



This form should be used for all taxonomic proposals. Please complete all those modules that are applicable (and then delete the unwanted sections).

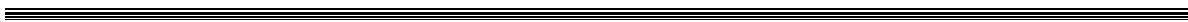
Code(s) assigned:	2008.018- 22V	(to be completed by ICTV officers)			
Short title: 2 species in new genus <i>Batrachovirus</i> (e.g. 6 new species in the genus <i>Zetavirus</i> ; re-classification of the family <i>Zetaviridae</i> etc.)					
Modules attached (please check all that apply):	1 <input type="checkbox"/>	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:

Herpesvirales Study Group; P. Pellett, Chair; ppellett@med.wayne.edu
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ICTV-EC or Study Group comments and response of the proposer:

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MODULE 4: NEW GENUS

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

Code	2008.018V	(assigned by ICTV officers)
To create a new genus assigned as follows:		
Subfamily:		Fill in all that apply. Ideally, a genus should be placed within a higher taxon, but if not put "unassigned" here.
Family:	<i>Alloherpesviridae</i>	
Order:	<i>Herpesvirales</i>	

Code	2008.019V	(assigned by ICTV officers)
To name the new genus: <i>Batrachovirus</i>		

Code	2008.020V	(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.		
<ul style="list-style-type: none"> • 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. 		
<i>Ranid herpesvirus 1</i>		
<i>Ranid herpesvirus 2</i>		

Code	2008.021V	(assigned by ICTV officers)
Note: every genus must have a type species		
To designate the following as the type species in the new genus:		
<i>Ranid herpesvirus 1</i>		

Argument to justify the creation of a new genus:

Ranid herpesvirus 1 is commonly known as Lucké tumor herpesvirus. Ranid herpesvirus 2 is commonly known as frog virus 4 and has no known pathology. Ranid herpesvirus 1 has not been grown in cell culture, whereas ranid herpesvirus 2 has. Both viruses infect the leopard frog, and they are biologically distinct. They are unassigned in the family.

Complete genome sequence data show the two viruses are distinct from each other and are more closely related to each other than to other herpesviruses. Ranid herpesvirus 1 has 132 genes and ranid herpesvirus 2 has 147 genes. They share 40 homologous genes with each other, 19 of which have homologues in ictalurid herpesvirus 1 (in the genus *Ictalurivirus*).

Origin of the new genus name:

Batrachos, frog

Argument to justify the choice of type species:

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Ranid herpesvirus 1 was the first to be described, as the causative agent of the Lucké tumor. It was much worked on in its day. Ranid herpesvirus 2 can be cultured *in vitro*, but causes no known disease. Very little work has been done with it.

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 two viruses appear to meet these criteria.

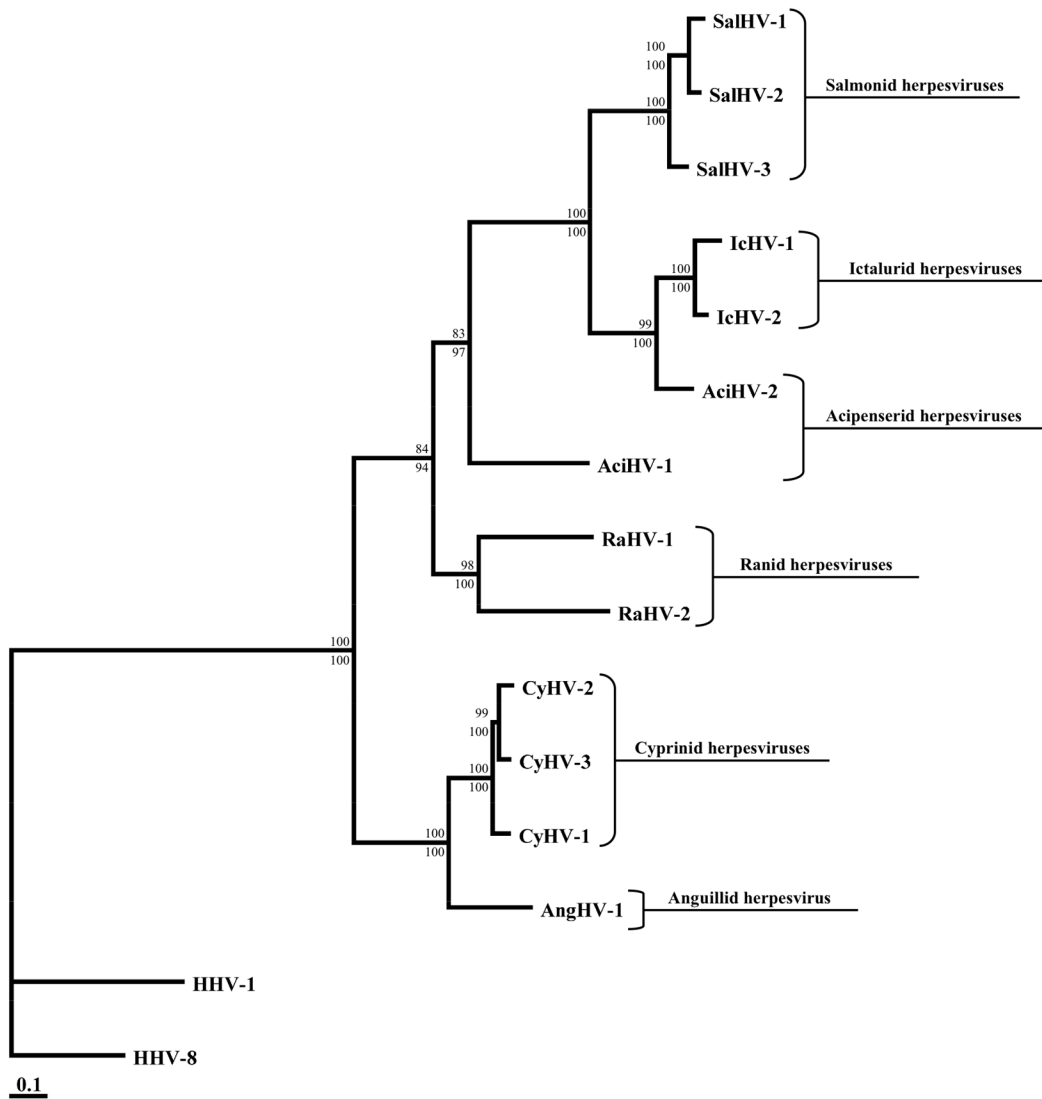
References:

Davison AJ, Cunningham C, Sauerbier W, McKinnell RG. 2006. Genome sequences of two frog herpesviruses. *J Gen Virol* 87:3509-14. Accessions: ranid herpesvirus 1, DQ665917; ranid herpesvirus 2, DQ665652.

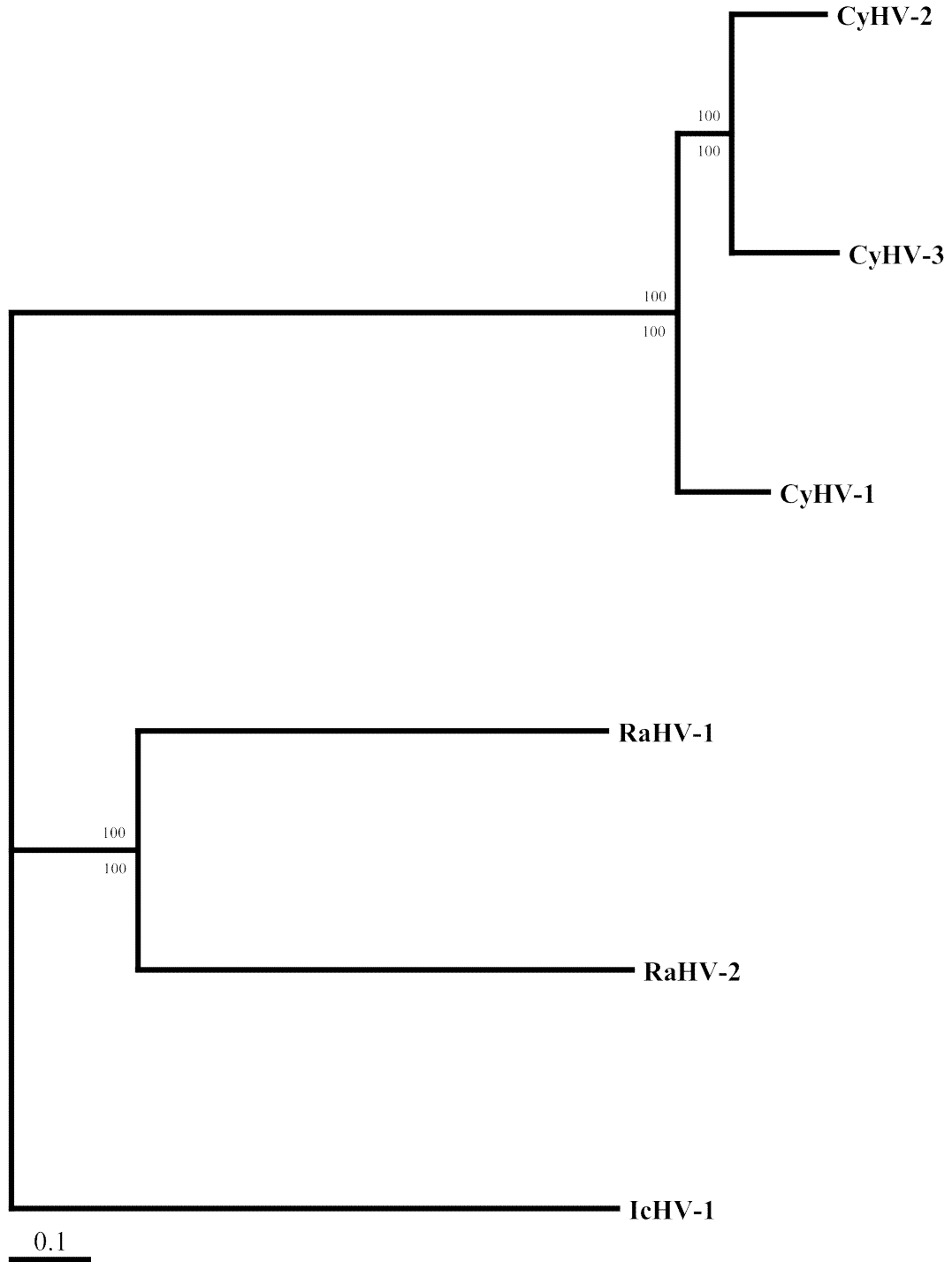
Annexes:

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

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.



MODULE 5: **NEW SPECIES**

Code	2008.022V	(assigned by ICTV officers)
To create 2 new species assigned as follows:		
Genus:	<i>Batrachovirus</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>Alloherpesviridae</i>	
Order:	<i>Herpesvirales</i>	

Name(s) of proposed new species:

<i>Ranid herpesvirus 1</i> <i>Ranid herpesvirus 2</i>
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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:

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Annexes:

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

