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:	***2016.019aD***	(to be completed by ICTV officers)

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

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

Author(s):

Heléne Norder and 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:	July 12, 2016
Date of this revision (if different to above):	August 2, 2016

ICTV-EC comments and response of the proposer:

Decision:
Response:

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	***2016.019aD***	(assigned by ICTV officers)

Create 1 new species in the genus *Orthohepadnavirus*

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)**
Pomona bat hepatitis B virus	Pomona bat hepatitis B virus (PB HBV; isolate PEPR7)	KF939649

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

Bats are important reservoirs for zoonotic viruses, therefore 42 bats belonging to three species (*Hipposideros pomona*, *Rhinolophus affinis* and *R. sinicus*) were collected in Yunnan in China for identification of new viruses (He et al., 2015). All liver samples were screened for orthohepadnaviruses and 20 % of the samples from *H. pomona* were positive. Three isolates were selected for full genome sequencing. Analysis of the genomes showed the presence of all four ORFs identified in the members of the genus *Orthohepadnavirus*. The strains were similar to other identified bat hepatitis B viruses, from which they diverged by more than 30%. The genetic differences between the different species in this genus are tentatively more than or equal to 20%. Phlyogenetic analysis confirmed that this virus represent an additional bat hepadnavirus species in the *Orthohepadnavirus* genus. The suggested naming is according to the general policy in the family, i.e. by applying the English host name and adding hepatitis B virus. Since there is already a roundleaf bat hepatitis B virus from Gabon and this new roundleaf bat hepatitis B virus, both hosts belonging to the bat genus *Hipposideros*, we have chosen to use the species name of the host “*pomona*” to the name of this new hepatitis B virus species.

MODULE 11: **APPENDIX**: supporting material

References:

He B, Zhang F, Xia L, Hu T, Chen G, Qiu W, Fan Q, Feng Y, Guo H, Tu C (2015) Identification of a novel orthohepadnavirus in pomona roundleaf bats in China. Arch. Virol. 160:335-7.

The complete sequence and sequence comparison of the new bat hepadnavirus has been published (He et al., 2015). The following phylogenetic tree (Fig. 1) is based on complete hepadnavirus genomes. The percent nucleotide divergences of complete genomes are shown in Table 1.

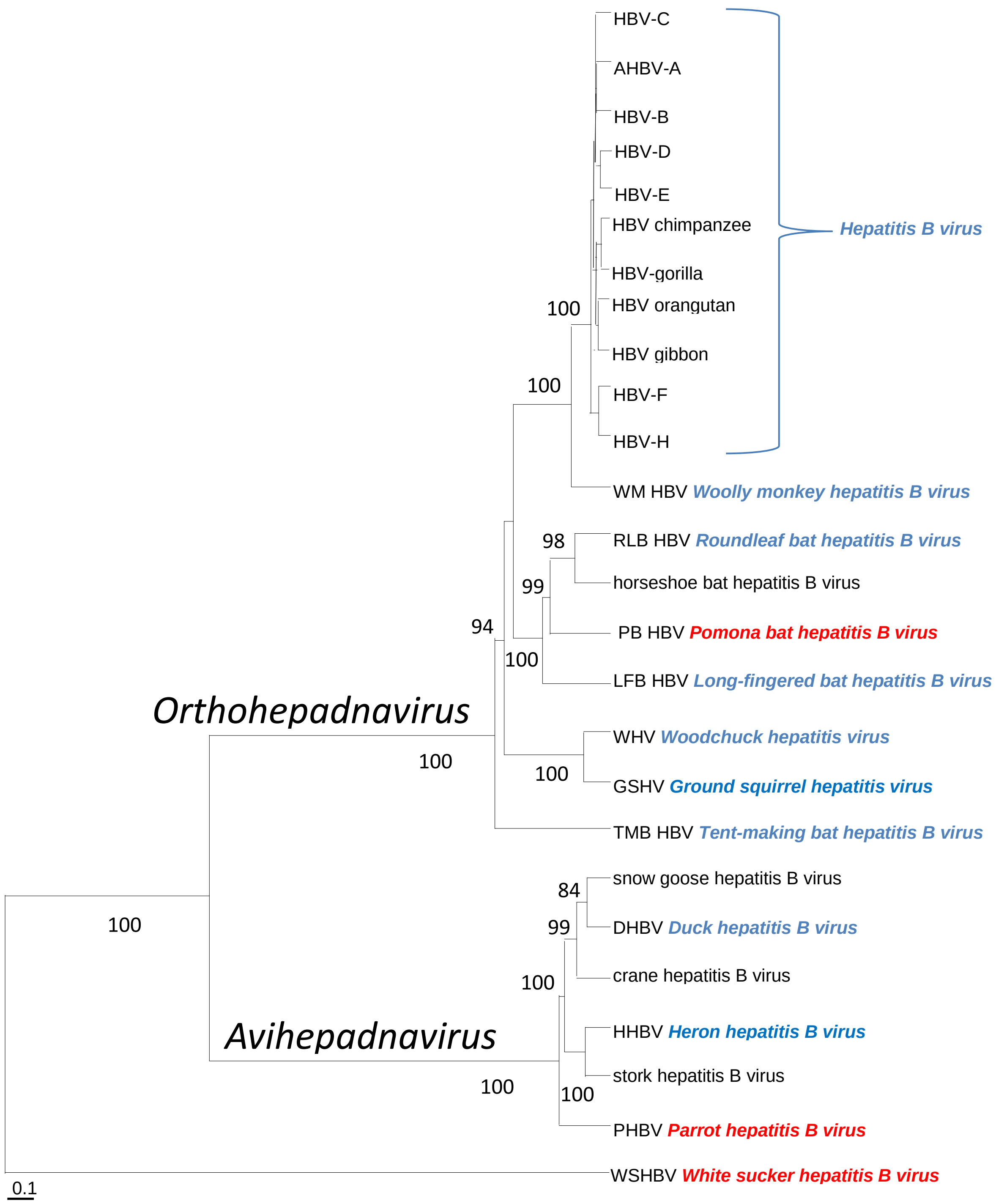

Fig. 1. Phylogenetic tree based on maximum likelihood analysis of complete genomes of members of genera *Avihepadnavirus* and *Orthohepadnavirus*. Bootstrap values of 1,000 replicas are given at the branches as percentage. The species names are shown in bold and italics, the suggested new species names in red, accepted species in blue. Abbreviations: HBV: hepatitis B virus; PB HBV: pomona bat HBV; PHBV: parrot hepatitis B virus; WSHBV: white sucker hepatitis B virus.

Table 1. Percent nucleotide divergence of complete orthohepadnavirus genomes.

Abbreviations: WM HBV: woolly monkey hepatitis B virus; TMB HBV: tent-making bat hepatitis B virus; RLB HBV: roundleaf bat hepatitis B virus; HSB HBV: horseshoe bat hepatitis B virus; PB HBV: pomona bat hepatitis B virus; LFB HBV: long-fingered bat hepatitis B virus; GSHV: ground squirrel hepatitis virus; ASHV: Arctic ground squirrel hepatitis B virus; WHV: woodchuck hepatitis virus

	1	2	3	4	5	6	7	8	9
1. HBV genotypes F-H	8.5								
2. HBV genotypes A-E	13.5-15.2	7.9-11							
3. ape HBVs	13-13.6	7.8-12.2							
4. WM HBV	22.4-23.5	21.7-22.7	21.6-21.7						
5. TMB HBV	37-38	38.6-38.9	38.3-38.7	38.6					
6. RLB HBV	33-33.8	34.2-35.5	34.1-34.6	35.5	40.9				
7. HSB HBV	34.2-34.9	34.5-35.9	34.9-35.3	35.5	40.7	20.7			
8. PB HBV	**34.9-36.1**	**35.5-36.7**	**35.4-36.2**	**36.3**	**40.1**	**31.1**	**31.2**		
9. LFB HBV	35.4-36.2	36.3-37.2	36-36.6	35.5	40.3	28.6	28.6	**31.3**	
10. GSHV, WHV	35.2-36.4	36.1-37.4	35.9-36.7	36-36.6	37.7-38.2	37.7-38.2	38.3-38.7	**36.4-37.1**	37.7-38.2