



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**

Code assigned:	2011.022a-dV	(to be completed by ICTV officers)			
Short title: create genus <i>Aurivirus</i> in the family <i>Malacoherpesviridae</i> , order <i>Herpesvirales</i> (e.g. 6 new species in the genus <i>Zetavirus</i>)					
Modules attached (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 checked="" 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:

Keith Savin (Keith.Savin@dpi.vic.gov.au) and Andrew Davison (andrew.davison@glasgow.ac.uk)

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)

This proposal was considered and then approved by the Herpesvirales Study Group.

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

Date first submitted to ICTV:

June 21, 2011

Date of this revision (if different to above):

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. Wherever possible, provide sequence accession number(s) for one isolate of each new species proposed.

Code	2011.022aV	(assigned by ICTV officers)
To create 1 new species within:		
Genus:	<i>Aurivirus</i> (new)	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:	Unassigned	
Family:	<i>Malacoherpesviridae</i>	
Order:	<i>Herpesvirales</i>	
And name the new species:		GenBank sequence accession number(s) of reference isolate:
<i>Haliotid herpesvirus 1</i>		HM631981.1, HM631982.2

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.
- Further material in support of this proposal may be presented in the Appendix, Module 9

The single paper relevant to this proposal is Savin *et al.* (2010).

An agent that is morphologically a herpesvirus has been associated in Australia and Taiwan with outbreaks of acute ganglioneuritis – some devastatingly lethal – in various species of an edible gastropod mollusc, the abalone. A total of 39 full-length gene coding regions have been sequenced, and these have closest relatives in ostreid herpesvirus 1, which infects bivalves. A phylogenetic tree derived from an alignment of the concatenated DNA polymerase and terminase amino acid sequences indicates that the abalone herpesvirus groups with ostreid herpesvirus 1 in the family *Malacoherpesviridae*, separated by a distance that is similar to those that separate genera in the order *Herpesvirales*.

A herpesvirus may be classified as a species if it has distinct epidemiological or biological characteristics and a distinct genome that represents an independent replicating lineage. The abalone herpesvirus fulfils these criteria. Herpesvirus species are named after a taxon of the host from which they are isolated, usually the family, which for abalones is the family Haliotidae. Therefore, we propose classifying the abalone herpesvirus as the species *Haliotid herpesvirus 1*. Precise demarcation criteria for establishing herpesvirus genera do not exist, but it seems reasonable, on the basis of genetic divergence, to establish the new genus *Aurivirus* to contain this species. The family *Malacoherpesviridae* currently contains a single species (*Ostreid herpesvirus 1*) in a single genus (*Ostreavirus*). Should this proposal be adopted, it would then contain two species, each in its own genus.

MODULE 3: **NEW GENUS**

creating a new genus

Ideally, a genus should be placed within a higher taxon.

Code	2011.022bV	(assigned by ICTV officers)
To create a new genus within:		
Subfamily:	Unassigned	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 family is specified, enter “ unassigned ” in the family box
Family:	Malacoherpesviridae	
Order:	Herpesvirales	

naming a new genus

Code	2011.022cV	(assigned by ICTV officers)
To name the new genus: <i>Aurivirus</i>		

Assigning the type species and other species to a new genus

Code	2011.022dV	(assigned by ICTV officers)
To designate the following as the type species of the new genus		
<i>Haliotid herpesvirus 1</i>		Every genus must have a type species. This should be a well characterized species although not necessarily the first to be discovered
The new genus will also contain any other new species created and assigned to it (Module 2) and any that are being moved from elsewhere (Module 7b). Please enter here the TOTAL number of species (including the type species) that the genus will contain:		
1		

Reasons to justify the creation of a new genus:

Additional material in support of this proposal may be presented in the Appendix, Module 9

See Modules 2 and 9

Origin of the new genus name:

From the Latin word for “ear” (auris) and secondarily from the Latin word for “gold” (aurum), to reflect a common name for abalones (ear-shell) and the shiny, iridescent layer of nacre on the inside of the shell

Reasons to justify the choice of type species:

First member of species

Species demarcation criteria in the new 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.

Not applicable

MODULE 9: **APPENDIX**: supporting material

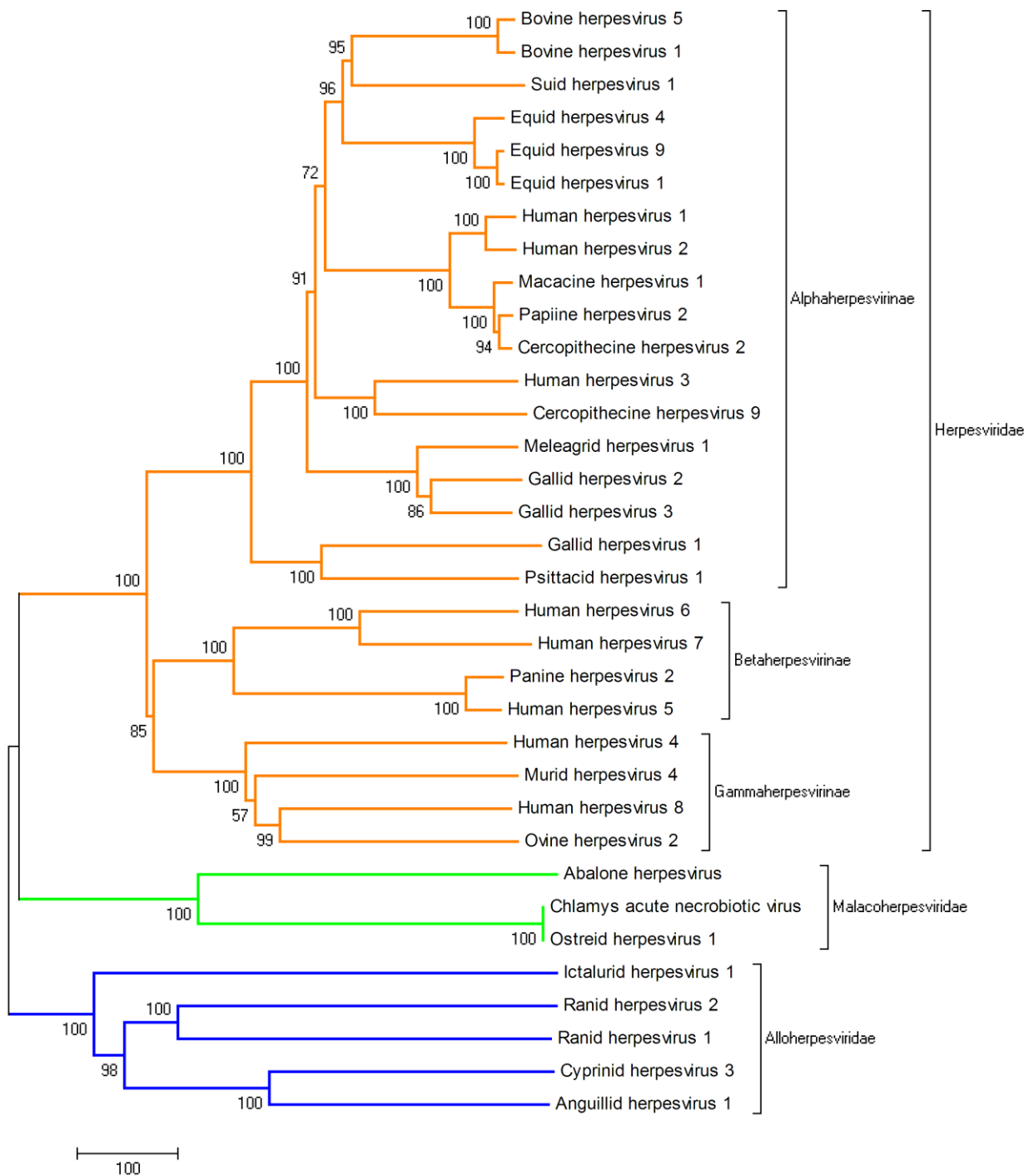
additional material in support of this proposal

References:

Savin KW, Cocks BG, Wong F, Sawbridge T, Cogan N, Savage D, Warner S (2010). A neurotropic herpesvirus infecting the gastropod, abalone, shares ancestry with oyster herpesvirus and a herpesvirus associated with the amphioxus genome. *Virology* 7:308.

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.



Dendrogram of herpesvirus protein sequences.

Dendrogram illustrating the evolutionary relationship of abalone, scallop (*Chlamys*) and oyster herpesviruses to 32 other herpesviruses based on the concatenated full length protein sequences of DNA polymerase and the ATPase subunit of the terminase for each virus. The tree was inferred with MEGA4 using the Minimum Evolution (ME) method and a model based on the number of amino acid differences detected after an alignment using ClustalW. The percentage of replicate trees in which the associated taxa clustered together in the bootstrap test (5000 replicates) are shown next to the branches. The scale bar for the branch lengths = 100 amino acid sequence differences.