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:	***2011.013aV***	(to be completed by ICTV officers)

Short title: Create species *Cricetid herpesvirus 2* in the genus *Rhadinovirus*, subfamily *Gammaherpesvirinae*, family *Herpesviridae*, order *Herpesvirales*
(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 (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* Study Group

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

After a discussion period, the proposal was approved by the *Herpesvirales* Study Group without dissent.

Date first submitted to ICTV:	March 11, 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	*2011.013aV*	(assigned by ICTV officers)

To create 1 new species within:

Genus:	***Rhadinovirus***
Subfamily:	***Gammaherpesvirinae***
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.

And name the new species:	**GenBank sequence accession number(s) of reference isolate:**
Cricetid herpesvirus 2	HQ221963

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 Loh *et al.* (2011), to which reference should be made in relation to the following comments.

A virus was isolated from the lung homogenate of a pygmy rice rat (*Oligoryzomys microtis*, a member of the family Cricetidae) trapped in July 1996 in a grassy field in Iquitos, Peru. It was found to kill suckling mice after intracranial inoculation, and was shown subsequently to be able to establish acute and latent infections in laboratory mice. The complete genome sequence is that of a herpesvirus, which was named rodent herpesvirus Peru (RHVP). The gene order is similar to that of members of subfamily *Gammaherpesvirinae*. A phylogenetic tree (Fig. 4 in Loh et al.) based on concatenated amino acid sequences from glycoprotein B and DNA polymerase showed that RHVP is most closely related to murid herpesvirus 4 (MuHV-4; genus *Rhadinovirus*, subfamily *Gammaherpesvirinae*) and other rodent rhadinoviruses, though clearly distinct from these viruses (e.g. the RHVP and MuHV-4 DNA polymerase amino acid sequences are only 61% identical). RHVP lacks some of the niche genes of MuHV-4, and contains its own set, whose properties indicate immunomodulatory functions.

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. RHVP fulfils these criteria. The virus was isolated on a single occasion, and, since it is uncertain whether epidemiological surveys will be carried out, we recommend classification of RHVP at this stage. It would be a dereliction to leave a completely sequenced virus unclassified for what is otherwise likely to be an indefinite period.

Herpesvirus species are named after the taxon of the host from which they are isolated. However, assigning RHVP to the new species *Cricetid herpesvirus 1* would be problematic. Various ICTV reports and other expert publications mention an unclassified virus named cricetid herpesvirus (hamster herpesvirus, ostensibly a betaherpesvirus) dating from over 50 years ago (Smith, 1959). Although this name is not usually followed by a number, the abbreviation is (CrHV-1). In order to avoid confusion, we propose classifying RHVP into the new species *Cricetid herpesvirus 2*, even though CrHV-1 probably does not now exist in a laboratory and no sequence data are available. If a hamster cytomegalovirus is isolated in future and characterized by sequencing, it could reasonably be assigned to the new species *Cricetid herpesvirus 1*.

We conclude that RHVP meets the criteria to be classified into a new species, and recommend the name *Cricetid herpesvirus 2*, being added to the existing species in the genus *Rhadinovirus,* namely *Ateline herpesvirus 2, Ateline herpesvirus 3, Bovine herpesvirus 4, Human herpesvirus 8, Macacine herpesvirus 5, Murid herpesvirus 4, Saimiriine herpesvirus 2* and (currently under consideration) *Murid herpesvirus 7*.

MODULE 9: **APPENDIX**: supporting material

additional material in support of this proposal

References:

Loh J, Zhao G, Nelson CA, Coder P, Droit L, Handley SA, Johnson LS, Vachharajani P, Guzman H, Tesh RB, Wang D, Fremont DH, Virgin HW (2011). Identification and sequencing of a novel rodent gammaherpesvirus that establishes acute and latent infection in laboratory mice. J Virol 85:2642-56.

Smith MG (1959). The salivary gland viruses of man and animals (cytomegalic inclusion disease). Prog Med Virol 2:171–202.

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.