Taxonomic proposal to the ICTV Executive Committee

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:	***2008.023-27V***	(to be completed by ICTV officers)

Short title: 3 species in new genus Cyprinivirus
(e.g. 6 new species in the genus *Zetavirus*; re-classification of the family *Zetaviridae* etc.)

Modules attached (please check all that apply):	**1** ☐ **2** ☐ **3** ☐ **4** ☒ **5** ☒ **6** ☐ **7** ☐

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

Herpesvirales Study Group; P. Pellett, Chair; ppellett@med.wayne.edu

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

MODULE 4: **NEW GENUS**

(if more than one genus is to be created, please complete additional copies of this section)

Code ***2008.023V*** (assigned by ICTV officers)

To create a new genus assigned as follows:

Subfamily:	
Family:	***Alloherpesviridae***
Order:	***Herpesvirales***

Fill in all that apply. Ideally, a genus should be placed within a higher taxon, but if not put “unassigned” here.

Code ***2008.024V*** (assigned by ICTV officers)

To name the new genus: *Cyprinivirus*

Code ***2008.025V*** (assigned by ICTV officers)

To assign the following as species in the new genus:

You may list several species here. For each species, please state whether it is new or existing.

- If the species is new, please complete Module 5 to create it.
- If the species already exists, please state whether it is unassigned or is to be removed from another genus and, if the latter, complete module 6(a) to ‘REMOVE’ it from that genus.

Cyprinid herpesvirus 1
Cyprinid herpesvirus 2
Cyprinid herpesvirus 3

Code ***2008.026V*** (assigned by ICTV officers)

Note: every genus must have a type species

To designate the following as the type species in the new genus:
Cyprinid herpesvirus 3

Argument to justify the creation of a new genus:

Cyprinid herpesvirus 1 is commonly known as carp pox herpesvirus, cyprinid herpesvirus 2 as haematopoietic necrosis herpesvirus of goldfish, and cyprinid herpesvirus 3 as koi herpesvirus. The viruses are biologically distinct. Cyprinid herpesviruses 1 and 3 infect the carp, and cyprinid herpesvirus 2 the goldfish. Cyprinid herpesvirus 3 has been classified in species *Cyprinid herpesvirus 3*, and the other two viruses are unassigned in the family.

Partial genome sequence data show that the three viruses are distinct from each other and monophyletic. Cyprinid herpesviruses 2 and 3 are more closely related to each other than to cyprinid herpesvirus 1. The three viruses are more distantly related to genus *Ictalurivirus*. Complete genome sequence data show that cyprinid herpesvirus 3 is a distant relative of ictalurid herpesvirus 1 (in the genus *Ictalurivirus*), with only 15 homologous genes in common.

The complete genome sequence of cyprinid herpesvirus 1 has been determined, but has not

Argument to justify the creation of a new genus:

yet been published.

Origin of the new genus name:

Cyprinus, carp

Argument to justify the choice of type species:

Cyprinid herpesvirus 1 was the first to be described, but cyprinid herpesvirus 3 causes the most significant disease.

Species demarcation criteria in the genus:

If there will be more than one species in the new genus, list the criteria being used for species demarcation and explain how the proposed members meet these criteria.

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 HHV-1 and HHV-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.

The three viruses appear to meet these criteria.

References:

Waltzek TB, Kelley GO, Stone DM, Way K, Hanson L, Fukuda H, Hirono I, Aoki T, Davison AJ, Hedrick RP. 2005. Koi herpesvirus represents a third cyprinid herpesvirus (CyHV-3) in the family *Herpesviridae*. J Gen Virol 86:1659-67. Accessions: cyprinid herpesvirus 1, AY939865, AY939868, AY939860, AY939858, AY939866; cyprinid herpesvirus 2, DQ085628, DQ085627, DQ085626, AY939863, AY939861, AY939867; cyprinid herpesvirus 3, see below.

Aoki T, Hirono I, Kurokawa K, Fukuda H, Nahary R, Eldar A, Davison AJ, Waltzek TB, Bercovier H, Hedrick RP. 2007. Genome sequences of three koi herpesvirus isolates representing the expanding distribution of an emerging disease threatening koi and common carp worldwide. J Virol 81:5058-65. Accessions: cyprinid herpesvirus 3, DQ657948, DQ177346, AP008984.

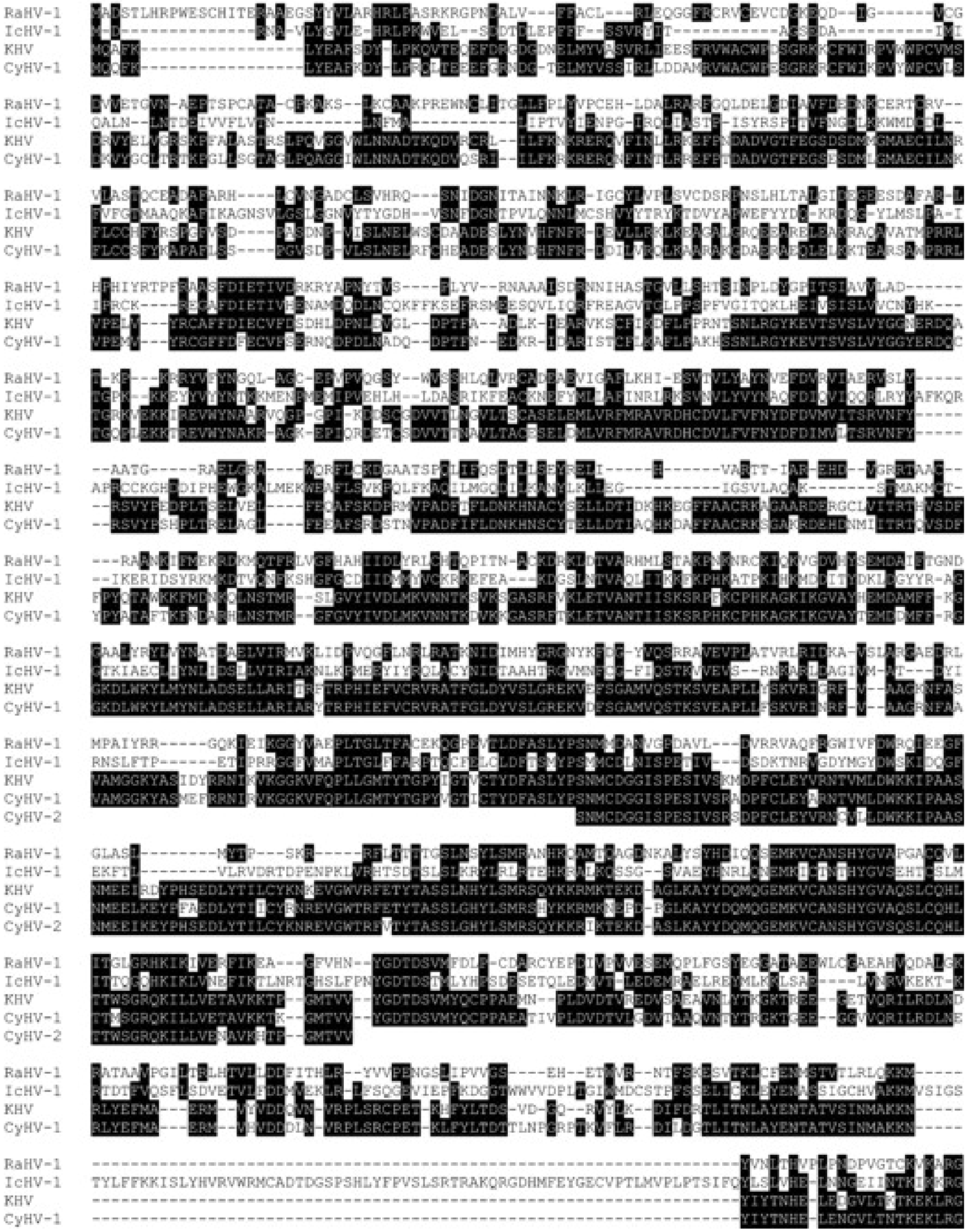
Annexes:

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

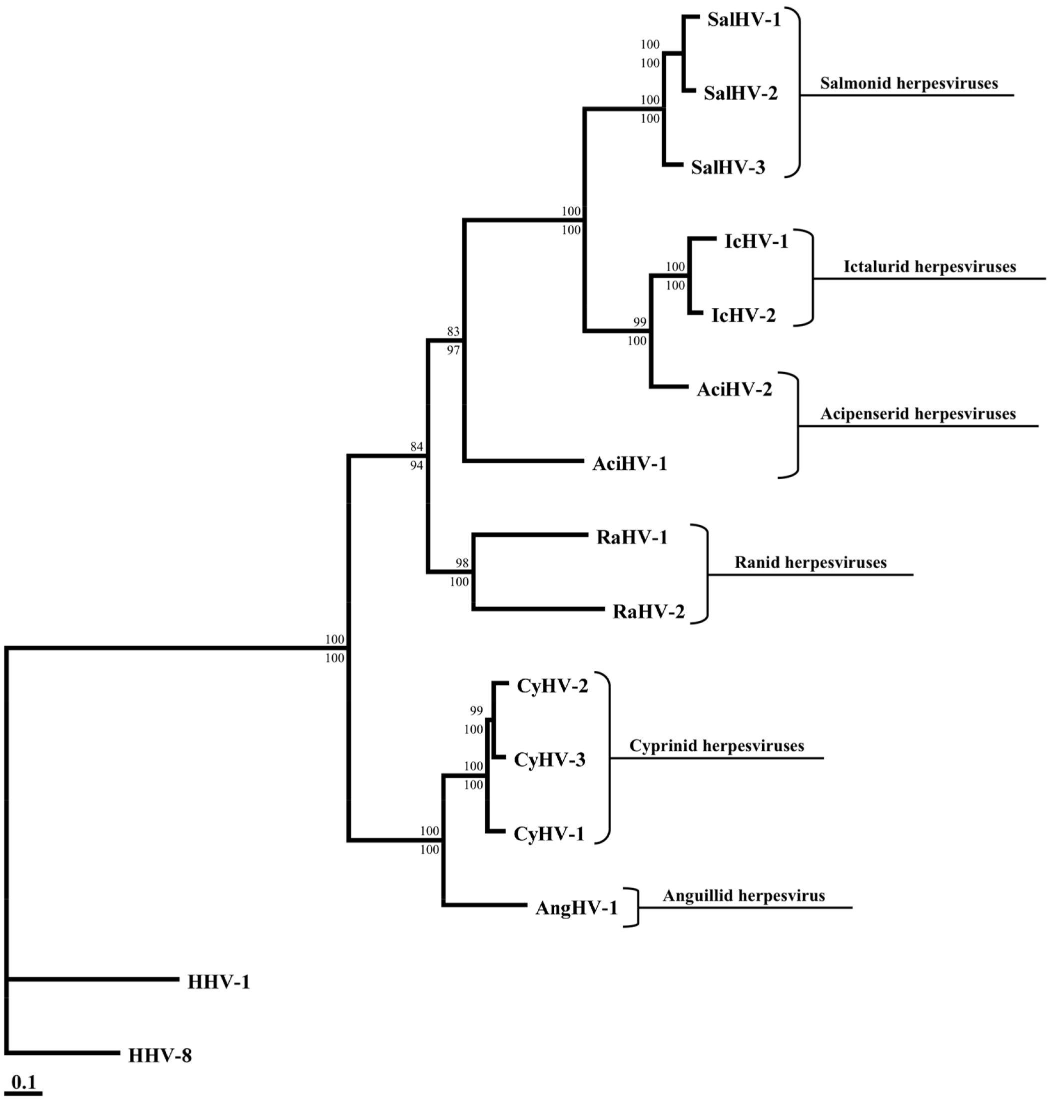
Amino acid sequence alignment for the complete DNA polymerase of ranid herpesvirus 1 (RaHV-1), ictalurid herpesvirus 1(IcHV-1), cyprinid herpesvirus 3 (KHV), cyprinid herpesvirus 1 (CyHV-1) and a partial sequence for cyprinid herpesvirus 2 (CyHV-2). From

Waltzek *et al.* (2005). Additional alignments are provided in this paper.

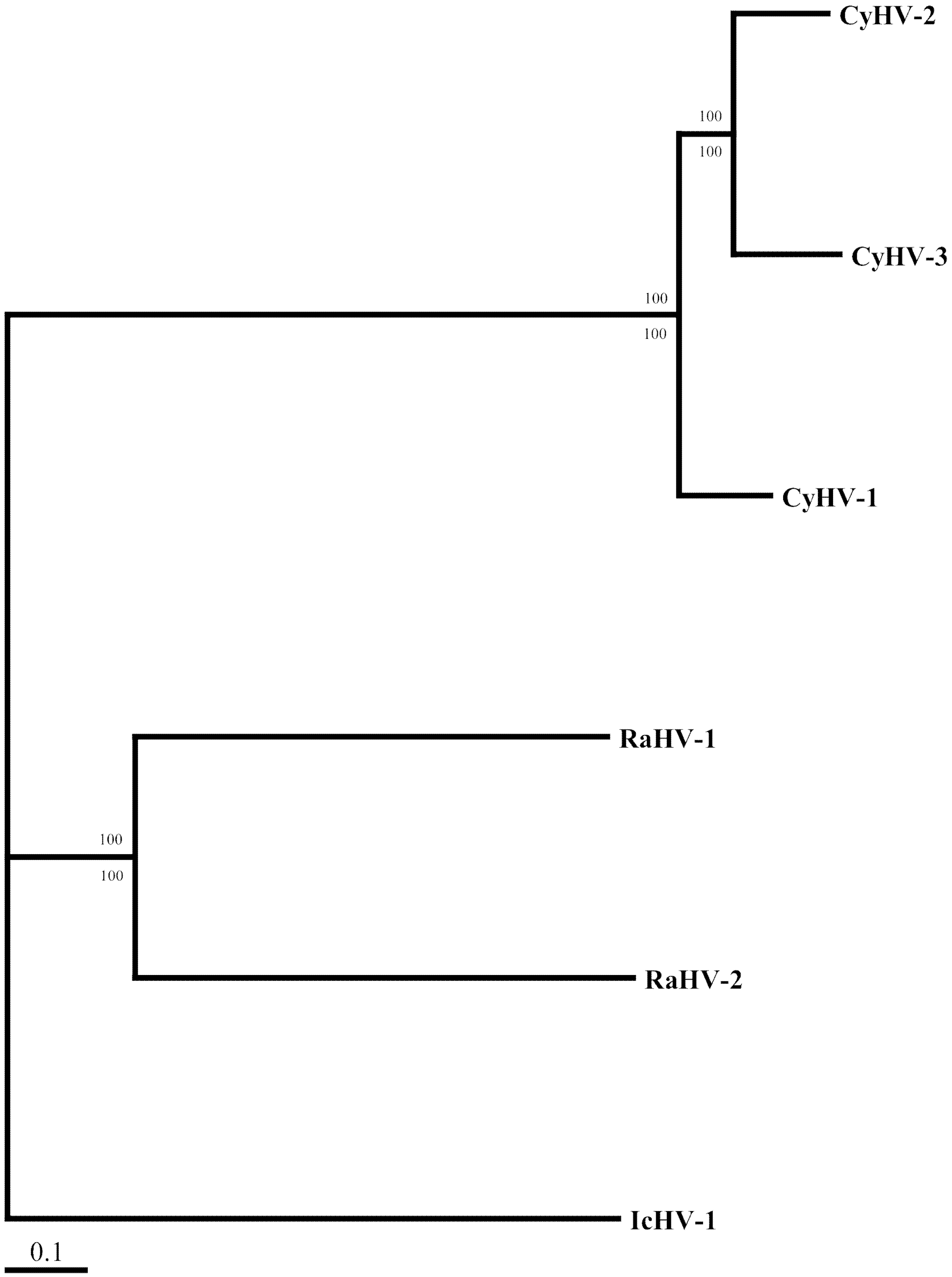
(c) DNA polymerase



Phylogram depicting relationships among fish and amphibian herpesviruses, based on the concatenated partial deduced amino acid sequences of the DNA polymerase and terminase genes. 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 >70 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. TB Waltzek, unpublished.



Phylogram depicting relationships among fish and amphibian herpesviruses, based on the concatenated deduced amino acid sequences of the full length terminase, helicase and triplex protein genes, plus the partial DNA polymerase gene. The tree is not rooted. The first number in each pair represents the quartet puzzling probability (values >70 shown) of the maximum likelihood analysis and the second number represents the posterior probability (values >90 shown) of the Bayesian analysis. The branch lengths are based on the number of inferred substitutions, as indicated by the scale. TB Waltzek, unpublished.


CyHV-2
100
100
CyHV-3
100
100
CyHV-1
RaHV-1
100
100
RaHV-2
IcHV-1
0.1

MODULE 5: **NEW SPECIES**

Code	***2008.027V***	(assigned by ICTV officers)

To create 2 new species assigned as follows:

Genus:	***Cyprinivirus***
Subfamily:	
Family:	***Alloherpesviridae***
Order:	***Herpesvirales***

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)

Name(s) of proposed new species:

Cyprinid herpesvirus 1
Cyprinid herpesvirus 2

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.

See module 4 above.

References:

Annexes:

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