



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:	2012.006aV	(to be completed by ICTV officers)
Short title: Create 4 new species in genus <i>Cytomegalovirus</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 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

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

The original proposal recommended the creation of species *Saimiriine herpesvirus 3*. However, the Study Group pointed out that a different virus had already been given this name. No corresponding species had been created, but the existence of publications using the name and a 171 bp sequence in GenBank might cause confusion. The proposers opted to modify the proposed species name to *Saimiriine herpesvirus 4*, and to accept that the species name *Saimiriine herpesvirus 3* would remain undesignated for the foreseeable future.

Date first submitted to ICTV:

18 June 2012

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	2012.006aV	(assigned by ICTV officers)
To create 4 new species within:		
Genus:	<i>Cytomegalovirus</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:	<i>Betaherpesvirinae</i>	
Family:	<i>Herpesviridae</i>	
Order:	<i>Herpesvirales</i>	
And name the new species:		GenBank sequence accession number(s) of reference isolate:
<i>Papiine herpesvirus 3</i>		AC090446
<i>Aotine herpesvirus 1</i>		FJ483967
<i>Saimiriine herpesvirus 4</i>		FJ483970
<i>Cebine herpesvirus 1</i>		JQ264772

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 genus *Cytomegalovirus* consists of primate herpesviruses that are classified in the species *Cercopithecine herpesvirus 5* (green monkey viruses), *Human herpesvirus 5* (human viruses), *Macacine herpesvirus 3* (macaque viruses) and *Panine herpesvirus 2* (chimpanzee viruses). Sequence data are available on four viruses from additional primate species (three from the New World and one from the Old World) that evidently belong to this genus.

- Owl monkey cytomegalovirus strain S 34E (ATCC VR-606). This virus was originally dubbed *Herpesvirus aotus* type 1 (Daniel *et al.*, 1973), and listed in ICTV Reports as tentative species (now unassigned virus) aotine herpesvirus 1 in the genus *Cytomegalovirus*. The complete genome sequence is in GenBank. The proposal is to classify this virus in the new species *Aotine herpesvirus 1*.
- Squirrel monkey cytomegalovirus strain SqSHV (ATCC VR-1398). The complete genome sequence is in GenBank. The proposal is to classify this virus in the new species *Saimiriine herpesvirus 4*.
- Baboon cytomegalovirus strain OCOM4-37. A major proportion of the genome sequence is in GenBank. The proposal is to classify this virus in the new species *Papiine herpesvirus 3*.
- Capuchin monkey cytomegalovirus strain 5567. The complete DNA polymerase gene sequence is in GenBank. The proposal is to classify this virus in the new species *Cebine herpesvirus 1*.

A supporting phylogenetic tree based on the DNA polymerase gene (UL54) is presented in Fig.

1. Proposals 1-3 also find strong support in the phylogenetic analysis of genes UL55 and UL56 by Leendertz *et al.* (2009); data relevant to proposal 4 were not available for that study.

We make three further recommendations regarding primate cytomegaloviruses that, although not in the ICTV's purview, would represent useful clarifications in the field.

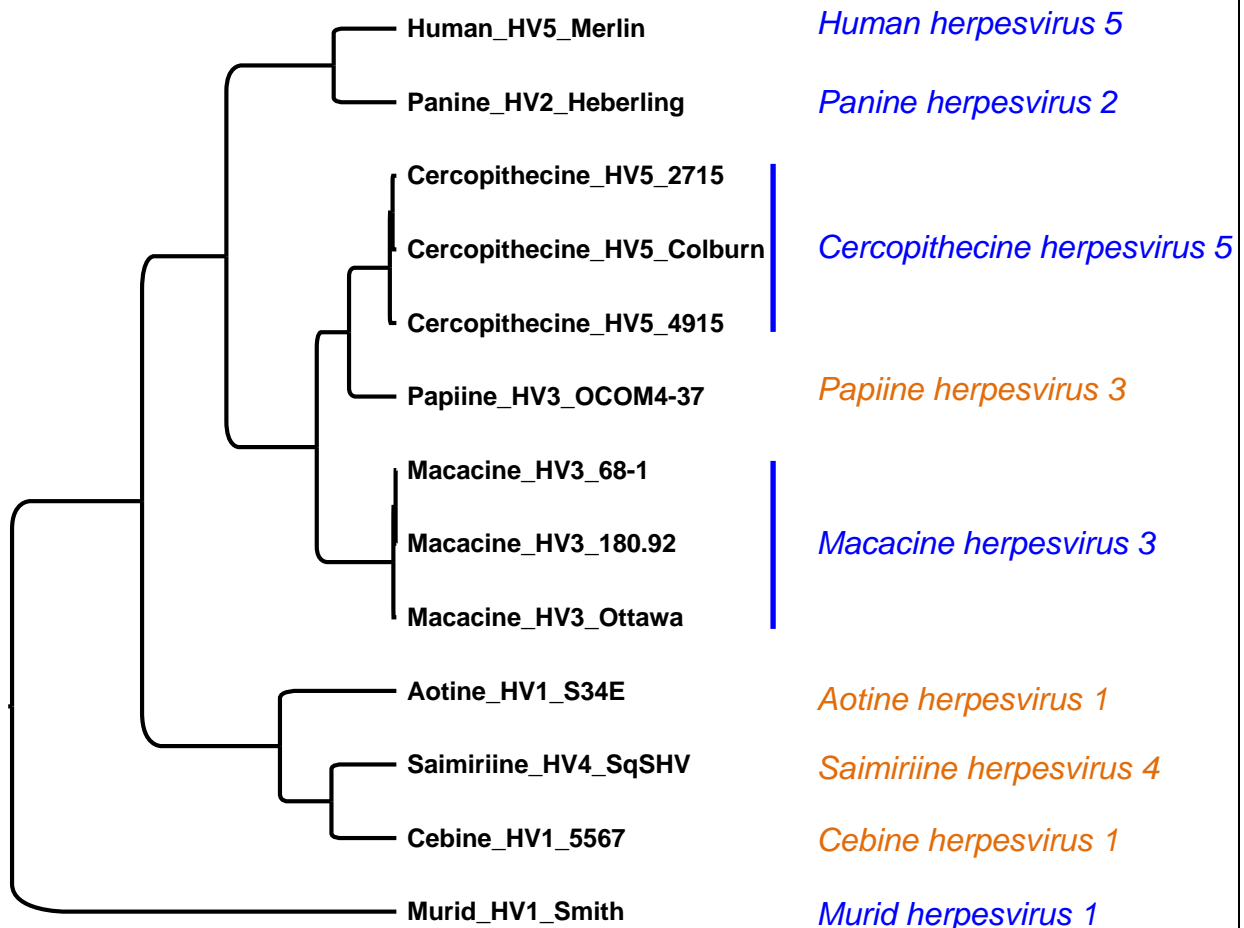
1. Cynomolgous macaque cytomegalovirus strain Ottawa is listed as a separate species by GenBank. The complete genome sequence is in GenBank (Marsh *et al.*, 2011; JN227533). However, this virus is very closely related throughout its genome to rhesus macaque cytomegalovirus (macacine herpesvirus 3), as is illustrated for gene UL54 by the phylogeny in Fig. 1. Indeed, the two viruses are far more closely related than would be expected if they had coevolved with their hosts, which diverged 2.4 million years ago. We recommend that cynomolgous macaque cytomegalovirus strain Ottawa be included in species *Macacine herpesvirus 3*, and GenBank so informed. It is possible that circulation of rhesus cytomegaloviruses and cynomolgous macaque cytomegalovirus strain Ottawa is confined to the eponymous host species, but there is no convincing evidence for this.
2. Like aotine herpesvirus 1, aotine herpesvirus 3 (*Herpesvirus aotus* type 3) was also listed in ICTV reports as a tentative species in the genus *Cytomegalovirus*. We support the recommendation made by Ebeling *et al.* (1983) from studies of the electrophoretic properties of genome restriction fragments and virion proteins, and from DNA hybridization experiments, that this virus (for which no sequence data are available) be included in the new species *Aotine herpesvirus 1*.
3. Cercopithecine herpesvirus 3 strain SA6 was listed as an unassigned virus in the family. It is clear from the phylogenetic analysis in Alcendor *et al.* (2009) that this virus belongs in the species *Cercopithecine herpesvirus 5*, and we recommend that it be so included.

The 9th Report of the ICTV states that 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. An additional explanatory note indicates that sequence information is required for formal recognition of new herpesvirus species. Replicating lineages of herpesviruses are now identified primarily on the basis of information derived from genomic sequences. Sequence information sufficient to demonstrate that a novel virus represents a replicating lineage distinct from known herpesvirus species is taken as evidence that the virus in question exists in nature, occupies a distinct ecological niche and thus can be recognized as a herpesvirus species. For some well-studied genes, there are levels of sequence difference beyond which there are no instances in which the viruses in question do not have distinct epidemiological and biological properties; such viruses can be reliably recognized as species on the basis of limited sequence information. There are also closely related viruses that have relatively small differences in the sequences of individual genes, but genetic differences extend across the respective genomes in a manner indicative of them representing independent replicating lineages. These viruses also have distinct epidemiological and biological characteristics (e.g. host identity, pathogenic and epidemiological properties, and the lack of occurrence of natural recombinants) and thus meet the definition of herpesvirus species. In the context of species established previously in the genus *Cytomegalovirus* (e.g. in regard to phylogenetic distance and biological properties), the present proposals adhere to the species demarcation criteria.

The 9th Report of the ICTV also states that herpesvirus species name consists of three parts. (i) A term derived from a taxon of the host that in its natural setting harbors the virus. The default taxon employed is that of family, and, except for the species of humans, it ends in '-id'. Exceptions are species from the family Bovidae, which are designated by host subfamily or

genus, and nonhuman primates (host genus); these names end in ‘-ine’. (ii) The word “herpesvirus”. (iii) An Arabic numeral, which, in combination with (i), provides a unique name. The proposed species names fulfil this requirement, with the numerals chosen to succeed those already utilized for established species. We note that Lewis *et al.* (1976) described the isolation of two capuchin monkey cytomegaloviruses, which were named subsequently in ICTV reports as unassigned viruses cebine herpesviruses 1 and 2 in the family *Herpesviridae* (i.e. they have not been classified formally). Nonetheless, we recommend that the new species containing capuchin monkey cytomegalovirus strain 5567 be named *Cebine herpesvirus 1* rather than *Cebine herpesvirus 3*. This is because all of the viruses concerned were isolated from capuchin monkeys and have been characterized as cytomegaloviruses, and no additional data (including sequence information) is available, or likely to be available, on the two earlier viruses. The proposed species name for squirrel monkey cytomegalovirus strain SqSHV is *Saimiriine herpesvirus 4* rather than *Saimiriine herpesvirus 3* because, although the latter does not exist, a lymphocryptovirus has been named saimiriine herpesvirus 3 (Cho *et al.*, 2001) and a short sequence has been deposited in GenBank (AF229063).

Fig. 1. Bayesian phylogenetic tree for cytomegaloviruses, determined from the complete DNA sequences of the DNA polymerase gene. Posterior probability values were all 1, except for that at the node leading to Cercopithecine_HV5_2715 and Cercopithecine_HV5_Colburn, which was 0.97. The tree was rooted by using Murid_HV1_Smith (a rodent virus; genus *Muromegalovirus*) as the outgroup. Established species names are in blue, and proposed species names in orange. Abbreviation: HV, herpesvirus, followed by the appropriate number and strain designation.



MODULE 9: **APPENDIX**: supporting material

additional material in support of this proposal

References:

- Alcendor DJ, Zong J, Dolan A, Gatherer D, Davison AJ, Hayward GS (2009) Patterns of divergence in the vCXCL and vGPCR gene clusters in primate cytomegalovirus genomes. *Virology* 395:21-32.
- Cho Y, Ramer J, Rivaller P, Quink C, Garber RL, Beier DR, Wang F (2001) An Epstein-Barr-related herpesvirus from marmoset lymphomas. *Proc Natl Acad Sci USA* 98:1224-9.
- Daniel MD, Melendez LV, King NW, Barahona HH, Fraser CE, Garcia FG, Silva D (1973) Isolation and characterization of a new virus from owl monkeys: *Herpesvirus aotus* type 3. *Am J Phys Anthropol* 38:497-500.
- Ebeling A, Keil G, Nowak B, Fleckenstein B, Berthelot N, Sheldrick P (1983) Genome structure and virion polypeptides of the primate herpesviruses *Herpesvirus aotus* types 1 and 3: comparison with human cytomegalovirus. *J Virol* 45:715-26.
- Leendertz FH, Deckers M, Schempp W, Lankester F, Boesch C, Mugisha L, Dolan A, Gatherer D, McGeoch DJ, Ehlers B (2009) Novel cytomegaloviruses in free-ranging and captive great apes: phylogenetic evidence for bidirectional horizontal transmission. *J Gen Virol* 90:2386-94.
- Lewis MA, Frye LD, Gibbs CJ Jr, Chou SM, Cutchins EC, Gajdusek DC, Ward G (1976) Isolation and characterization of two new herpes-like viruses from capuchin monkeys. *Infect Immun* 14:759-66.
- Marsh AK, Willer DO, Ambagala AP, Dzamba M, Chan JK, Pilon R, Fournier J, Sandstrom P, Brudno M, Macdonald KS (2011) Genomic sequencing and characterization of cynomolgus macaque cytomegalovirus. *J Virol* 85:12995-3009.

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.
