



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**

<b>Code assigned:</b>	<b>2010.015aV</b>	(to be completed by ICTV officers)			
<b>Short title:</b> New species <i>Anguillid herpesvirus 1</i> in the genus <i>Cyprinivirus</i> , family <i>Alloherpesviridae</i> , order <i>Herpesvirales</i> . (e.g. 6 new species in the genus <i>Zetavirus</i> )					
<b>Modules attached</b> (modules 1 and 9 are required)	1 <input checked="" type="checkbox"/> 6 <input type="checkbox"/>	2 <input checked="" type="checkbox"/> 7 <input type="checkbox"/>	3 <input type="checkbox"/> 8 <input type="checkbox"/>	4 <input type="checkbox"/> 9 <input checked="" type="checkbox"/>	5 <input type="checkbox"/>

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

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**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)

Herpesvirales Study Group

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

This proposal has had a full round of discussion and has been approved without dissent by the Herpesvirales Study Group.

Date first submitted to ICTV:

to Study Group Chair Feb. 3, 2010  
communicated to SG Feb. 9, 2010  
Final SG vote completed April 7,  
2010.

Date of this revision (if different to above):

June 4, 2010

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.

Code	<b>2010.015aV</b>	(assigned by ICTV officers)
<b>To create 1 new species within:</b>		
Genus:	<i>Cyprinivirus</i>	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.
Subfamily:		
Family:	<i>Alloherpesviridae</i>	
Order:	<i>Herpesvirales</i>	
<b>And name the new species:</b>		
<i>Anguillid herpesvirus 1</i>		

**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.
- Provide accession numbers for genomic sequences
- Further material in support of this proposal may be presented in the Appendix, Module 9

In 1990 a new virus was isolated from cultured Japanese eels (*Anguilla japonica*) and European eels (*Anguilla anguilla*) in Japan (Sano et al., 1990). The virus appeared to consist of a core with a large DNA genome, surrounded by an icosahedral nucleocapsid with a diameter of about 110 nm, that is surrounded by a tegument, all enclosed by an envelope with a diameter of about 200 nm (Davidse et al., 1999; Sano et al., 1990). Based on these biological properties the virus was classified as a herpesvirus, designated anguillid herpesvirus 1 (AngHV-1) after the host family, with herpesvirus anguillae as the Latinized name and eel herpesvirus as the vernacular name (Sano et al., 1990). Other formerly used names for the same virus include eel herpesvirus in Formosa (Ueno et al., 1992; Ueno et al., 1996), gill herpesvirus of eel (Lee et al., 1999) and European eel herpesvirus (Chang et al., 2002).

Related herpesviruses are classified as distinct species if (a) their genomes differ in a readily assayable and distinctive manner across the entire genome and (b) if the virus can be shown to have distinct epidemiologic and biologic characteristics (Roizman *et al.*, 1992).

AngHV-1 is commonly observed in Japanese and European eels and has never been detected in other species than the freshwater eels of the genus *Anguilla* (Chang et al., 2002; Davidse et al., 1999; Haenen et al., 2002; Jakob et al., 2009; Kobayashi and Miyazaki, 1997; Lee et al., 1999; Ueno et al., 1992; van Ginneken et al., 2004). AngHV-1 can cause a hemorrhagic disease in freshwater eels, potentially resulting in an increased mortality (Chang et al., 2002; Davidse et al., 1999; Haenen et al., 2002; Hangalapura et al., 2007; Kobayashi and Miyazaki, 1997; Sano et al., 1990; Shih et al., 2003; Ueno et al., 1992; van Ginneken et al., 2004; van Nieuwstadt et al., 2001).

Recently, the complete genome of the Dutch AngHV-1 isolate 500138 was sequenced (RefSeq accession number NC\_013668). AngHV-1 has a genome length of 248,531 bp, a direct terminal repeat length of 10,634 bp, and 136 predicted protein coding open reading frames (van Beurden et al., 2009). The genome characteristics clearly differ from those of the other completely sequenced herpesviruses infecting bony fish and amphibians: *Ictalurid herpesvirus 1* (IcHV-1), *Cyprinid herpesvirus 3* (CyHV-3), *Ranid herpesvirus 1* (RaHV-1) and *Ranid herpesvirus 2* (RaHV-2).

AngHV-1 isolates from European eels in Europe and Asia can be considered as a single virus species as is indicated by serological, molecular and limited sequence data (Chang et al., 2002; Rijsewijk et al., 2005; Waltzek et al., 2009). This conclusion was confirmed by comparing sequence data of four conserved genes of the Dutch AngHV-1 isolate 500138 with sequence data of the Japanese AngHV-1 isolate C3P2, kindly provided by Dr. H. Fukuda, Tokyo University of Fisheries, Japan (Haenen et al., 2002; Rijsewijk et al., 2005) (GenBank accession numbers GU233797 (capsid triplex protein 2), GU233798 (DNA helicase), GU233799 (the major capsid protein) and GU233800 (DNA polymerase)). Sequence comparison revealed the following nucleotide identities between the Dutch and the Japanese AngHV-1 isolates: capsid triplex protein 2 99.6%, DNA helicase 99.9%, DNA polymerase 99.8% and the major capsid protein 99.7%.

Within the family *Alloherpesviridae* only 13 genes are conserved among all members (Aoki et al., 2007). Closer related alloherpesviruses show more homology with each other, for example IcHV-1 and both ranid herpesviruses share 19 genes and the ranid herpesviruses share 40 genes (Davison et al., 2006). Similarity searches for AngHV-1 carried out against non-redundant protein sequences available at the NCBI database by using BLASTP showed that AngHV-1 is clearly distinctive with only 12 genes shared with the other completely sequenced herpesviruses (van Beurden et al., 2009). A total of 40 genes appeared to be convincingly conserved between AngHV-1 and CyHV-3, indicating a relatively close relationship

The criteria for the establishment of new genera within the family *Alloherpesviridae* have not been stated yet, nor have rules been formulated for deciding whether species should belong to a particular genus. Currently, genera and their respective assigned species are assigned based largely on available phylogenetic analyses; species phylogenetically closely related are assigned to the same genus. In the majority of the cases this classification happens to follow the grouping of alloherpesviruses infecting the same host. See for example the recently established genera *Cyprinivirus* comprising the three cyprinid herpesviruses, *Batrachovirus* comprising two species of ranid herpesviruses, and *Salmonivirus* comprising the three salmonid herpesviruses species (*Salmonid herpesvirus 1* (denoted Salmonid herpesvirus 1, abbreviated as SalHV-1), *Salmonid herpesvirus 2* (Salmonid herpesvirus 1, SalHV-2), *Salmonid herpesvirus 3* (Salmonid herpesvirus 3, SalHV-3)). Phylogenetic distances between the members of these genera differ considerably, however. Compare for example the distance between the ranid herpesviruses RaHV-1 and RaHV-2 with the distances between *Cyprinid herpesvirus 1* (Cyprinid herpesvirus 1, CyHV-1), *Cyprinid herpesvirus 2* (Cyprinid herpesvirus 2, CyHV-2) and CyHV-3 (Waltzek et al., 2009). Furthermore, herpesviruses infecting the same host are not necessarily phylogenetically closely related. For example acipenserid herpesvirus 1 (AciHV-1) and *Acipenserid herpesvirus 2* (Acipenserid herpesvirus 2, AciHV-2) are distantly related (Doszpoly et al., 2008). With the classification of AciHV-2, IcHV-1 and *Ictalurid herpesvirus 2* (*Ictalurid herpesvirus 2*, IcHV-2) into the genus *Ictalurivirus*, it was illustrated that a genus can comprise herpesvirus species infecting different host families.

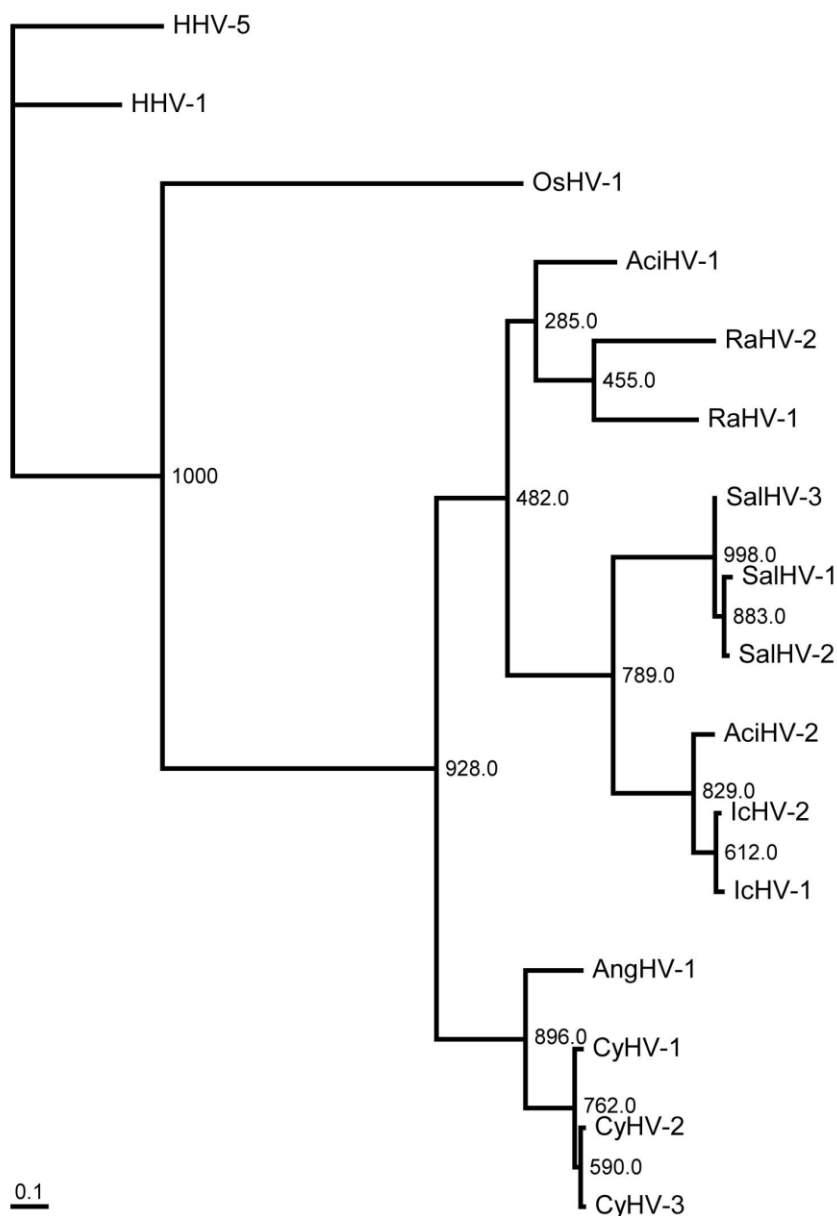
Recent genomic and phylogenetic analyses of the family *Alloherpesviridae* indicate AngHV-1 to be clearly distinctive from, but closest related to the cyprinid herpesviruses (van Beurden et al., 2009). Together, the anguillid and the cyprinid herpesviruses form a phylogenetic group more distantly related to the other members of the family *Alloherpesviridae* (van Beurden et al., 2009; Waltzek et al., 2009). Although AngHV-1 infects anguillid species rather than cyprinid species, the genomic homology and phylogenetic distances within the clade consisting of AngHV-1 and the cyprinid herpesviruses are comparable to the homology and distances within the other established genera in the family. Therefore, we propose that anguillid herpesvirus 1 is a new virus species in the family *Alloherpesviridae*, and that it should be assigned to the genus *Cyprinivirus*.

MODULE 9: **APPENDIX**: supporting material

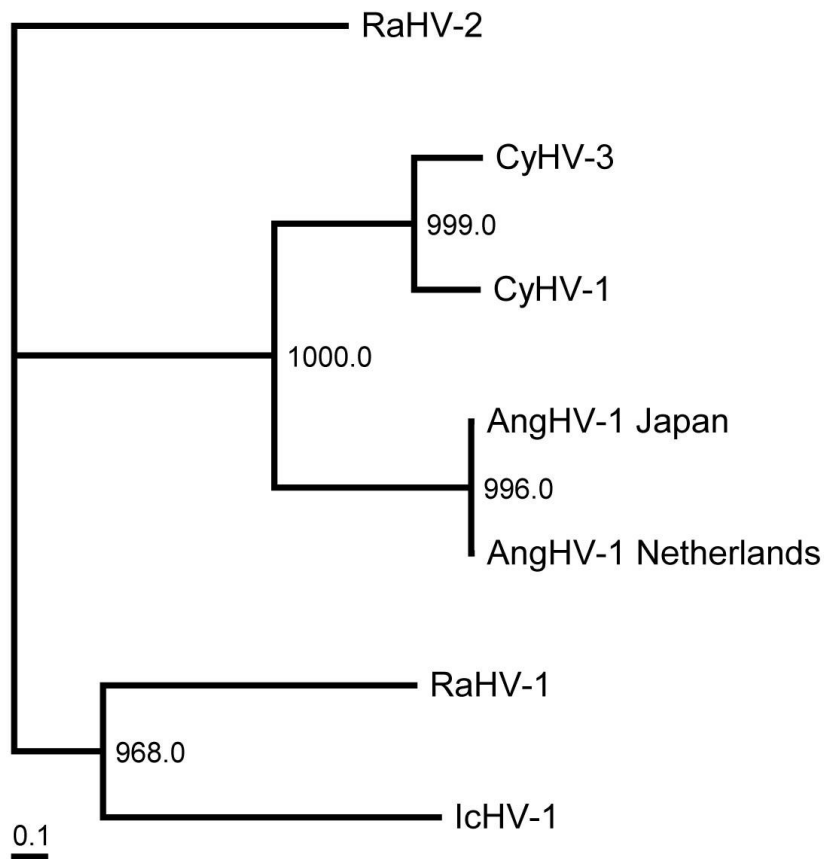
**Table 1.** Completely sequenced and annotated *Alloherpesviridae*.

Name	Abbreviation	Genome length	Terminal repeat length	G+C content	Number of ORFs	ORF density	RefSeq accession	Reference
<i>Ictalurid herpesvirus 1</i>	IcHV-1	134,226	18,556	56.2%	79	0.68	NC_001493	(Davison, 1992)
<i>Cyprinid herpesvirus 3</i>	CyHV-3	295,146	22,469	59.2%	156	0.57	NC_009127	(Aoki et al., 2007)
<i>Ranid herpesvirus 1</i>	RaHV-1	220,859	636	54.6%	132	0.60	NC_008211	(Davison et al., 2006)
<i>Ranid herpesvirus 2</i>	RaHV-2	231,801	912	52.8%	147	0.63	NC_008210	(Davison et al., 2006)
anguillid herpesvirus 1	AngHV-1	248,531	10,634	53.0%	136	0.57	NC_013668	(van Beurden et al., 2009)

**Figure 1.** Unrooted maximum-likelihood phylogenetic tree (1000 replicates) based upon a 116 residue deduced amino acid sequence alignment of the terminase gene depicting the relationships within the family *Alloherpesviridae*, with human herpesviruses 1 and 5 as representatives of the *Herpesviridae* subfamilies *Alphaherpesvirinae* and *Betaherpesvirinae*, respectively, and *Ostreid herpesvirus 1* as representative of the family *Malacoherpesviridae*. Sequences were retrieved from RefSeq and GenBank: CyHV-1 (accession number ACD84552), CyHV-2 (ACD84549), CyHV-3 (NC\_009127), AngHV-1 (NC\_013668), RaHV-1 (NC\_008211), RaHV-2 (NC\_008210), AciHV-1 (ABQ10589), AciHV-2 (ABQ10592), IcHV-1 (NC\_001493), IcHV-2 (ACD84542), SalHV-1 (ACD84543), SalHV-2 (ACD84544), SalHV-3 (ACD84548), human herpesvirus 1 (HHV-1; NC\_001806), human herpesvirus 5 (HHV-5; NC\_006273), and *Ostreid herpesvirus 1* (OsHV-1; NC\_005881). Reliability of the branching is indicated as number of replications at the nodes. The branch lengths indicate phylogenetic distance.



**Figure 2.** Unrooted maximum-likelihood phylogenetic tree depicting the relationship between six alloherpesviruses based upon the deduced amino acid sequences of full length DNA polymerase, DNA helicase, the major capsid protein and capsid triplex protein 2. Sequences were retrieved from RefSeq and GenBank: CyHV-1 (accession numbers AY939868, AY939858, AY939865 and AY939860), CyHV-3 (NC\_009127), IcHV1 (NC\_001493), RaHV-1 (NC\_008211), RaHV-2 (NC\_008210), AngHV-1 Netherlands (NC\_013668) and AngHV-1 Japan (GU233797, GU233798, GU233799 and GU233800). The concatenated alignment of the four conserved genes resulted in a dataset of 4341 residues. Reliability of the branching is indicated at the nodes. Reliability of the branching is indicated as number of replications at the nodes. The branch lengths indicate phylogenetic distance.



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## 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.

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