



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:	2008.0051	(to be completed by ICTV officers)
Short title: Creation of a new species in the genus, Cripavirus, family Dicistroviridae (e.g. 6 new species in the genus <i>Zetavirus</i> ; re-classification of the family <i>Zetaviridae</i> etc.)		
Modules attached (please check all that apply):	1 <input type="checkbox"/>	2 <input type="checkbox"/>
	3 <input type="checkbox"/>	4 <input checked="" 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:

Dicistroviridae Study Group:
 Nobuhiko Nakashima (nakaji@affrc.go.jp), Karyn Johnson (karynj@uq.edu.au); Frank van der Wilk (Frank.van.der.Wilk@rivm.nl); Les Domier: (l-domier@uiuc.edu); Peter Christian (pchristian@nibsc.ac.uk); Judy Chen (ChenJ@ba.ars.usda.gov) ; Tamas Bakonyi (Bakonyi.Tamas@aotk.szie.hu).

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

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MODULE 5: NEW SPECIES

Code	2008.0051	(assigned by ICTV officers)
To create <i>Homalodisca coagulata virus-1</i>, a new species assigned as follows:		
Genus:	<i>Cripavirus</i>	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)
Subfamily:		
Family:	<i>Dicistroviridae</i>	
Order:	<i>Picornavirales</i>	

Name(s) of proposed new species:

Homalodisca coagulata 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.

HoCV-1 was found from the glassy winged sharp shooter, *Homalodisca coagulata* (Hemiptera, Insecta) (*Homalodisca coagulata* is a synonym of *Homalodisca vitripennis* but

Argument to justify the creation of the new species:

the nomenclature used in the original publications is retained for clarity)

The HoCV-1 genome has an organization typical of the dicistroviruses, i.e., a long 5' UTR followed by ORF1 from which a polyprotein precursor is translated that includes the nonstructural proteins in order of helicase, protease, and RNA dependent RNA polymerase. This ORF is followed by an intergenic region and then ORF2 which encodes the capsid protein precursor.

Phylogenetic analysis of deduced amino acid sequence for RNA polymerase of positive-sense RNA viruses indicates that HoCV-1 is most closely related to PSIV, HiPV and TrV, which are isolated from hemipteran insects (Figure 1 below)

The smallest capsid protein VP4 is assumed to be located between VP2 and VP3, similar to other cripaviruses.

The intergenic region of HoCV-1 can form a secondary structure which is typically formed in cripaviruses (Figure 2).

Serological relation to other member of dicistroviruses is not reported but sequence identities of CPs (25%-29%) indicate that HoCV-1 should be a distinct species in the genus *Cripavirus*.

References:

Hunnicut L.E, Mozoruk J, Hunter W.B, Crosslin J.M, Cave R.D, Powell C.A. (2007) Prevalence and natural host range of Homalodisca coagulata virus-1 (HoCV-1). Arch. Virol. 153, 61-67.

Hunnicut L.E, Hunter W.B, Cave R.D, Powell C.A, Mozoruk J.J. (2006) Genome sequence and molecular characterization of Homalodisca coagulata virus-1, a novel virus discovered in the glassy-winged sharpshooter (Hemiptera: Cicadellidae). Virology 350, 67-78.

Annexes:

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

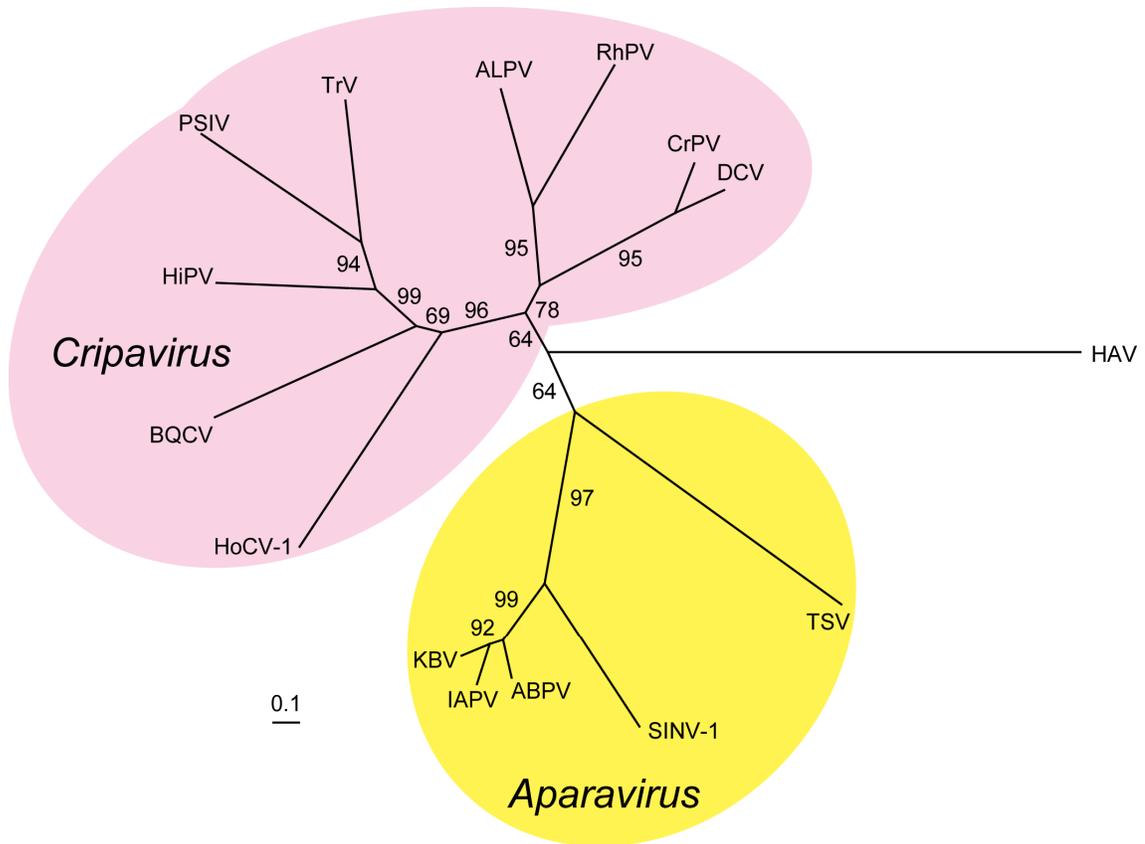


Figure 1.

Neighbour joining tree constructed from an alignment of the deduced amino acid sequence of structural proteins encoding ORF2 of dicistroviruses. Deduced amino acid sequence for capsid protein precursor of hepatitis A virus was used for outgroup. Cripaviruses: ALPV, aphid lethal paralysis virus, AF536531; BQCV, black queen-cell virus, AF183905; CrPV, cricket paralysis virus, AF218039; DCV, *Drosophila C* virus, AF014388; HiPV, himetobi P virus, AB017037; HoCV-1, *Homalodisca coagulata* virus-1, DQ288865; PSIV, *Plautia stali* intestine virus, AB006531; RhPV, *Rhopalosiphum padi* virus, AF022937; TrV, *Triatoma* virus, AF178440. Aparaviruses; ABPV, acute bee paralysis virus, AF150629; IAPV, Israeli acute paralysis virus, EF219380; KBV, Kashmir bee virus, AY275710; SiNV-1, *Solenopsis invicta* virus-1, AY634314; TSV, *Taura syndrome* virus, AF277675.

Data on isolates of the newly proposed species in the family: *Homalodisca coagulata* virus-1 (HoCV-1) (*Cripavirus*) and Israeli acute paralysis virus (IAPV) (*Aparavirus*) are also included in this figure (see Module 5).

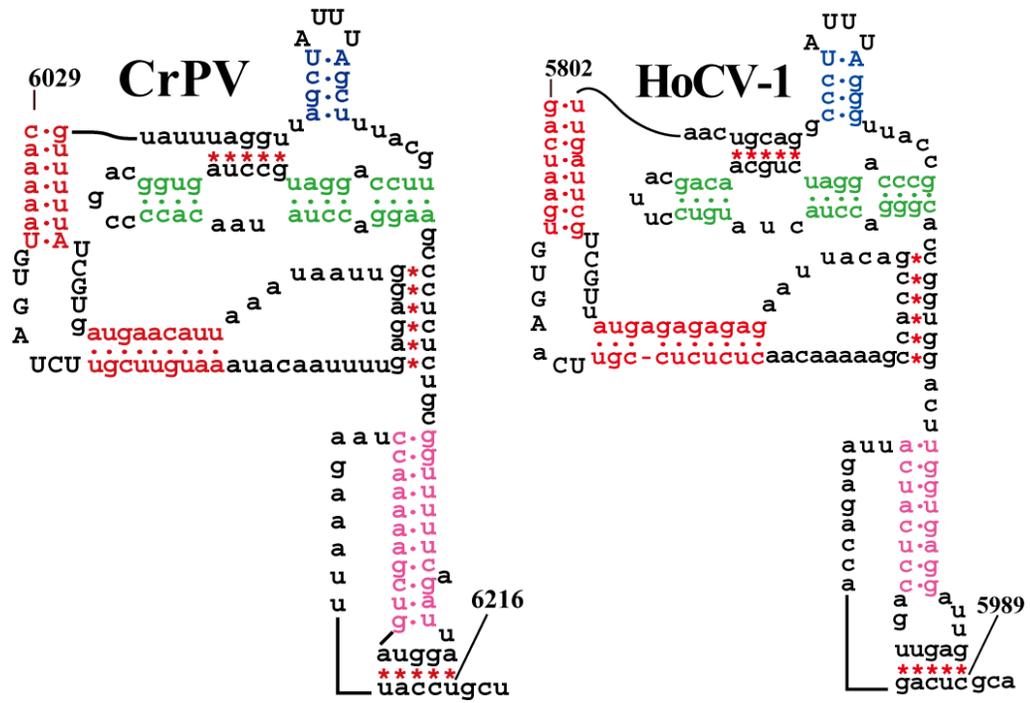


Figure 2
Secondary structures of IGR-IRES elements in the type species CrPV (left) and HoCV-1 (right).