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.

The Word module explains and justifies your proposal. The Excel module is a critical document that will be used to implement the proposed taxonomic changes once they are approved and ratified. If proposals presented in the Word module are not presented accurately in the Excel module, the taxonomic changes cannot proceed.

For guidance, see the notes written in blue, below, and the Help Notes in file Taxonomic\_Proposals\_Help\_2019.

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

|  |  |  |  |  |
| --- | --- | --- | --- | --- |
| **Code assigned:** | ***2019.007D*** | | |  |
| **Short title:** Create three new species in the genus *Orthohepadnavirus*, family *Hepadnaviridae* | | | | |
|  | | | | |
| **Author(s) and email address(es):** | | | | |
| List authors in a single line *Archives of Virology* citation format (e.g. Smith AB, Huang C-L, Santos, F) | | Provide email address for each author in a single line separated by semi-colons | | |
| Magnius LO | | [Lars.magnius@gmail.com](mailto:Lars.magnius@gmail.com) | | |
| **Author(s) institutional address(es) (optional):**   |  | | --- | | Provide institutional addresses, each on a single line followed by author(s) initials (e.g. University of Woolloomooloo [SAB, HCL]) | | Ulf Lundahls Foundation, Stockholm, Sweden [LOM] | | | | | |
| **Corresponding author** | | | | |
| Lars O Magnius | | | | |
| **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 and Hepatitis delta virus SG | |
| ICTV Study Group comments (if any) and response of the proposer: | | | | |
|  | | | | |
|  | | | | |
| Date first submitted to ICTV: | | | | 19 May 2019 |
| Date of this revision (if different to above): | | | | 2 September 2019 |

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

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

|  |
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| **Name of accompanying Excel module:** 2019.007D.A.v1.Orthohepadnavirus\_3sp.xlxs |

The taxonomic changes you are proposing should be presented on an accompanying Excel module, 2019\_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, please provide a tree where branch length is **proportional to genetic** distance, generated using an appropriate algorithm (Neighbour-Joining, Maximum Likelihood, or Bayesian) and provide evidence of the reliability of the branching (e.g., by bootstrapping).   Please refer to the Help Notes file (Taxonomic\_Proposals\_Help\_2019) for more information  Three new species is proposed in *Orhtohepadnaviridae* for the first recorded hepadnaviruses in their respective mammalian order, i.e. Insectivora, Carnivora and Artiodactylia.  *Chinese shrew hepatitis B virus*  A novel hepadnavirus, Asian grey shrew hepatitis B virus (AGS HBV), 3,165 bp in genomic length, was identified in liver tissue of 2 species of Crocidura and in *Anourosorex squamipes* shrews collected in 2016 and 2017 in the Hubei and Zheijang provinces in China. Although viruses were recovered from two different genera of shrews they diverged by <10 per cent from each other but by >35% as compared to other orthohepadnaviruses and thus representing a new species. (The species demarcation criterion for orthohepadnaviruses is >20% nucleotide divergence at the level of complete genomes.) CSHBV had all four ORFs of orthohepadnaviruses although the pre core sequence was divergent.  *Domestic cat hepatitis B virus*  By high-throughput transcriptome sequencing of lymphoma tissue from a male domestic cat infected with feline immune deficiency virus (FIV), a new orthohepadnavirus was discovered. The genome of the domestic cat hepatitis B virus (DCHBV) comprised 3,187 bp and diverged by more than 33% from all other orthohepadnaviruses and thus represents a new species. Infection with this new virus was revealed by PCR in 3.2% of 63 cats not infected by FIV but in 10% of 60 FIV infected cats.  *Tai Forest hepatitis B virus*  At postmortem virome capture sequencing of samples originating from one of six dead Maxwell's duiker antilops (*Philantomba maxwellii*, Order Artiodactylia) found in the Taï National Park in Côte d'Ivoire, a new orthohepadnavirus was disclosed. High viral copy numbers revealed in spleen, lung, blood and liver in a range compatible with that found in humans with active chronic hepatitis suggest a causative role for the death of this virus in the diseased animal.  Its genome comprised 3,128 bp and differed by >31% from all other orthohepadnaviruses. Phylogenetic analysis revealed no close relation to any other species of orthohepadnaviruses but it formed a clade with all known rodent and most known bat hepadnaviruses. The designation Tai Forest hepadnavirus was suggested by the authors and we suggest to name the species *Tai Forest hepatitis B virus*. The virus could not be demonstrated in any of 29 other duikers, which is why a spillover from another mammalian host cannot be excluded.  X02763 HBV-A  AJ131569 HBV-gib I  D00220 chHBV  X69798 HBV-F  KY703886 CMHBV  AF046996 WMHBV  U29144 ASHV.  K02715 GSHV.  J02442 WHV.  **MH307930 DCHBV**  **MK620908 TFo HBV**  JX941466 LFB HBV  KF939649 PBHBV  KC790377 HSB HBV  KC790376 RLB HBV  KC790381 TMB HBV  **MH484438 AGS HBV**  KX058435 TFHBV  93  100  100  58  100  100  84  100  100  100  99  100  71  53  100  200 |

Figure 1. Phylogenetic tree of members of the genus *Orthohepadnavirus* based on Beast analysis of complete genomes and using the Tibetan frog virus, TFHBV, as outgroup. The new suggested species are marked in bold. Abbreviations: AGSH: Arctic ground squirrel hepatitis B virus; AGS HBV: Asian grey shrew hepatitis B virus; chHBV: chimp hepatitis B virus; CMHBV: capuchin monkey hepatitis B virus; DCHBV: domestic cat hepatitis B virus; GSHV: ground squirrel hepatitis virus; HBV-gib I: gibbon hepatitis B virus; HSBHBV: horseshoe bat hepatitis B virus; LFB HBV: long-fingered bat hepatitis B virus; PBHBV: Pomona bat hepatitis B virus; RLB HBV: roundleaf bat hepatitis B virus; TFo HBV: Taï Forest hepatitis B virus; TMB HBV: tent-making bat hepatitis B virus; WHV: woodchuck hepatitis B virus, WMHBV: woolly monkey hepatitis B virus.

Table 1. Percent nucleotide divergence of complete genomes

|  |  |  |  |
| --- | --- | --- | --- |
|  | AGS HBV | DCHBV | TFo HBV |
| HBV-A | 35 | 35 | 33 |
| chHBV | 35 | 34 | 33 |
| HBV-gib I | 35 | 35 | 33 |
| HBV-F | 37 | 35 | 34 |
| WMHBV | 37 | 35 | 32 |
| CMHBV | 37 | 35 | 34 |
| WHV | 38 | 36 | 34 |
| GSHV | 37 | 36 | 34 |
| AGSHV | 38 | 37 | 35 |
| LFB HBV | 38 | 33 | 31 |
| RLB HBV | 38 | 33 | 32 |
| HSB HBV | 38 | 34 | 32 |
| PBHBV | 38 | 33 | 31 |
| TMB HBV | 35 | 37 | 35 |
| CSHBV | - | 38 | 38 |
| DCHBV | 38 | - | 33 |

Abbreviations: chHBV: chimp HBV; HBV-gib I: gibbon HBV; WMHBV: woolly monkey HBV; CMHBV: capuchin monkey HBV; WHV: woodchuck HBV; GSHV: ground squirrel HBV; AGSHV: Artic ground squirrel HBV; TMB HBV: tent making bat hepatitis B virus; RLB HBV: roundleaf bat hepatitis B virus; HSB HBV: horseshoe bat hepatitis B virus; LFB HBV: long-fingered bat hepatitis B virus; AGS HBV: Asian grey shrew HBV; DCHBV: domestic cat HBV; TFo HBV: Taï Forest hepatitis B virus.

| **References:** |
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| Nie FY, Tian JH, Lin XD, Yu B, Xing JG, Cao JH, Holmes EC, Ma RZ, Zhang YZ. Discovery of a highly divergent hepadnavirus in shrews from China. Virology 2019, 531:162-170. doi: 10.1016/j.virol.2019.03.007. Epub 2019 Mar 11. PMID: 30884426.  Aghazadeh M, Shi M, Barrs VR, McLuckie AJ, Lindsay SA, Jameson B, Hampson B, Holmes EC, Beatty JA. A novel hepadnavirus identified in an immunocompromised domestic cat in Australia. Viruses. 2018, 10(5): E269. doi: 10.3390/v10050269. PMID: 29772771; PMCID: PMC5977262  Gogarten JF, Ulrich M, Bhuva N, Garcia J, Jain K, Lee B, Löhrich T, Oleynik A, Couacy-Hymann E, Fuh Neba T, Mishra N, Briese T, Calvignac-Spencer S, Lipkin WI, Leendertz FH. A novel orthohepadnavirus identified in a dead Maxwell's duiker (*Philantomba maxwellii*) in Taï National Park, Côte d'Ivoire. Viruses. 2019, 11(3):E279. doi: 10.3390/v11030279. PMID: 30893858; PMCID: PMC6466360. |