This form should be used for all taxonomic proposals. Please complete all those modules that are applicable (and then delete the unwanted sections).

Code(s) assigned:	***2009.014aV*** (to be completed by ICTV officers)

Short title: Create species Leporid herpesvirus 4 in genus Simplexvirus, subfamily Alphaherpesvirinae, family Herpesviridae, order Herpesvirales
(e.g. 6 new species in the genus *Zetavirus*; re-classification of the family *Zetaviridae* etc.)

Modules attached (please check all that apply):	**1** ☐	**2** ☐	**3** ☐	**4** ☐	**5** ☒	
	6 ☐	**7** ☐				

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

The Herpesvirales Study Group; Phil Pellett <ppellett@med.wayne.edu>

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

MODULE 5: **NEW SPECIES**

Code	***2009.014aV***	(assigned by ICTV officers)

To create 1 new species assigned as follows:

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

Fill in all that apply. Ideally, species should be placed within a genus, but it is acceptable to propose a species that is within a Subfamily or Family but not assigned to an existing genus (in which case put "unassigned" in the genus box)

Name(s) of proposed new species:

Leporid herpesvirus 4

Argument to justify the creation of the new species:
If the species are to be assigned to an existing genus, list the criteria for species demarcation and explain how the proposed members meet these criteria.

Related herpesviruses are classified as distinct species if (a) their nucleotide sequences differ in a readily assayable and distinctive manner across the entire genome and (b) they occupy different ecological niches by virtue of their distinct epidemiology and pathogenesis or their distinct natural hosts. A paradigm is provided by HHV-1 and HHV-2, which differ in their sequence throughout the genome, tend to infect different epithelial surfaces and exhibit distinct epidemiological characteristics. These two viruses recombine readily in culture, but despite the fact that they can infect the same sites in the host, no recombinants have been isolated in nature, and the two viruses appear to have evolved independently for millions of years.

This virus appears to meet these criteria.

References:

Jin L, Löhr CV, Vanarsdall AL, Baker RJ, Moerdyk-Schauwecker M, Levine C, Gerlach RF, Cohen SA, Alvarado DE, Rohrmann GF (2008) Characterization of a novel alphaherpesvirus associated with fatal infections of domestic rabbits. Virology 378:13-20. Accession number EU119871.

Annexes:
Include as much information as necessary to support the proposal. The use of Figures and Tables is strongly recommended.

A virus was found to be associated with a severe disease affecting rabbits on a farm near Anchorage, Alaska. Extracts from the skin of infected rabbits produced syncytia and cell lysis in cultured rabbit skin, rabbit kidney, and Vero cells. Examination of the infectious agent by electron microscopy revealed an icosahedral nucleocapsid surrounded by an envelope with a diameter of about 120 nm, suggesting that it was a herpesvirus. The viral genome was determined to be composed of double-stranded DNA of 120–130 kbp. PCR using degenerate

primers to two conserved herpesvirus genes (encoding the subunits of ribonucleotide reductase, RR1 and RR2) and parts of two flanking genes was used to amplify sequences from purified viral DNA. Analysis of these data for the completely sequenced genes indicated that the virus is most closely related to bovine herpesvirus 2. The next most closely related viruses are human herpesviruses 1 and 2, and a number of cercopithecine herpesviruses. Experimental exposure of domestic rabbits to the isolate resulted in severe clinical disease and necrosis in the spleen and lymph node. In addition, viral DNA was identified in a variety of tissues by PCR, consistent with a systemic infection. Taken together, these data suggest that this virus, leporid herpesvirus 4 (LHV-4) is highly pathogenic for domestic rabbits and belongs to the family *Herpesviridae*, subfamily *Alphaherpesvirinae*, genus *Simplexvirus*.

Three other, different leporid herpesviruses (LHV-1, LHV-2 and LHV-3) have been classified tentatively in the genus *Rhadinovirus*, subfamily *Gammaherpesvirus*.

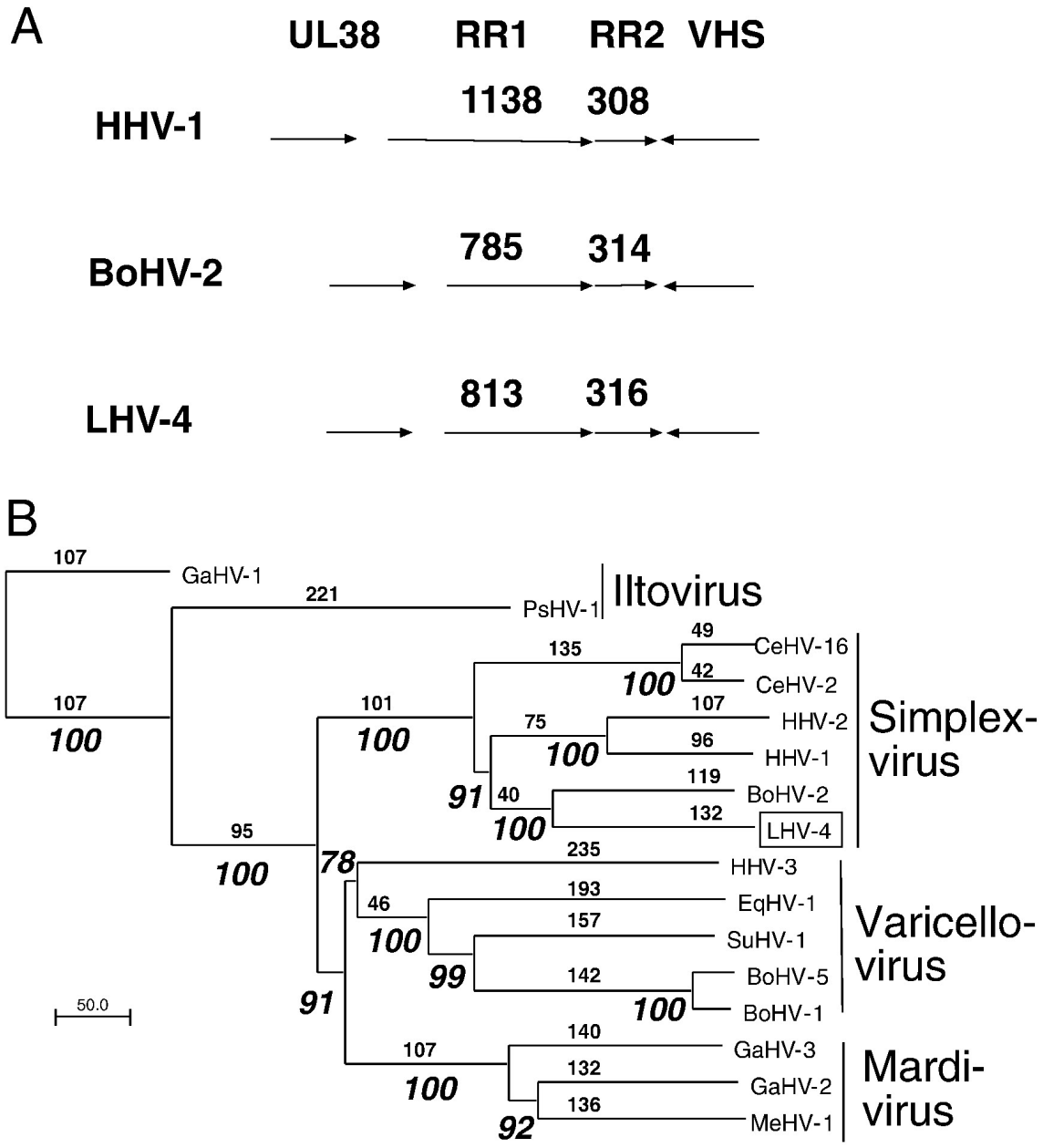

Fig. 6. Organization and phylogenetic analysis of the LHV-4 RR1 and RR2 genes. (A) Gene organization in HHV-1, BoHV-2, and LHV-4. The numbers indicate the sizes in codons of the open reading frames. The positions of the UL38 and VHS genes, for which partial LHV-4 sequences were obtained, are indicated. (B) Phylogenetic tree of the concatenated amino acid sequences of the RR1 and RR2 subunits. The scale bar represents genetic distance (nucleotide substitutions per site), and branch lengths are given in small font. Bootstrap values are shown in large font. The abbreviations in the virus names are as follows: Bo, bovine; Ce, cercopithecine; Eq, equine; Ga, gallid; H, human; L, leporid; Me, meleagrid; Ps, psittacid; Su, suid.