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:	***2011.004aI***	(to be completed by ICTV officers)

Short title: create species *Mud crab virus* in the genus *Aparavirus*, family *Dicistroviridae*, order *Picornavirales*
(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:

Dicistroviridae Study Group:
Yanping (Judy) Chen (judy.chen@ars.usda.gov); Nobuhiko Nakashima (nakaji@affrc.go.jp); Peter Christian (tyttenhangerpete@hotmail.co.uk); Tamas Bakonyi (Bakonyi.Tamas@aotk.szie.hu); Bryony C. Bonning (BBonning@iastate.edu); Steven M. Valles (steven.valles@ars.usda.gov); Donald Lightner (dvl@u.arizona.edu)

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)	***Dicistroviridae* Study Group**

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

Date first submitted to ICTV: Yes
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. Wherever possible, provide sequence accession number(s) for one isolate of each new species proposed.

Code	***2011.004aI***	(assigned by ICTV officers)

To create a new species within:

Genus:	***Aparavirus***
Subfamily:	
Family:	***Dicistroviridae***
Order:	***Picornavirales***

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:	**GenBank sequence accession number(s) of reference isolate:**
Mud crab virus	HM777507

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

The species demarcation criteria in the family *Dicistroviridae* are

- Natural host range: species can be differentiated on the basis of their natural host range and their relative ability to replicate in a range of cultured insect cells.
- Serology: species are serologically distinct.
- Sequence identity between the capsid proteins (CPs) of isolates and strains of a species is above 90%.

A newly identified virus has been reported by Zhang et al. (2010, 2011) to infect the mud crab, *Scylla cerrata*, and was originally termed *Mud crab dicistrovirus*. The complete genome sequence of the new virus has been deposited in the GenBank database under accession NUMBER HM777507. This virus shows the following features that fulfills the *Dicistroviridae* family inclusion criteria:

Virus particles: Spherical in shape, 30 nm in diameter, icosahedral symmetry and no envelop.

Genome: Positive-sense, single stranded RNA genome which is approximately 10436 nt long and contains two large open reading frames (ORF) flanked by 323 nt of 5′-UTR and 338 nt of 3′-UTR and separated by an intergenic region (IGR)(positive 6863-7245). The N-terminal ORF encodes the nonstructural polyprotein of 2179 amino acid residues while the C-terminal ORF encode the structural CPs of 950 amino acid residues.

Phylogeny: Phylogenetic tree constructed with the amino acid sequences of viral non structure polyprotein shows that the virus clusters together with the members of *Dicistroviridae* (Fig. 1). Comparison of the structural CPs showed that the new virus appears to be closely related to the Taura Syndrome Virus (TSV) (Fig. 2). The sequence identity of the capsid proteins between the new virus and TSV is 61.5%.

Natural host range: Has been isolated only from the mud crab, *S. cerrata*.

Antigenic properties: Serologically distinct.

The IGR of the new virus contains bulge sequences (UGGUUACC) and forms a stem loop structure (Figure 3), which are typical features of the genus, *Aparavirus* (Fig. 3).

The above data suggest that this new virus represents a new species within the genus *Aparavirus* family *Dicistroviridaee*. The name proposed is *Mud Crab Virus* (MCV). To follow the standard nomenclatural format of dicistroviruses, the “*dicistro*” was removed from the original name.

MODULE 9: **APPENDIX**: supporting material

additional material in support of this proposal

References:

Zhang, R., He, J. Su, H., Dong, C., Guo, Z., Ou, Y., Deng, X., Weng, S. (2011) Identification of the structural proteins of VP1 and VP2 of a novel mud crab Dicistrovirus. Journal of Virological Methods 171 (2011) 323–328.

Zhang, R., He, J., Su, H., Dong, C., Guo, Z., and Weng, S. (2010) Monoclonal antibodies produced against VP3 of a novel mud crab dicistrovirus. Hybridoma (Larchmt). 29(5):437-40.

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.

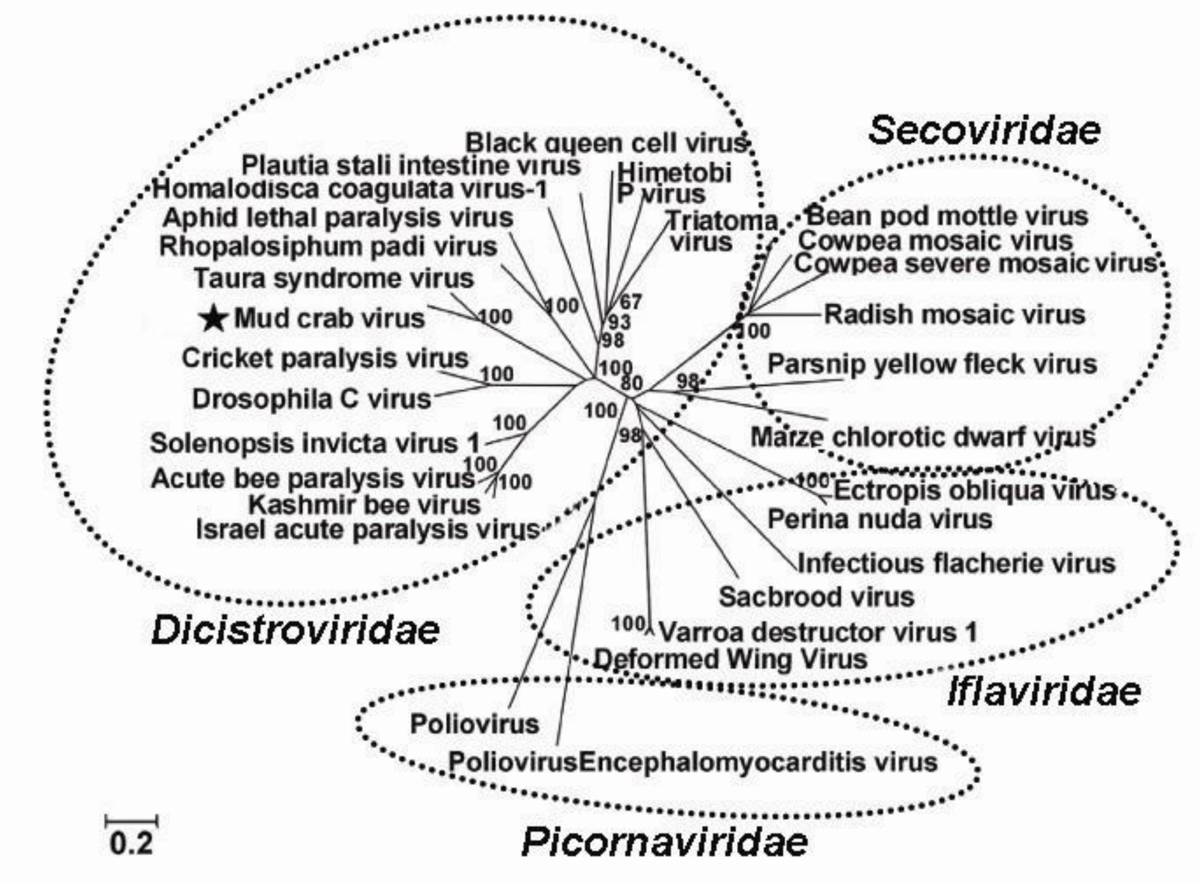

Fig 1. Unrooted phenogram showing the relationship of Mud crab virus and other viruses in the families *Dicistroviridae*, *Iflaviridae*, *Secoviridae* and *Picornaviridae*. The phylogenetic analysis was conducted in MEGA4 (Tamura et al., 2007) based on amino acid sequences of the putative non-structural polyprotein using the Neighbor-Joining method. The tree is

drawn to scale, with branch lengths in the same units as those of the evolutionary distances used to infer the phylogenetic tree. The scale bar shows the number of substitutions per base. The neighbour-jointing phenogram was boostraped 500 times with values greater than 50% given at nodes. Taxa used (with virus name and accession number) were: ***Dicistroviridae*** – Mud crab virus (HM777507), Acute bee paralysis virus (AF150629), Black queen cell virus (AF183905), Cricket paralysis virus (AF218039), Drosophila C virus (AF014388), Kashmir bee virus (AY27571O), Rhopalosiphum padi virus (AF022937), Solenopsis invicta virus-l (AY6343 14), Taura syndrome virus (AF277675), Israeli acute paralysis virus (EF219380), Aphid lethal paralysis virus (AF536531), Homalodisca coagulata virus-1 (DQ288865), Plautia stali intestine virus (AB006531), Himetobi P virus (AB017037), and Triatoma virus (AF178440); ***Iflaviridae* -** Deformed wing virus (AY292384), Ectropis obliqua virus (AY365064), Infectious flacherie virus (AB000906), Perina nuda virus (AF323747), Sacbrood virus (AF092924), and Varroa destructor virus 1 (AY251269); ***Secoviridae* -** Parsnip yellow fleck virus (D14066), Cowpea severe mosaic virus (M83830), Maize chlorotic dwarf virus (NP619716), Bean pod mottle virus (NP612349, Radish mosaic virus (YP001911126), and Cowpea mosaic virus (NP613283); ***Picornaviridae* -** Poliovirus (VOl149), and Encephalomyocarditis virus (M81861).

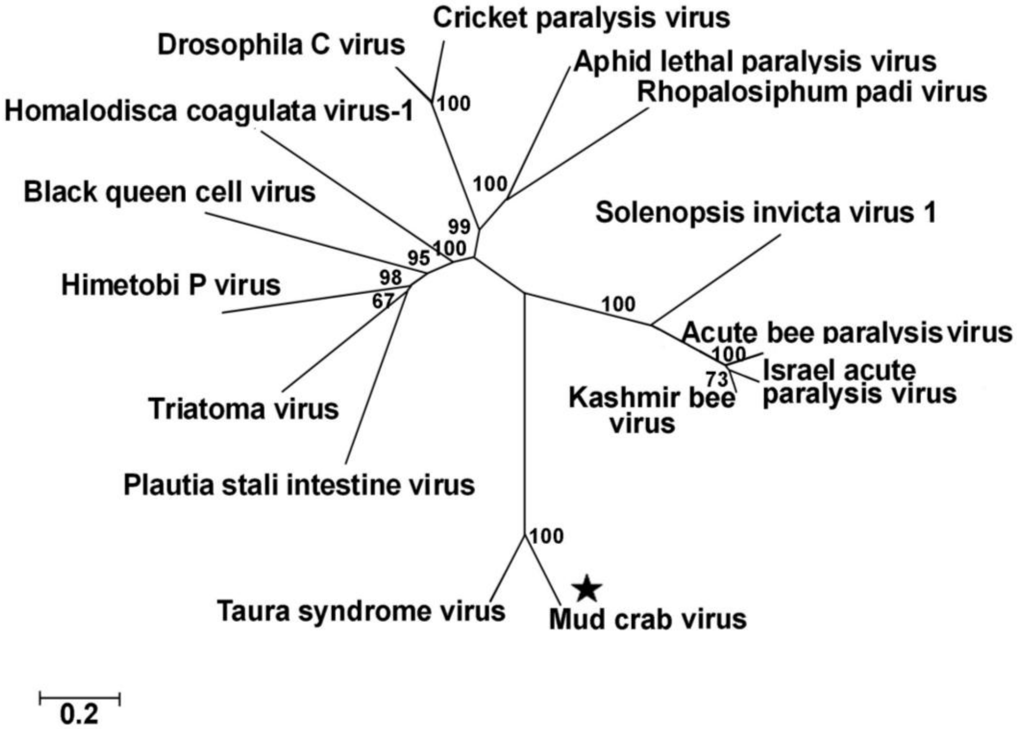

Fig 2. Neighbour-jointing tree showing the relationship between MCDV and other members of the *Dicistroviridas*. Phylogenetic analysis was conducted in MEGA4 (Tamura et al., 2007) based on amino acid sequences of the structural capsid proteins. The neighbour-jointing phenogram was bootstrapped 500 times with values greater than 50% given at nodes. The names and accession numbers of dicistrovirus taxa are the same as above Fig. 1.

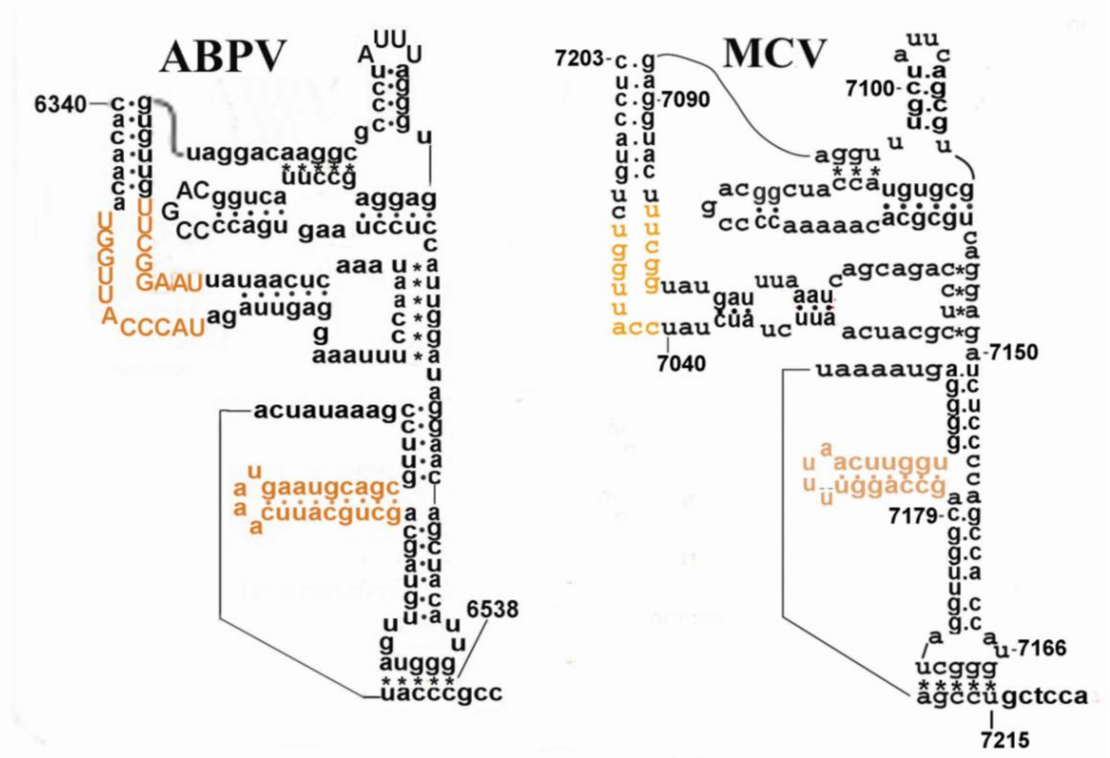

Fig. 3. Structure of IGR-IRES elements of aparaviruses. Like other aparaviruses, such as type species Acute bee paralysis virus (ABPV), the IGR of Mud crab virus contains bulge sequences (UGGUUACC) and forms a stem loop structure which are shown in orange color.