



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:	2016.017aD	(to be completed by ICTV officers)
Short title: One new species in <i>Hepadnaviridae</i> (e.g. 6 new species in the genus <i>Zetavirus</i>)		
Modules attached (modules 1 and 11 are required)	6 <input type="checkbox"/> 7 <input type="checkbox"/> 8 <input type="checkbox"/> 9 <input type="checkbox"/> 10 <input type="checkbox"/>	
	2 <input checked="" type="checkbox"/>	3 <input type="checkbox"/> 4 <input type="checkbox"/> 5 <input type="checkbox"/>

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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 (there are six virus subcommittees: animal DNA and retroviruses, animal ssRNA-, animal ssRNA+, fungal and protist, plant, bacterial and archaeal)

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:

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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	2016.017aD	(assigned by ICTV officers)	
To create 1 new species within:			
Genus:	unassigned	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.	
Subfamily:			
Family:	<i>Hepadnaviridae</i>		
Order:			
Name of new species:	Representative isolate: (only 1 per species please)	GenBank sequence accession number(s)	
<i>White sucker hepatitis B virus</i>	white sucker hepatitis B virus (WSHBV) isolate RR173	KR229754	

<p>Reasons to justify the creation and assignment of the new species:</p> <ul style="list-style-type: none"> • Explain how the proposed species differ(s) from all existing species. <ul style="list-style-type: none"> ○ 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
<p>The white sucker fish (<i>Catostomus commersonii</i>, Cypriniformes, Actinopterygii) is used as a sentinel organism to monitor the development of tumors as an indicator of exposure to environmental pollutants. Hahn et al. (2015) identified a novel hepatitis B like-virus during the development of a hepatic transcriptome in the white sucker. Phylogenetic analysis proved that it was a new hepadnavirus with all known ORFs apart from the X-gene. The white sucker virus diverges with more than 30% from all previously known hepadnaviruses, and formed a root in the phylogenetic tree based on complete genomes of all <i>Hepadnaviridae</i> members. The sequence has been published (Hahn et al., 2015). We await the description of more hepadnaviruses similar to this virus isolated from other species before proposing the establishment of a new genus for this fish hepadnavirus.</p>

MODULE 11: **APPENDIX**: supporting material

additional material in support of this proposal

References:

Hahn CM, Iwanowicz LR, Cornman RS, Conway CM, Winton JR, Blazer VS (2015)
Characterization of a novel hepadnavirus in the white sucker (*Catostomus commersonii*) from the Great Lakes region of the United States. *J. Virol.* 89:11801-11.

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.

The complete sequence and sequence comparison of the white sucker hepatitis B virus has been published (Hahn et al., 2015). The percent nucleotide divergences of complete white sucker hepadnavirus genome compared to complete genomes of orthohepadnaviruses and avihepadnaviruses are shown in Table 1. The following phylogenetic tree (Fig. 1) is based on complete hepadnavirus genomes.

Table 1. Percent nucleotide divergence of complete white sucker hepadnavirus genome compared to complete avihepadnavirus (duck hepatitis B virus) and orthohepadnavirus genomes (tent-making bat HBV, TMB HBV, and human/ape HBV).

	white sucker HBV	duck HBV	TMB HBV
<i>Avihepadnavirus</i> duck hepatitis B virus	42.11		
<i>Orthohepadnavirus</i> TMB HBV	46.4	53.8	
HBV	44.3-45.8	51.6- 52.6	37.1-38.9

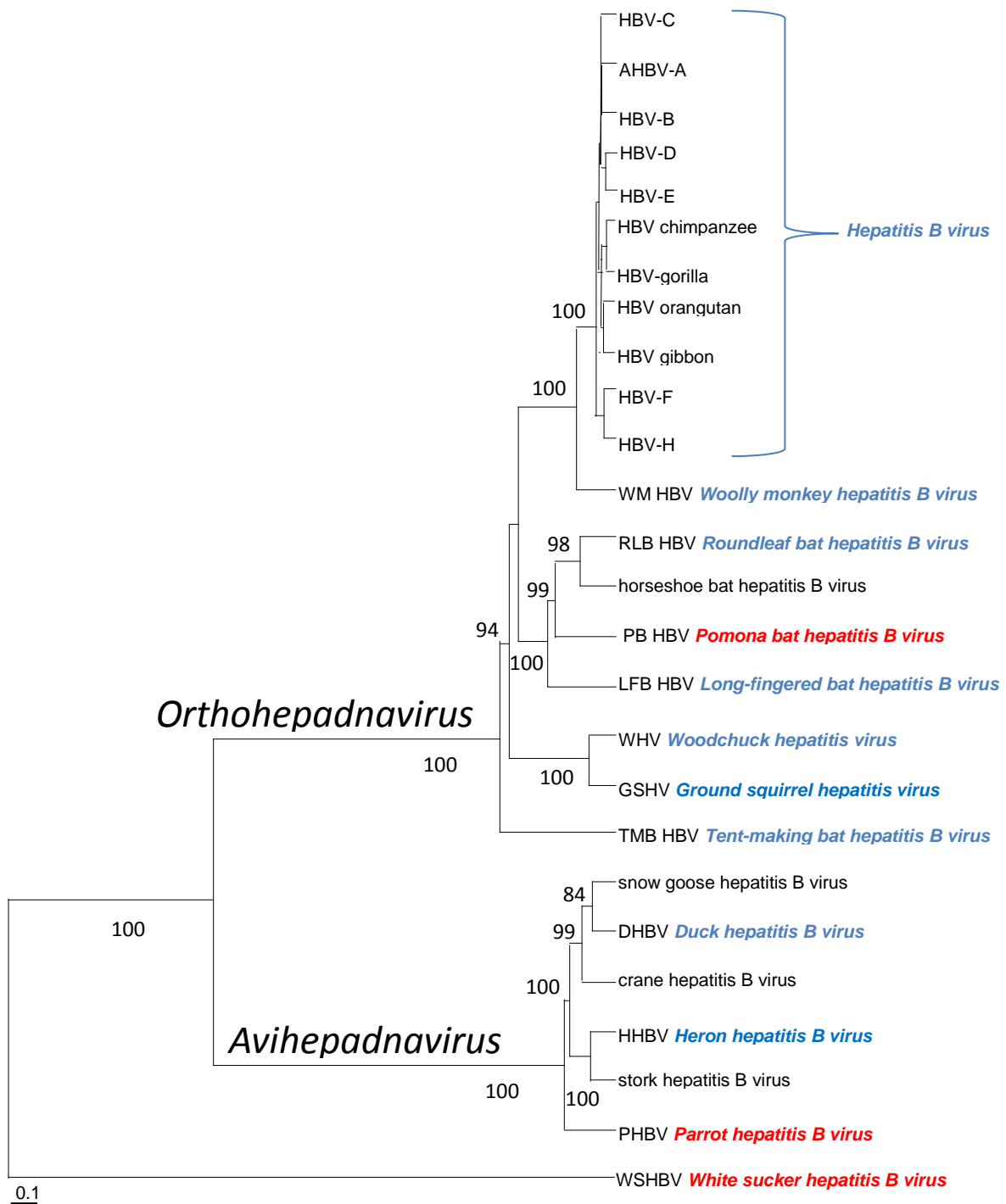


Fig. 1. Phylogenetic tree based on maximum likelihood analysis of complete genomes of members of genera *Avihepadnavirus* and *Orthohepadnavirus*. Bootstrap values of 1,000 replicas are given at the branches as percentage. The species names are shown in bold and italics, the suggested new species names 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.