



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:	2009.016aV	(to be completed by ICTV officers)
Short title: Create species Ictalurid herpesvirus 2 and Acipenserid herpesvirus 2 in genus Ictalurivirus, family Alloherpesviridae, order Herpesvirales (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 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:

Andrew Davison; a.davison@mrcvu.gla.ac.uk; adopted by the Herpesvirales Study Group.

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



MODULE 5: **NEW SPECIES**

Code	<i>2009.016aV</i>
To create 2 new species assigned as follows:	
Genus:	<i>Ictalurivirus</i>
Subfamily:	
Family:	<i>Alloherpesviridae</i>
Order:	<i>Herpesvirales</i>

Name(s) of proposed new species:

<i>Ictalurid herpesvirus 2</i> <i>Acipenserid herpesvirus 2</i>
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Argument to justify the creation of the new species:

Related herpesviruses are classified as distinct species if (a) their nucleotide sequences differ in a readily assayable and distinctive manner across the entire genome and (b) they occupy different ecological niches by virtue of their distinct epidemiology and pathogenesis or their distinct natural hosts. A paradigm is provided by human herpesviruses 1 and 2, which differ in their sequence throughout the genome, tend to infect different epithelial surfaces and exhibit distinct epidemiological characteristics. These two viruses recombine readily in culture, but despite the fact that they can infect the same sites in the host, no recombinants have been isolated in nature, and the two viruses appear to have evolved independently for millions of years.

Ictalurid herpesvirus 1 (IcHV1) represents the species *Ictalurid herpesvirus 1* in the genus *Ictalurivirus*, and is associated with economically important epidemics in channel catfish (*Ictalurus punctatus*). Ictalurid herpesvirus 2 (IcHV2) is associated with similar epidemics in the black bullhead (*Ameiurus melas*), and has been isolated. IcHV2 does not react with polyclonal rabbit or monoclonal antibodies directed to IcHV1 in either neutralization or indirect immunofluorescence assays, and is distinct from IcHV1 when compared by restriction fragment length polymorphisms of genomic DNA (Hedrick *et al.*, 2003). Sequence analysis of portions of the DNA polymerase and terminase genes shows that the two viruses are distinct from each other, though closely related (Figures 1 and 2). Classification into the genus *Ictalurivirus* under the species name *Ameiurine herpesvirus 1* was recommended in Doszpoly *et al.* (2008), and this remains the view of the senior author (M Benkő). On the other hand, classification into this genus under the species name *Ictalurid herpesvirus 2* was recommended in Waltzek *et al.* (2009). The former name is derived from the host genus and the latter from the host family (Acipenseridae). I support *Ictalurid herpesvirus 2* as the species name, as this is consistent with the general convention for naming herpesvirus species after the host family.

Acipenserid herpesvirus 2 (AciHV2) causes mortality in intensively reared juvenile white sturgeon (*Acipenser transmontanus*). The virus has been isolated. Sequence analysis of portions of the DNA polymerase and terminase genes shows that this virus is most closely

Argument to justify the creation of the new species:

related to ICHV1 and ICHV2 (Figures 1 and 2). This virus is phylogenetically more distant from another herpesvirus of white sturgeon, acipenserid herpesvirus 1 (AciHV1) (Figures 1 and 2), and neutralizing sera against it do not neutralize AciHV1 (Watson *et al.*, 1995). More than 60 kbp of sequence from the AciHV2 genome has been determined, and every gene so far discovered has an identical position and orientation and a similar size to its counterpart in ictalurid herpesvirus 1 (M Benkő, unpublished data). Classification into the genus *Ictalurivirus* was recommended in Doszpoly *et al.* (2008) and Waltzek *et al.* (2009), the latter suggesting the species name *Acipenserid herpesvirus 2*. I support this recommendation.

References:

- Doszpoly A, Kovács ER, Bovo G, LaPatra SE, Harrach B, Benkő M. 2008. Molecular confirmation of a new herpesvirus from catfish (*Ameiurus melas*) by testing the performance of a novel PCR method, designed to target the DNA polymerase gene of alloherpesviruses. Arch Virol :2123-7.
- Hedrick RP, McDowell TS, Gilad O, Adkison M, Bovo G. 2003. Systemic herpes-like virus in catfish *Ictalurus melas* (Italy) differs from Ictalurid herpesvirus 1 (North America). Dis Aquat Organ 55:85-92.
- Kurobe T, Kelley GO, Waltzek TB, Hedrick RP. 2008. Revised phylogenetic relationships among herpesviruses isolated from sturgeons. J Aquat Anim Health 20:96-102.
- Waltzek TB, Kelley GO, Alfaro, ME, Kurobe T, Davison AJ, Hedrick RP. 2009. Phylogenetic relationships in the family *Alloherpesviridae*. Dis Aquat Org 84:179-194.
- Watson LR, Yun SC, Groff JM, Hedrick RP (1995) Characteristics and pathogenicity of a novel herpesvirus isolated from adult and subadult white sturgeon *Acipenser transmontanus*. Dis Aquat Org 22:199-210.

Annexes:

Figure 1. Phylogenetic (distance matrix) tree reconstructions based on distance matrix analysis of partial DNA polymerase aa sequences available from frog and fish alloherpesviruses. (a) Tree calculated on a short (99 aa) alignment with Kimura matrix. (b) Tree based on a longer (501 aa) alignment with JTT matrix. High bootstrap values confirm the tree topology. AmHV-1, ameurine herpesvirus 1 (a synonym for ICHV2). From Doszpoly *et al.* (2008). Accession numbers therein.

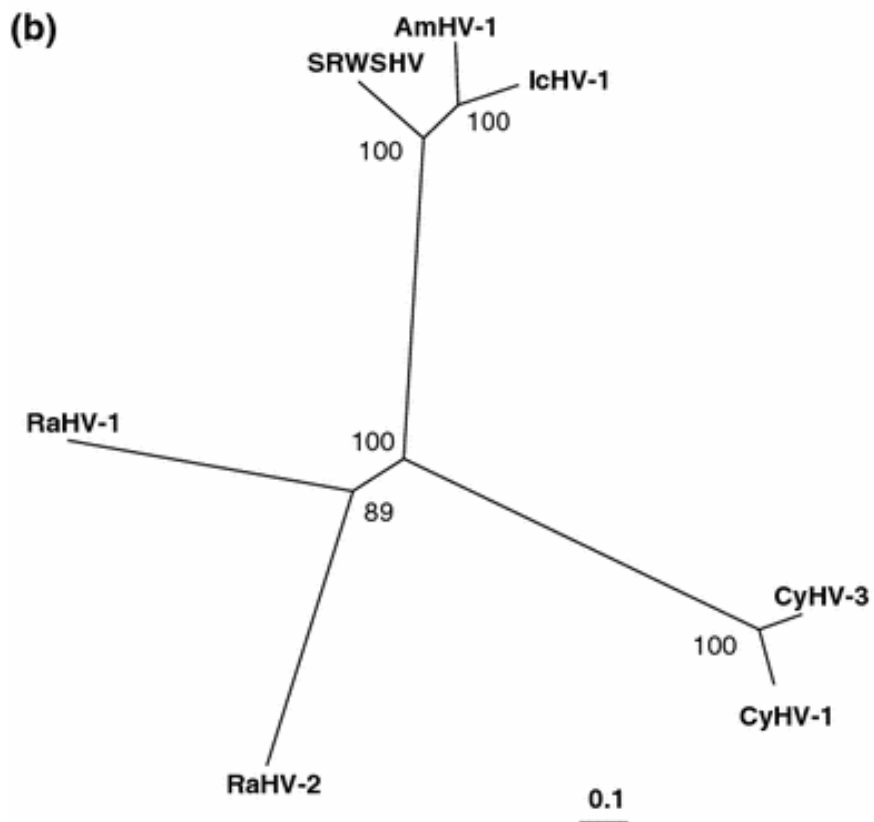
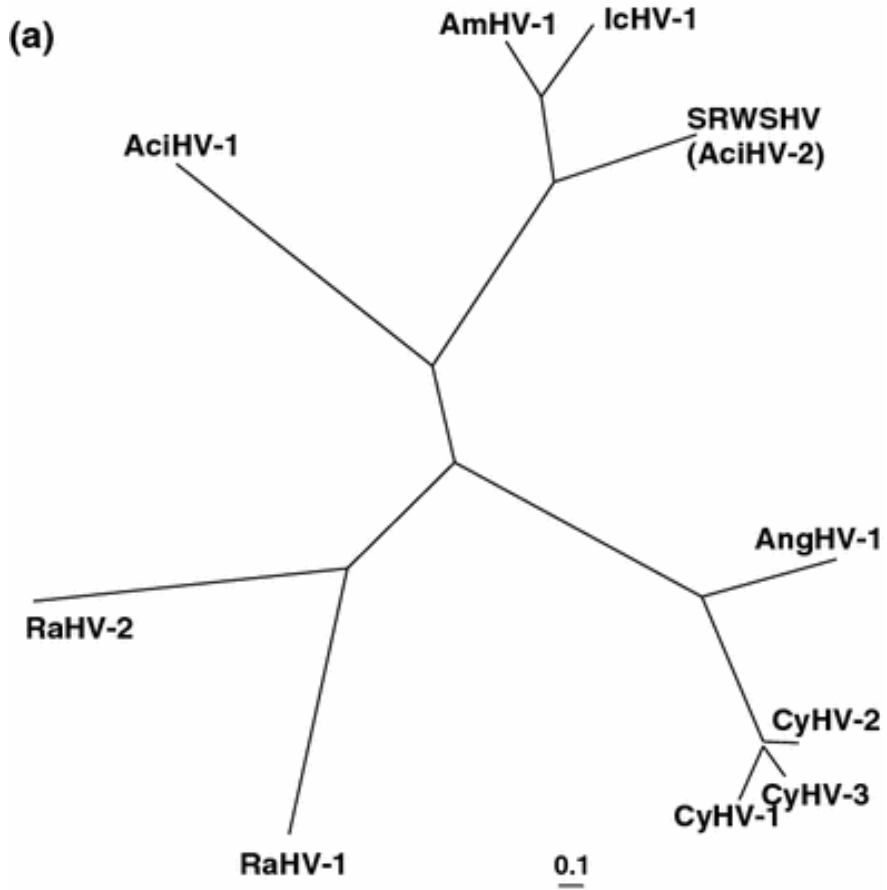


Figure 2. Phylogram depicting relationships among fish and amphibian herpesviruses, based on the concatenated deduced partial amino acid sequences of the DNA polymerase and terminase genes (309 aa). The quartet puzzling maximum likelihood tree was rooted with human herpesviruses 1 and 8 (HHV-1 and HHV-8) in the family *Herpesviridae*. The numbers above each node represent quartet puzzling probabilities (values >80 shown) of the maximum likelihood analysis, and the numbers below represent posterior probabilities (values >90 shown) of the Bayesian analysis. The branch lengths are based on the number of inferred substitutions, as indicated by the scale. From Waltzek *et al.* (2009). Accession numbers therein.

