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:	***2015.009a,bD***	(to be completed by ICTV officers)

Short title: Two new species in the genus *Orthohepadnavirus*
(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):

Lars Magnius

Corresponding author with e-mail address:

lars.magnius@gmail.com

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)	Hepadnaviridae & Hepatitis delta virus Study Group

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

Date first submitted to ICTV:	6/26/15
Date of this revision (if different to above):	1/28/16

ICTV-EC comments and response of the proposer:

Decision: Ac. provide improved phylogenetic tree.

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	***2015.009aD***	(assigned by ICTV officers)

To create 2 new species within:

Genus:	***Orthohepadnavirus***
Subfamily:	
Family:	***Hepadnaviridae***
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)**
Tent-making bat hepatitis B virus	tent-making bat hepatitis B virus	KC790381
Roundleaf bat hepatitis B virus	roundleaf bat hepatitis B virus	KC790376

Reasons to justify the creation and assignment of the new species:

Phylogenetic calculations and host range differences proved the existence of at least three different bat hepadnavirus species (two of them being new) (Drexler et al., 2013). The phylogenetic differences among their members are tentatively more than or equal to 20%. Their naming was according to the general policy in the family, i.e., by applying the English host name and to add hepatitis B virus.

MODULE 8: **RENAME**

Use this module to change the name of one or more existing taxa (but note that stability of nomenclature is encouraged wherever possible). Insert extra lines in the table if needed.
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Renaming one or more taxa

Code	***2015.009bD***	(assigned by ICTV officers)

To rename the following taxon (or taxa):

Current name	**Proposed name**
Bat hepatitis virus	***Long-fingered bat hepatitis B virus***

Reasons to justify the renaming:

Earlier there was only a single bat hepatitis virus, while now there are at least three bat hepatitis virus species proven to belong to the genus *Orthohepadnavirus*. For the moment there is just one isolate of horseshoe bat hepatitis B virus, which diverges <20 % from round leaf bat HBV and therefore will not be classified as a new species. After the finding of the novel bat hepadnaviruses, we propose to rename the original bat hepadnavirus species to reflect its host species in line with the proposed designations of the two new bat hepadnavirus species.

MODULE 10: **APPENDIX**: supporting material

References:

Drexler JF, Geipel A, König A, Corman VM, van Riel D, Leijten LM, Bremer CM, Rasche A, Cottontail VM, Maganga GD, Schlegel M, Müller MA, Adam A, Klose SM, Carneiro AJ, Stöcker A, Franke CR, Gloza-Rausch F, Geyer J, Annan A, Adu-Sarkodie Y, Oppong S, Binger T, Vallo P, Tschapka M, Ulrich RG, Gerlich WH, Leroy E, Kuiken T, Glebe D, Drosten C (2013) Bats carry pathogenic hepadnaviruses antigenically related to hepatitis B virus and capable of infecting human hepatocytes. *Proc Natl Acad Sci U S A.* **110**, 16151-56.

He B, Fan Q, Yang F, Hu T, Qiu W, Feng Y, Li Z, Li Y, Zhang F, Guo H, Zou X, Tu C (2013) Hepatitis virus in long-fingered bats, Myanmar. Emerg Infect Dis. **19,** 638-40.

The complete sequence and sequence comparison of the new bat hepadnaviruses has been published (Drexler et al., 2013; He et al., 2013). The following phylogenetic tree (Fig. 1) is based on complete hepadnavirus genomes. The percent nucleotide divergence of complete genomes are shown in Table 1.

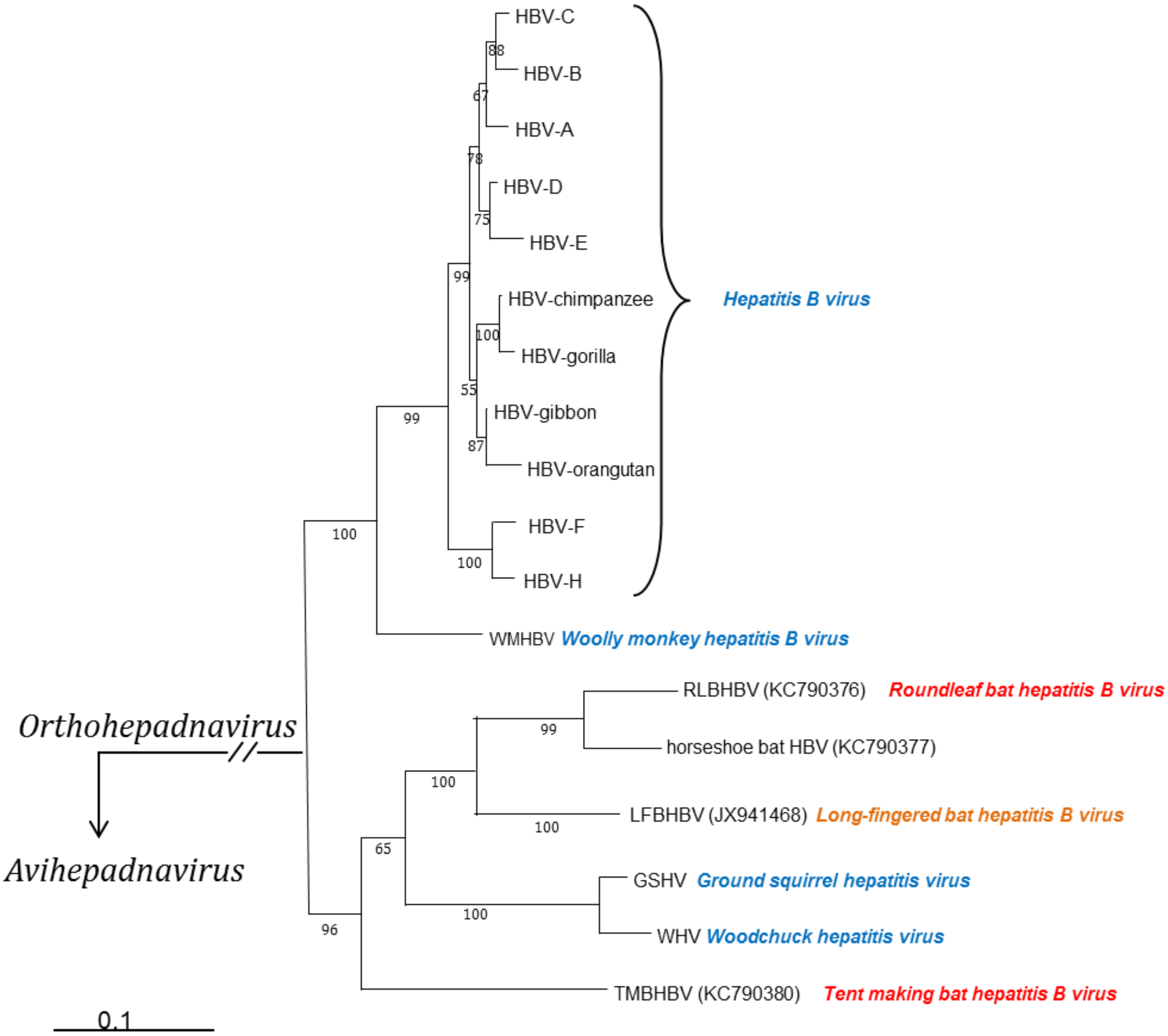

Fig. 1. Phylogenetic tree of the genus *Orthohepadnavirus* based on Maximum likelihood analysis of complete genomes of members of genera *Avihepadnavirus* and *Orthohepadnavirus*. Primate and rodent Orthohepadnavirus species are shown. Bootstrap values of 1,000 replicas are given at the branches. The species names are shown in bold and italics, the suggested new species names in red, the proposed renamed species in orange, accepted species in blue. One virus (horseshoe bat HBV) in the tree diverges <20% from round leaf bat HBV and may thus be considered another isolate of the latter virus. Abbreviations: HBV: hepatitis B virus; WMHBV: woolly monkey hepatitis B virus; GSHV: ground squirrel hepatitis virus; WHV: woodchuck HBV; TMHBV: tent making hepatitis B virus

Table 1. Percent nucleotide divergence of complete genomes. Data obtained from Drextler et al., 2013 supplemented with divergence of complete genomes of LFBHBV from other bat hepadnaviruses. Abbreviations: WMHBV: woolly monkey hepatitis B virus; TMBHBV: tent-making bat hepatitis B virus; RLBHBV: roundleaf bat hepatitis B virus; HSBHBV: horseshoe bat hepatitis B virus; LFBHBV: long-fingered bat hepatitis B virus; ND= not determined; GSHV: ground squirrel hepatitis virus; ASHV: Arctic ground squirrel hepatitis B virus; WHV: woodchuck hepatitis virus.

	1	2	3	4	5	6	7	8
1. HBV (genotypes F-H)	8.4							
2. HBV (genotypes A-E)	13.3–14.7	7.4–12.6						
3. WMHBV	22.7–23	21.7–22.	6 0					
4. Ape HBV	12.9–13.5	9.3–12.4	21.2–22.2	5.9–9.8				
5. TMBHBV	38.1–38.8	38.8–39.5	39–39.3	38.5–39.5	0.1–2.3			
6. RLBHBV	34.9–35.3	34.9–36	35.7–35.8	35–35.4	40.1–40.4	0.4–0.5		
7. HSBHBV	35.1–35.7	34.3–35.6	35.4–35.4	34.9–35.6	39.6–39.8	18.9–19.	1 0	
8. LFBHBV	ND	ND	ND	ND	37.1	28.6	28.4	-
9. GSHV, ASHV, WHV	36.5–37.8	36.3–38.1	36.6–37.8	36.1–37.5	40.3–41.3	36.3–37.2	29.7–30	14.8–16