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:	***2015.006aD***	(to be completed by ICTV officers)

Short title: One new species in genus *Simplexvirus*, subfamily *Alphaherpesvirinae*, family *Herpesviridae*
(e.g. 6 new species in the genus *Zetavirus*)

Modules attached (modules 1 and 10 are required)	**1** ☒	**2** ☒	**3** ☐	**4** ☐	**5** ☐
	6 ☐	**7** ☐	**8** ☐	**9** ☐	**10** ☒

Author(s):

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Corresponding author with e-mail address:

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)	*Herpesvirales*

ICTV Study Group comments (if any) and response of the proposer:

This proposal was discussed by the Herpesvirales study group and received unanimous support

Date first submitted to ICTV:	June 10, 2015
Date of this revision (if different to above):	January 27, 2016

ICTV-EC comments and response of the proposer:

Decision: Ac. Provide species name consistent with 2015.010aD.

Response: Done.

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	***2015.006aD***	(assigned by ICTV officers)

To create 1 new species within:

Genus:	***Simplexvirus***
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 genus is specified, enter "**unassigned**" in the genus box.

Name of new species:	**Representative isolate:**	**GenBank sequence accession number(s)**
Panine alphaherpesvirus 3	Chimpanzee herpesvirus strain 105640	JQ360576

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 10

Chimpanzee herpesvirus (ChHV) strain 105640 was isolated from a tongue lesion biopsy from a female chimpanzee (Luebcke *et al.*, 2006). This animal was one of five individuals sharing housing that developed oral and pharyngeal ulcers at around the same time. The virus exhibited growth properties in Vero cell culture that were similar to those of the human virus herpes simplex virus type 1 (HSV-1). Serological testing indicated that ChHV is similar to, but distinct from, the human virus herpes simplex virus type 2 (HSV-2). DNA sequence analysis of several regions across the genome implicated HSV-2 as the closest relative of ChHV, and phylogenetic analyses (see Fig. 1 in Module 9) supported this conclusion.

Determination of the complete genome sequence of ChHV subsequently confirmed the close relationship to, but distinctiveness from, HSV-2, and showed that the average level of amino acid sequence identity is 91% (Severini *et al.*, 2013). These authors concluded that the serological and genetic data indicate that ChHV is not an HSV-2 variant but a genuine chimpanzee virus related to HSV-2. As a result, these authors proposed that ChHV be considered for formal designation as the founding member of a new species, *Panine herpesvirus 3*, named in line with the accepted nomenclature of members of the order *Herpesvirales*.

The statement in the 9th ICTV Report on species demarcation criteria within the order *Herpesvirales* is as follows.

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. 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.

The proposed classification of ChHV into a new species fits these criteria, in that the virus has distinct genetic, biological and evolutionary properties, for example in terms of sequence divergence across the entire genome, phylogenic relationships, host association and perceived co-evolution with the host. It should be noted that a maximal value for sequence identity has not been adopted as a criterion for the classification of herpesvirus species. However, the raw level of nucleotide sequence identity between the ChHV and HSV2 genomes (89.1%) is somewhat greater than that (85.4%) between members of the most closely related established species, *Cercopithecine herpesvirus 2* and *Papiine herpesvirus 2*.

Addendum: A proposal to incorporate the subfamily designation into herpesvirus species names is being considered in parallel by the ICTV. In line with this, the name of the species to which ChHV is assigned above is *Panine alphaherpesvirus 3* rather than *Panine herpesvirus 3*.

MODULE 10: **APPENDIX**: supporting material

additional material in support of this proposal

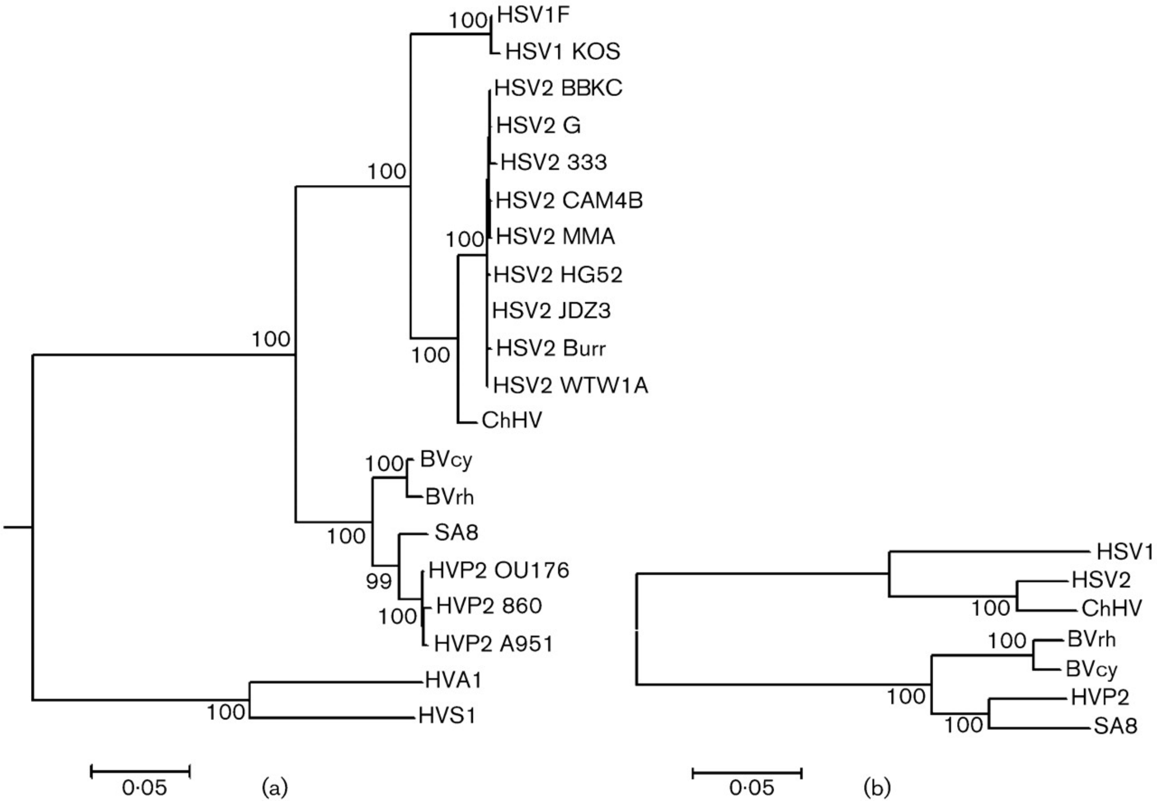
References:

Luebcke E, Dubovi E, Black D, Ohsawa K, Eberle R. 2006. Isolation and characterization of a chimpanzee alphaherpesvirus. J Gen Virol 87:11-9.

Severini A, Tyler SD, Peters GA, Black D, Eberle R. 2013. Genome sequence of a chimpanzee herpesvirus and its relation to other primate alphaherpesviruses. Arch Virol 158:1825-8.

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.



Luebcke E et al. J Gen Virol 2006;87:11-19

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Fig. 1. Phylogenetic relationships of the primate alphaherpesviruses. Predicted amino acid sequences were aligned, and all positions in the alignment having a gap character were excluded from the analysis.

Pairwise distances were calculated and trees were constructed by neighbour-joining using the Mega 3.1 program package. Bootstrap confidence levels are shown for major interior branches. The trees shown were generated by using (a) UL27 (glycoprotein B, gB) sequences or (b) concatenated sequences derived from 12 different genes (UL13, UL14, UL23, UL24, UL27, UL28, UL44, UL47–UL49, US6 and US7). The gB-based tree was rooted by using the bovine herpesvirus 1 gB sequence as an outgroup (bovine herpesvirus 1 not shown); the tree shown in (b) is an unrooted tree. HSV1 (*Human herpesvirus 1*); HSV2 (*Human herpesvirus 2*); ChHV (proposed *Panine herpesvirus 3*); BV, B virus (*Macacine herpesvirus 1*); SA8, simian agent 8 (*Cercopithecine herpesvirus 2*); HVP2, herpesvirus papio 2 (*Papiine herpesvirus 2*); HVA1, herpesvirus ateles 1 (*Ateline herpesvirus 1*); and HVS1, herpesvirus saimiri 1 (*Saimiriine herpesvirus 1*). In many instances, abbreviations of viral names are followed by strain designations. Reproduced from Luebcke *et al.* (2006) by permission of the Society for General Microbiology.