ORF (nt positions 40-2038) and dsRNA2 codes for the CP ORF (nt positions of 72 to 2030). The RdRp and CP ORFs are represented by rectangular boxes.

Figure 2. Phylogenetic analysis of the RdRp conserved motifs and flanking sequences derived from aligned deduced amino acid sequences of members of the genus *Partitivirus* and two members of the genus *Alphacryptovirus* using the program CLUSTAL X. The phylogenetic tree was generated using the program PAUP*. Bootstrap numbers out of 1,000 replicates are indicated at the nodes. The tree was rooted with the RdRp of *Helminthosporium victoriae* virus (HvV-190S), a member of the genus *Totivirus* in the family *Totiviridae* (GenBank accession no. NC_003607), which was included as an outgroup.

Table 1. List of viruses in the genus *Partitivirus* with sequenced genomic dsRNAs^a

Virus	Abbreviation	dsRNA segment No. (size in bp; encoded protein, size in kDa)	GenBank Accession No.
Genus: <i>Partitivirus</i>			
Subgroup 1			
<i>Discula destructiva virus 1*</i>	DdV1	1 (1787; RdRp, 62) 2 (1585; CP, 48) 3 (1181; satellite) 4 (308; satellite)	NC_002797 NC_002800 NC_002801 NC_002802
<i>Discula destructiva virus 2*</i>	DdV2	1 (1781; RdRp, 62) 2 (1611; CP, 50)	NC_003710 NC_003711
<i>Fusarium solani virus 1*</i>	FsV1	1 (1645; RdRp, 60) 2 (1445; CP, 44)	D55668 D55669
<i>Gremmeniella abietina virus MS1*</i>	GaV-MS1	1 (1782; RdRp, 61) 2 (1586; CP, 47) 3 (1186; satellite)	NC_004018 NC_004019 NC_004020
Ophiostoma partitivirus 1	OPV1	1 (1744; RdRp, 63) 2 (1567; CP, 46)	AM087202 AM087203
Penicillium stoloniferum virus F	PsV-F	1 (1677; RdRp, 62) 2 (1500; CP, 47) 3 (677; satellite)	NC_007221 NC_007222 NC_007223
<i>Penicillium stoloniferum virus S*</i>	PsV-S	1 (1754; RdRp, 62) 2 (1582; CP, 47)	NC_005976 NC_005977
Subgroup 2			
<i>Atkinsonella hypoxylon virus*</i>	AhV	1 (2,180; RdRp, 78) 2 (2135; CP, 74) 3 (1790; satellite)	L39125 L39126 L39127
Ceratocystis resinifera virus 1	CrV1	1 (2207; RdRp, 77) 2 (2305; CP, 73)	AY603052 AY603051
<i>Fusarium poae virus 1*</i>	FpV1	1 (2203; RdRp, 78) 2 (2185; CP, 70)	NC_003884 NC_003883
<i>Heterobasidium annosum virus*</i>	HaV	1 (2325; RdRp, 87)	AF473549
<i>Helicobasidium mompa virus*</i>	HmV	V1-1 (2247; RdRp, 83)	AB110979
Pleurotus ostreatus virus 1	PoV1	1 (2296; RdRp, 82) 2 (2223; CP, 71)	NC_006961 NC_006960
<i>Rhizoctonia solani virus 717*</i>	RhsV-717	1 (2363; RdRp, 86) 2 (2206; CP, 76)	NC_003801 NC_003802
Rosellinia necatrix virus 1	RnV1	1 (2299; RdRp, 84) 2 (2279; CP, 77)	NC_007537 NC_007538

^a The list contains 10 approved members of the genus *Partitivirus* plus the proposed five new species (highlighted). An asterisk next to the virus name indicates it is presently recognized by ICTV as a member of the genus *Partitivirus*.

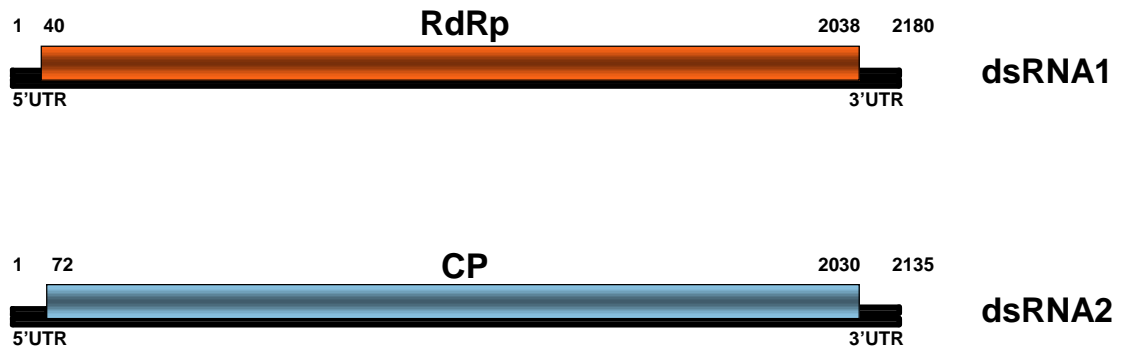


Fig. 1

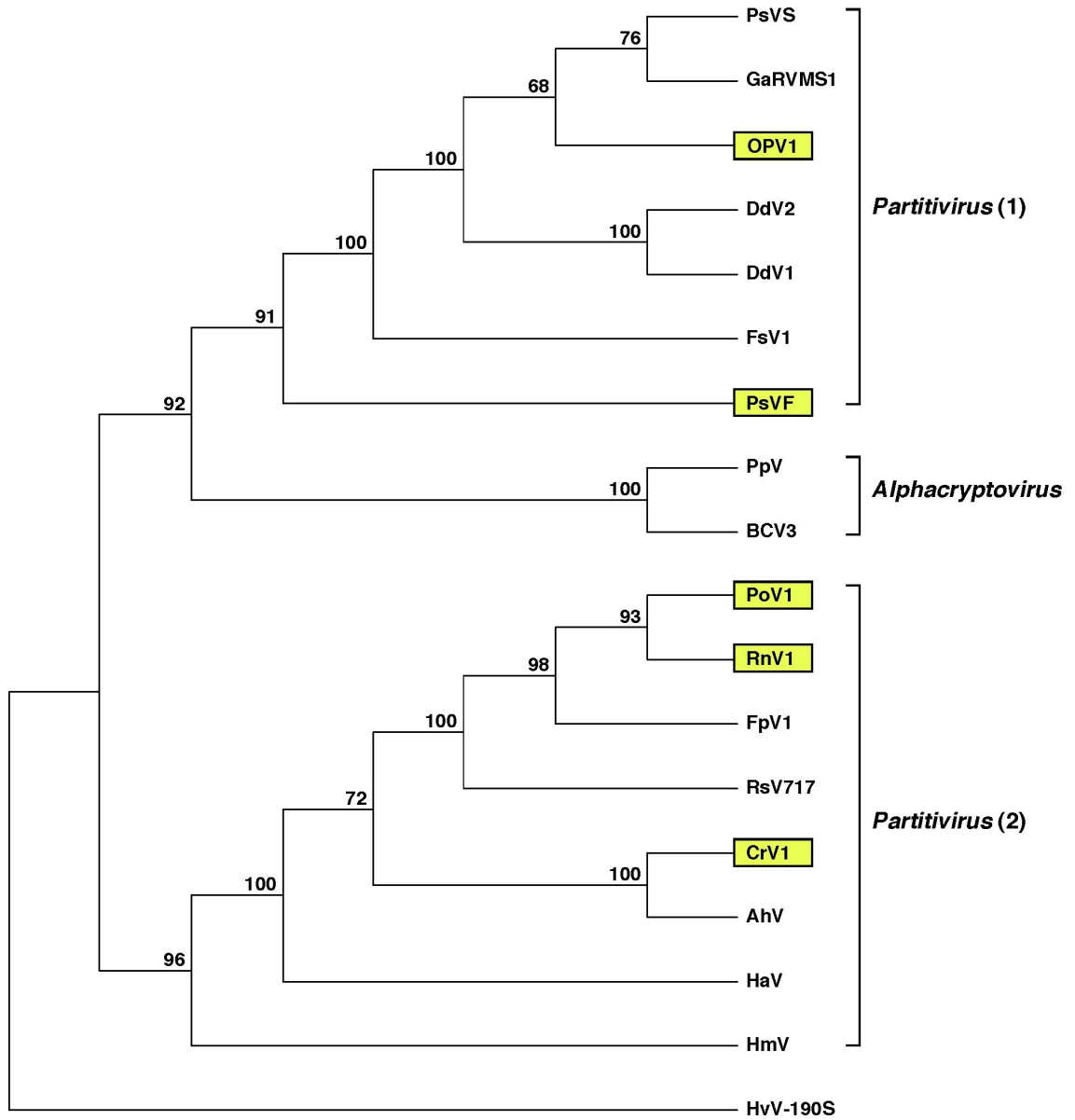


Figure 2