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:	***2016.021aD***	(to be completed by ICTV officers)

Short title: 1 new species in the genus *Lentivirus*
(e.g. 6 new species in the genus *Zetavirus*)

Modules attached (modules 1 and 11 are required)	**2** ☒ **3** ☐ **4** ☐ **5** ☐ **6** ☐ **7** ☐ **8** ☐ **9** ☐ **10** ☐

Author(s):

Welkin Johnson

Corresponding author with e-mail address:

Welkin Johnson welkin.johnson@bc.edu

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)	Retroviridae SG

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

Date first submitted to ICTV:	July 18, 2016
Date of this revision (if different to above):	August 3, 2016

ICTV-EC comments and response of the proposer:

MODULE 2: **NEW SPECIES**

Code	***2016.021aD***	(assigned by ICTV officers)

To create new species within:

Genus:	***Lentivirus***
Subfamily:	***Orthoretrovirinae***
Family:	***Retroviridae***
Order:	

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: (only 1 per species please)**	**GenBank sequence accession number(s)**
Jembrana disease virus	Jembrana disease virus isolate Tabanan/87	U21603

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 11

Jembrana disease in Bali cattle (*Bos javanicus*) was first described in the 1960s, and the causative agent, Jembrana disease virus (JDV) is a lentivirus most closely related to bovine immunodeficiency virus (BIV) (Desport and Lewis, 2010). The genetic distance between JDV and BIV is similar or greater than the distance between the caprine and ovine lentiviruses CAEV and SRLV, considered distinct species, although less than the distance between the two species of primate lentiviruses, HIV-1 and SIVmac (Gifford et al. 2008; Gifford, 2012); this is consistent with origins of JDV as a recent transmission of a BIV-related virus, whereas the timing of the last common ancestor of HIV-1 and SIVmac may be on the order of thousands–millions of years. As with HIV-1 and HIV-2, JDV is thought to have arisen by interspecies transmission – in this case, of a BIV-like virus into Bali cattle from an unknown reservoir or source; while BIV is found globally, JDV is thus far limited to Bali and neighboring regions (Desport and Lewis, 2010). Importantly, JDV pathogenesis is unique among lentiviruses, and is clearly distinct from the pathogenesis associated with BIV infection of cattle (Desport and Lewis, 2010). The JDV genome is the shortest of any known lentivirus, and has a number of in-frame deletions relative to BIV, as well as reported differences in cis-acting elements (Chadwick et al., 1995). Although JDV and BIV have cross-reactive epitopes, prior BIV infection reportedly did not prevent experimental JDV infection (McNab et al., 2010). Overall, the classification of JDV as a distinct species of lentivirus related to BIV is consistent with the four species demarcation criteria that include: differences in gene and genome sequence products, differences in natural host range, differences in pathogenicity, and differences in antigenic properties (9th Report of the ICTV). *Jembrana disease virus* would be an additional species, along with BIV, in the bovine "group" of the *Lentivirus* genus.

MODULE 11: **APPENDIX**: supporting material

additional material in support of this proposal

References:

Desport and Lewis. 2010. *Current HIV Research* 8:53-65

Gifford et al. 2008. *PNAS* 105:20362-20367

Gifford, R.J. 2012. *Trends in Genetics* 28:89-100

Chadwick et al. 1995. *J.Gen.Virol*. 76:1637-1650

McNab et al. 2010. *Virology* 404:261-268

9th Report of the ICTV, Part II, page 489, Genus *Lentivirus*

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.

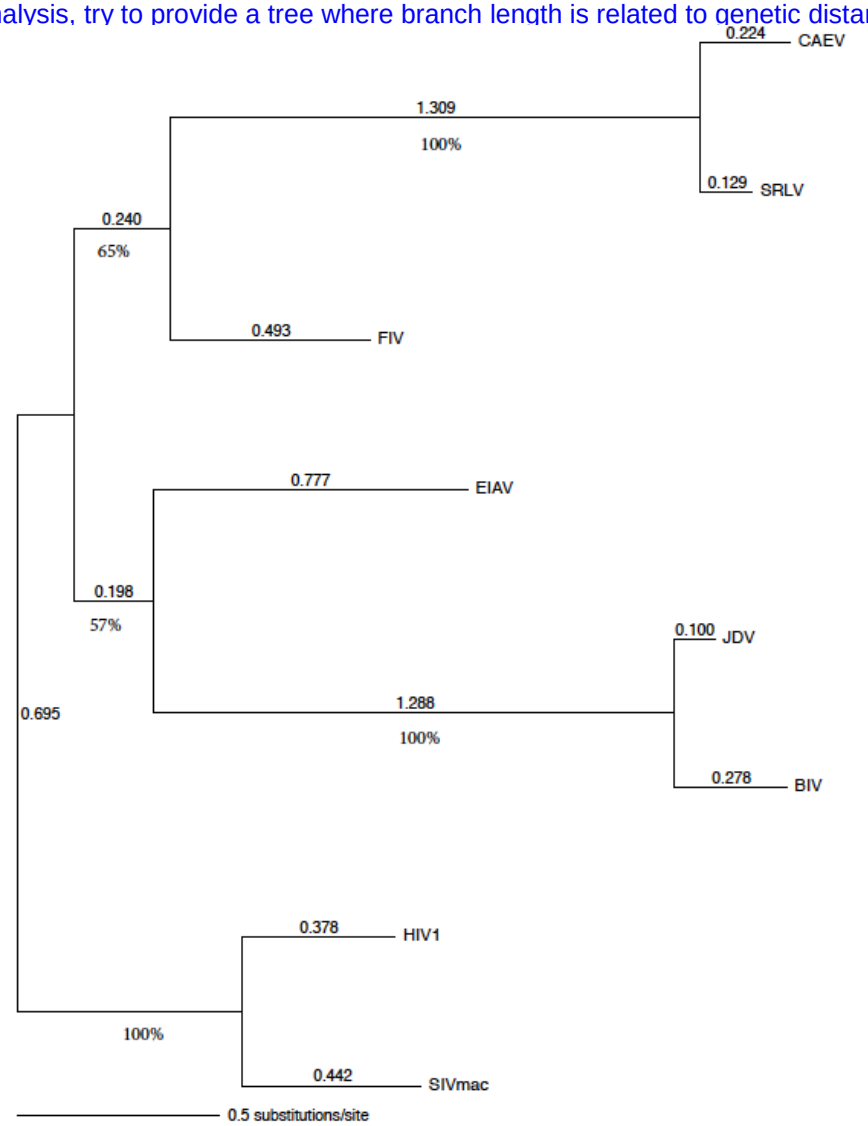

Fig. 1. Phylogenetic relationship of JDV to BIV and other lentiviruses. Tree was generated in PAUP* using the Likelihood criterion with the exhaustive search setting, based on an alignment of the reverse-transcriptase domain (RT) of the Pol protein sequences of eight representative lentiviruses. Identical topologies were also obtained with the Neighbor-Joining and Parsimony criteria, and topology is consistent with published reports (e.g., Gifford, 2012). Bootstrap support values (%) are based on 100 replicates.
Input taxa: caprine arthritis encephalitis virus of goats (CAEV, Genbank Acc.# AAG48629.1); a small ruminant lentivirus of sheep (SRLV, AAM51650.1, a member of species *Visna/maedi virus*), equine infectious anemia virus (EIAV, NP_056902.1), Jembrana disease virus (JDV, Q82851.1), bovine immunodeficiency virus (BIV, AAA42767.1), feline immunodeficiency virus (FIV, ABO69483.1), and two primate lentiviruses, human immunodeficiency virus 1 (HIV1, AMP41333.1) and simian immunodeficiency virus of macaques (SIVmac, AAU94530.1). To root the tree, the two primate lentiviruses (HIV1 and SIVmac) were designated as an outgroup.