This Word module should be used for all taxonomic proposals.

Please complete **Part 1** and:

either **Part 3** for proposals to create new taxa or change existing taxa

or **Part 2** for proposals of a general nature.

Submit the completed Word module, together with the accompanying Excel module named in Part 3, to the appropriate ICTV Subcommittee Chair.

For guidance, see the notes written in blue, below, and the help notes in file Taxonomic\_Proposals\_Help\_2018.

**Part 1:** **TITLE, AUTHORS, etc**

|  |  |  |
| --- | --- | --- |
| **Code assigned:** | ***2018.006D*** | (to be completed by ICTV officers) |
| **Short title:** 1 new species in the genus *Orthohepadnavirus*  |
|  |
| **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 (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: | 14/6/2018 |
| Date of this revision (if different to above): | 3/7/2018 |

|  |
| --- |
| **ICTV-EC comments and response of the proposer:** |
|       |

**Part 3:** **PROPOSED TAXONOMY**

|  |
| --- |
| **Name of accompanying Excel module: 2018.006D.N.v1.Orthohepadnavirus\_sp** |

The taxonomic changes you are proposing should be presented on an accompanying Excel module, 2017\_TP\_Template\_Excel\_module. Please enter the file name of the completed module in this box.

**Supporting material:**

| additional material in support of this proposal |
| --- |
| Please explain the reasons for the taxonomic changes you are proposing and provide evidence to support them. The following information should be provided, where relevant:* **Species demarcation criteria**: Explain how new species differ from others in the genus and demonstrate that these differences meet the criteria previously established for demarcating between species. If no criteriahave previously been established, and if there will now be more than one species in the genus, please state the demarcation criteria you are proposing.
* **Higher taxa**:
	+ There is no formal requirement to state demarcation criteria when proposing new genera or other higher taxa. However, a similar concept should apply in pursuit of a rational and consistent virus taxonomy.
	+ Please indicate the **origin of names** assigned to new taxa at genus level and above.
	+ For each new genus a **type species** must be designated to represent it. Please explain your choice.
* **Supporting evidence**: The use of Figures and Tables is strongly recommended (note that copying from publications will require permission from the copyright holder). For phylogenetic analysis, try to provide a tree where branch length is related to genetic distance.
 |

Analysis of sera from 124 New World monkey sera from zoos and shelters for confiscated animals in Bahia in Brazil has identified a new hepadnavirus in one female capuchin monkey *Sapajus xanthosternos* (de Carvalho Dominguez Souza et al., 2018). Five other monkeys belonging to three different *Sapajus spp*. were shown to carry antibodies to this virus.

Phylogenetic calculations and host range differences suggest that a new hepadnavirus species should be established for the capuchin monkey hepatitis B virus (CMHBV) and this species should belong to the genus *Orthohepadnavirus* (which contains all the known mammalian hepatitis B viruses). The nucleotide divergence from other othohepadnavirus members including woolly monkey HBV was more than 20% (which is the species demarcation criterion) and 20.4% from the latter virus. The naming of the species was according to the general policy in the family, i.e., by applying the English host name and adding hepatitis B virus.

0.1

D00330 HBV-B

AY123041 HBV-C

X02763 HBV-A

AJ131574 HBVgibV

AJ131572 HBV-gibIII

AJ131573 HBV-gibIV

AJ131571 HBV-gibII

AJ131569 HBV-gibI

AF193864 HBV-orangutan

D00220-chH

AJ131567 HBVgor

X75657 HBV-E

V01460 HBV-D

AF160501 HBV-G

X69798 HBV-F

AY090454 HBV-H

**KY703886 CMHBV**

AF046996 WMHBV

KC790377 HSBHBV

KC790376 RLBHBV

KF939649 PMBHBV

JX941466 LFBHBV

K02715 GSHV

U29144 ASHV

J02442 WHV

KC790381 TMBHBV

Human HBV

Ape HBV

Human HBV

Phylogenetic tree of the members of genus *Orthohepadnavirus* based on Beast analysis of complete genomes of orthohepadnaviruses. All human and ape hepadnaviruses belong to species *Hepatitis B virus*. Abbreviations and species they belong to (in italics): CMHBV: *Capuchin monkey hepatitis B virus* (proposed species); WMHBV: *Woolly monkey hepatitis B virus*; HSBHBV: horseshoe bat hepatitis B virus; RLBHBV: *Roundleaf bat hepatitis B virus*; PMBHV: *Pomonoma bat hepatitis B virus*; LFBHBV: *Long-fingered bat hepatitis B virus*; GSHV: *Ground squirrel hepatitis virus,* ASHV: Arctic ground squirrel hepatitis B virus; WHV: *Woodchuck hepatitis B virus* TMBHBV: *Tent-making bat hepatitis B virus*;.

 1 2 3 4 5 6 7 8 9

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

8. LFBHBV 33.8-33.9 34.5-36.4 35.3 33.5-34.6 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 41.7-41.9 19.2–22.1

10. CMHBV 21.3-22.4 20.7-21.8 20.4 20.6-21.4 37.8 36.1 34.7 35.3 36-36.6

Percent nucleotide divergence of complete genomes.

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*; GSHV: *Ground squirrel hepatitis virus,* ASHV: Arctic ground squirrel hepatitis B virus; WHV: *Woodchuck hepatitis B virus*; CMHBV: *Capuchin monkey hepatitis B virus*.

| **References:** |
| --- |
| de Carvalho Dominguez Souza BF, König A, Rasche A, de Oliveira Carneiro I,Stephan N, Corman VM, Roppert PL, Goldmann N, Kepper R, Müller SF, Völker C, deSouza AJS, Gomes-Gouvêa MS, Moreira-Soto A, Stöcker A, Nassal M, Franke CR,Rebello Pinho JR, Soares MDCP, Geyer J, Lemey P, Drosten C, Netto EM, Glebe D,Drexler JF. (2018). A novel hepatitis B virus species discovered in capuchin monkeyssheds new light on the evolution of primate hepadnaviruses. J Hepatol. 68:1114-1122. doi: 10.1016/j.jhep.2018.01.029.  |