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**

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| --- | --- | --- | --- | --- |
| **Code assigned:** | ***2019.008D*** | | |  |
| **Short title:** Create three newgenera in the 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: | | | | 20 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:** 2019.008D.A.v1.Hepadnaviridae\_3gen.xlsx |

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  With a metagenomic approach using the TP domain of the hepatitis B virus P-gene as search query in the NCBI public databases a new clade of teleost viruses has been identified. These share many features with hepadnaviruses and are therefore considered a sister family to this family (Lauber et al., 2017).They were designated as nackednaviruses, a name given due to their absence of an envelop considered a fundamental difference in level of organisation. We propose provisionally the name *Nudnaviridae* for this family, in agreement with the use of Latin to designate viral families.  By rooting the hepadnavirus phylogenetic tree with the recently described members of the provisional family *Nudnaviridae* and using them as outgroup, three new genera within *Hepadnaviridae* have been identified.  These new genera are proposed to be named *Herpetohepadnavirus*, *Metahepadnavirus* and *Parahepadnavirus,* respectively. *Herpetohepadnavirus* comprise reptilian and frog viruses (Gilbert el al., 2014). Members of both *Meta-* and *Parahepadnavirus* are teleostviruses as are those of the provisional *Nudnaviridae*. The majority of viruses in these genera have been identified by the metagenomic approaches. Only the bluegill and white sucker viruses have been found in the “wild” (Dill et al., 2016). For these viruses, TPs have previously been written and they have been approved by ICTV as unassigned species in the family of *Hepadnaviridae*. Now, they are proposed to be the type species for the presently proposed genera *Meta-* and *Parahepadnavirus*, respectively. For *Herpetohepadnavirus,* the proposed type species *Tibetan frog hepatitis B virus* has also previously been approved by ICTV as an unassigned species.  *Orthohepadnavirus*  BGHBV (bluegill HBV)  \*IMDV (Chionoraco hamatus HBV)  \*AMDV (Astatotilapia HBV)  \*TMDV (Astyanax mexicanus HBV)  *Avihepadnavirus*  \*SkHBV (Saproscincus basilicus HBV)  \*SLHBV (Scleroporus adleri HBV)  \*TFHBV (Tibetan frog HBV)  WSHBV (White succer HBV)  EENDV (Anguilla anguilla HBV)  KND-Lp1 (Lucania parva HBV)  100  100  100  100  100  74  100  93  87  72  100  100  *Meta-*  *hepadnavirus*  *Herpeto-*  *hepadnavirus*  *Parahepadnavirus*  Nudnaviridae |

Phylogenetic tree of the polymerase gene sequences of members of the *Hepadnaviridae* family based on Beast analysis using two members belonging to the proposed new family *Nudnaviridae* as outgroup. The tree was obtained by maximum likelihood with bootstrap of 1,000 replicas. The bootstrap values are given at the branches. The new suggested genera are given at the nodes. Type species in respective genus is marked in red. Species identified by metagenomics are marked with asterisk. Abbreviations; IMDV: ice fish metahepadnavirus, AMDV: Astatotilapia metahepadnavirus, TMDV: Tetra metahepadnavirus, SkHBV: skink hepatitis B virus, SLHBV: spiny lizard hepatitis B virus, EENDV: European eel nudnavirus, KND-Lp1: Killifish nudnavirus strain Lp1.

| **References:** |
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| Dill JA, Camus AC, Leary JH, Di Giallonardo F, Holmes EC, Ng TF. Distinct viral lineages from fish and amphibians reveal the complex evolutionary history of hepadnaviruses. J Virol. 2016, 90:7920-33. doi:10.1128/JVI.00832-16. PMID: 27334580; PMCID: PMC4988138.  Gilbert C, Meik JM, Dashevsky D, Card DC, Castoe TA, Schaack S. Endogenous hepadnaviruses, bornaviruses and circoviruses in snakes. Proc Biol Sci. 2014, 281 (1791):20141122. doi: 10.1098/rspb.2014.1122. PMID: 25080342; PMCID: PMC4132678.  Lauber C, Seitz S, Mattei S, Suh A, Beck J, Herstein J, Börold J, Salzburger W, Kaderali L, Briggs JAG, Bartenschlager R. Deciphering the origin and evolution of hepatitis B viruses by means of a family of non-enveloped fish viruses. Cell Host Microbe. 2017, 22 (3):387-399.e6. doi: 10.1016/j.chom.2017.07.019. PMID: 28867387; PMCID: PMC5604429. |