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:	***2010.016a-eV***	(to be completed by ICTV officers)

Short title: Create genus Scutavirus (type species: the currently unassigned species Chelonid herpesvirus 5) in subfamily Alphaherpesvirinae, family Herpesviridae
(e.g. 6 new species in the genus *Zetavirus*)

Modules attached (modules 1 and 9 are required)	**1** ☒	**2** ☐	**3** ☒	**4** ☐	**5** ☐
	6 ☐	**7** ☒	**8** ☐	**9** ☒	

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

Andrew Davison (a.davison@mrcvu.gla.ac.uk) & Duncan McGeoch

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 7 added July 4, 2010

MODULE 3: **NEW GENUS**

creating a new genus

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

Code	***2010.016aV***	(assigned by ICTV officers)

To create a new genus within:

Subfamily:	***Alphaherpesvirinae***
Family:	***Herpesviridae***
Order:	***Herpesvirales***

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

naming a new genus

Code	***2010.016bV***	(assigned by ICTV officers)

To name the new genus: *Scutavirus*

Assigning the type species and other species to a new genus

Code	***2010.016cV***	(assigned by ICTV officers)

To designate the following as the type species of the new genus

Chelonid herpesvirus 5	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

ICTV recognizes two turtle herpesvirus species, *Chelonid herpesvirus 5* and *Chelonid herpesvirus 6*. Both are classified into the subfamily *Alphaherpesvirinae*, but neither has been assigned to a genus. Viruses that belong to the species *Chelonid herpesvirus 5* are variously named Caretta caretta herpesvirus, Chelonia mydas herpesvirus, chelonid fibropapilloma-associated herpesvirus, fibropapilloma-associated turtle herpesvirus, fibropapillomatosis associated Chelonia mydas herpesvirus, green turtle herpesvirus (usually prefixed "Florida" or "Hawaiian"), Olive ridley turtle herpesvirus, loggerhead turtle herpesvirus and further alternatives. These viruses are denoted below as chelonid herpesvirus 5 (ChHV5). Viruses that belong to the species *Chelonid herpesvirus 6* are named lung-eye-trachea disease-associated herpesvirus.

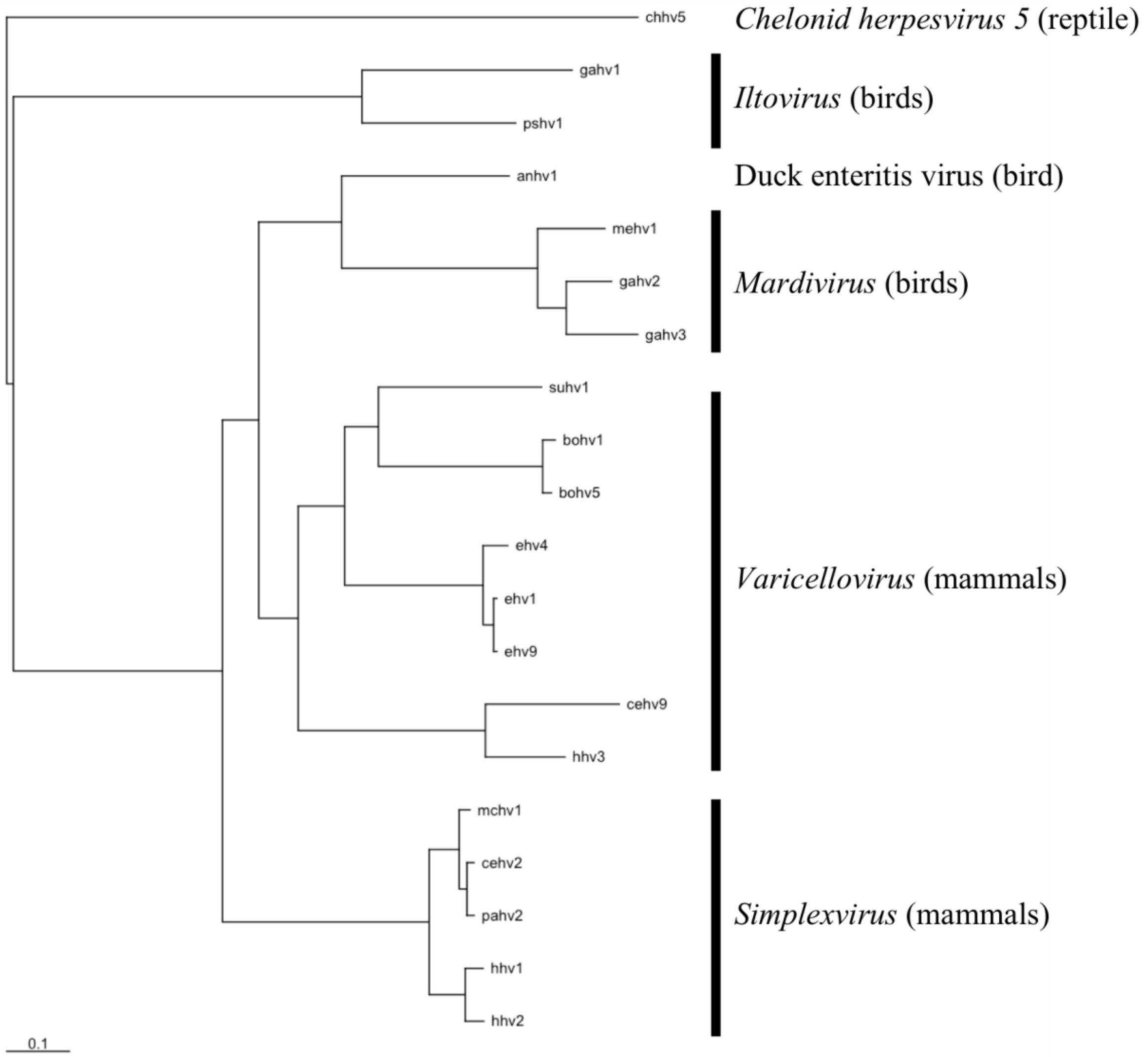
This proposal concerns the creation of a new genus to accommodate the species *Chelonid herpesvirus 5* as a result of recently published sequence data. Too few data are available to permit the assignment of *Chelonid herpesvirus 6* to a genus. The reason why species *Chelonid herpesvirus 1*, *Chelonid herpesvirus 2*, *Chelonid herpesvirus 3* and *Chelonid herpesvirus 4* have not been created is that viruses were given these names (as viruses not species) decades ago, in the absence of sequence data, and their relationship to sequenced members of species *Chelonid herpesvirus 5* and *Chelonid herpesvirus 6* are uncertain.

Using sequences representing the entire UL30 (DNA polymerase) and UL27 (glycoprotein B) genes and parts of genes UL28 and UL31, McGeoch & Gatherer (2005) showed that ChHV5 belongs phylogenetically to the subfamily *Alphaherpesvirinae* as a lineage separate from the four existing genera. More extensive sequence data are now available for strains of ChHV5, namely fibropapilloma-associated turtle herpesvirus (AY644454; 43843 bp) containing genes UL9 to UL30 and Hawaiian green turtle herpesvirus (AF035003; 23055 bp) containing genes UL23 to UL36.

To extend the phylogenetic analysis, we made amino acid sequence alignments for six large, well conserved genes from ChHV5 and 19 members or proposed members of the subfamily *Alphaherpesvirinae*. The genes were those encoding the single-stranded DNA-binding protein, glycoprotein B, the major capsid protein, DNA polymerase and two subunits of the DNA packaging terminase (genes UL29, UL27, UL19, UL30, UL15 and UL28, respectively). The alignments were trimmed, degapped and concatenated, yielding a final length of 5104 residues. From previous experience, this is a substantial length of alignment, appropriate to deriving a robust phylogenetic tree.

An initial neighbour-joining (NJ) tree (not shown) yielded the standard branching pattern for the subfamily *Alphaherpesvirinae* (McGeoch *et al.*, 2000) with the exception that the branching order of the genera *Simplexvirus* and *Mardivirus* was reversed. This exception affects neither the current classification nor this proposal. In the tree, ChHV5 formed an outgroup separate from the clades representing the existing genera. Bootstrap values (100 replicates) supported all nodes maximally except that defining the branching order of genera *Simplexvirus* and *Mardivirus*. A compute-intensive Bayesian Monte Carlo Markov chain (program MrBayes) was then conducted for one million generations, sampling every 100 and imposing a burn-in value of 5001. The topology of this tree (Figure 1) was the same as that of the NJ tree, with all nodes exhibiting maximal posterior probability and ChHV5 falling as the outgroup. We recommend that the species *Chelonid herpesvirus 5* should be classified in a new genus, *Scutavirus*. This genus would join genera *Iltovirus*, *Mardivirus*, *Varicellovirus* and *Simplexvirus* in the subfamily *Alphaherpesvirinae*.

Figure 1. Midpoint-rooted Bayesian phylogenetic tree of ChHV5 and 19 members or proposed members of the subfamily *Alphaherpesvirinae*. The prefixes for herpesvirus names are: ch, chelonid; ga, gallid; ps, psittacid; an, anatid; me, meleagrid; su, suid; bo, bovine; e, equid; ce, cercopithecine; h, human; mc, macacine; pa, papiine. The virus, genus or species names are shown, and the host groups that the viruses infect are indicated in parentheses.



Origin of the new genus name:

A scute or scutum (Latin *scutum*, “shield”) is a bony external plate or scale, as on the shell of a turtle, the skin of crocodilians, or the feet of some birds.

Reasons to justify the choice of type species:

First species to be classified into this genus.

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.

MODULE 7: **REMOVE and MOVE**

Use this module whenever an existing taxon needs to be removed:

- *Either* to abolish a taxon entirely (when only part (a) needs to be completed)
- *Or* to move a taxon and re-assign it e.g. when a species is moved from one genus to another (when BOTH parts (a) and (b) should be completed)

Part (a) taxon/taxa to be removed or moved

Code	***2010.016dV***	(assigned by ICTV officers)

To remove the following taxon (or taxa) from their present position:

Chelonid herpesvirus 5

The present taxonomic position of these taxon/taxa:

Genus:	***Unassigned***	Fill in all that apply.
Subfamily:	***Alphaherpesvirinae***	
Family:	***Herpesviridae***	
Order:	***Herpesvirales***	

If the taxon/taxa are to be abolished (i.e. not reassigned to another taxon) write “yes” in the box on the right	

Reasons to justify the removal:

Explain why the taxon (or taxa) should be removed

To permit reassignment to the new genus.

Part (b) re-assign to a higher taxon

Code	***2010.016eV***	(assigned by ICTV officers)

To re-assign the taxon (or taxa) listed in Part (a) as follows:

Genus:	***Scutavirus***	Fill in all that apply. • If the higher taxon has yet to be created write “**(new)**” after its proposed name and complete relevant module to create it. If no genus is specified, enter “**unassigned**” in the genus box.
Subfamily:	***Alphaherpesviridae***	
Family:	***Herpesviridae***	
Order:	***Herpesvirales***	

Reasons to justify the re-assignment:

- If it is proposed to re-assign species to an existing genus, please 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

See Module 3.

MODULE 9: **APPENDIX**: supporting material

additional material in support of this proposal

References:

McGeoch, D. J., Dolan, A. & Ralph, A. C. (2000). Toward a comprehensive phylogeny for mammalian and avian herpesviruses. J. Virol. 74, 10401-10406.

McGeoch, D. J. & Gatherer, D. (2005). Integrating reptilian herpesviruses into the family Herpesviridae. J. Virol. 79, 725-731.

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.