

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

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| **Code assigned:** | **to be assigned by ICTV officers** |  |
| **Short title:**  (1) Rename all currently listed viral species of the family Orthohepadnaviridae to the binominal nomenclature  (2) Introduce 7 new virus species in the genus Orthohepadnavirus and 2 new species in the genus Avihepadnavirus. | | |
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**Author(s) and email address(es)**

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**Corresponding author**

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**List the ICTV Study Group(s) that have seen this proposal**

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| --- |
| ICTV study group Hepadnaviridae |

**ICTV Study Group comments and response of proposer**

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| --- |
| The ICTV study group Hepadnaviridae core group (Glebe D, Drexler JF, Kramvis A together with external scientist Lehmann F) made the initial proposal that was discussed and voted within the whole ICTV study group (11 members, all 7 active members named in the authors list above agreed upon the proposal, while 4 members did not respond to the proposal and the voting at all). |

**ICTV Study Group votes on proposal**

|  |  |  |  |
| --- | --- | --- | --- |
| **Study Group** | **Number of members (11)** | | |
| **Votes support** | **Votes against** | **No vote** |
| Hepadnaviridae | 7 | 0 | 4 |

**Authority to use the name of a living person**

|  |  |
| --- | --- |
| **Is any taxon name used here derived from that of a living person (Y/N)** | N |

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| --- | --- | --- |
| **Taxon name** | **Person from whom the name is derived** | **Permission attached (Y/N)** |
|  |  |  |

**Submission dates**

|  |  |
| --- | --- |
| Date first submitted to SC Chair | 06/14/2023 |
| Date of this revision (if different to above) |  |

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

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**Part 2:** **NON-TAXONOMIC PROPOSAL**

**Text of proposal**

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**Part 3:** **TAXONOMIC PROPOSAL**

**Name of accompanying Excel module**

|  |
| --- |
| 2023.014N.v1.1\_Hepadnaviridae\_19renam\_9nsp.xlsx |

**Abstract**

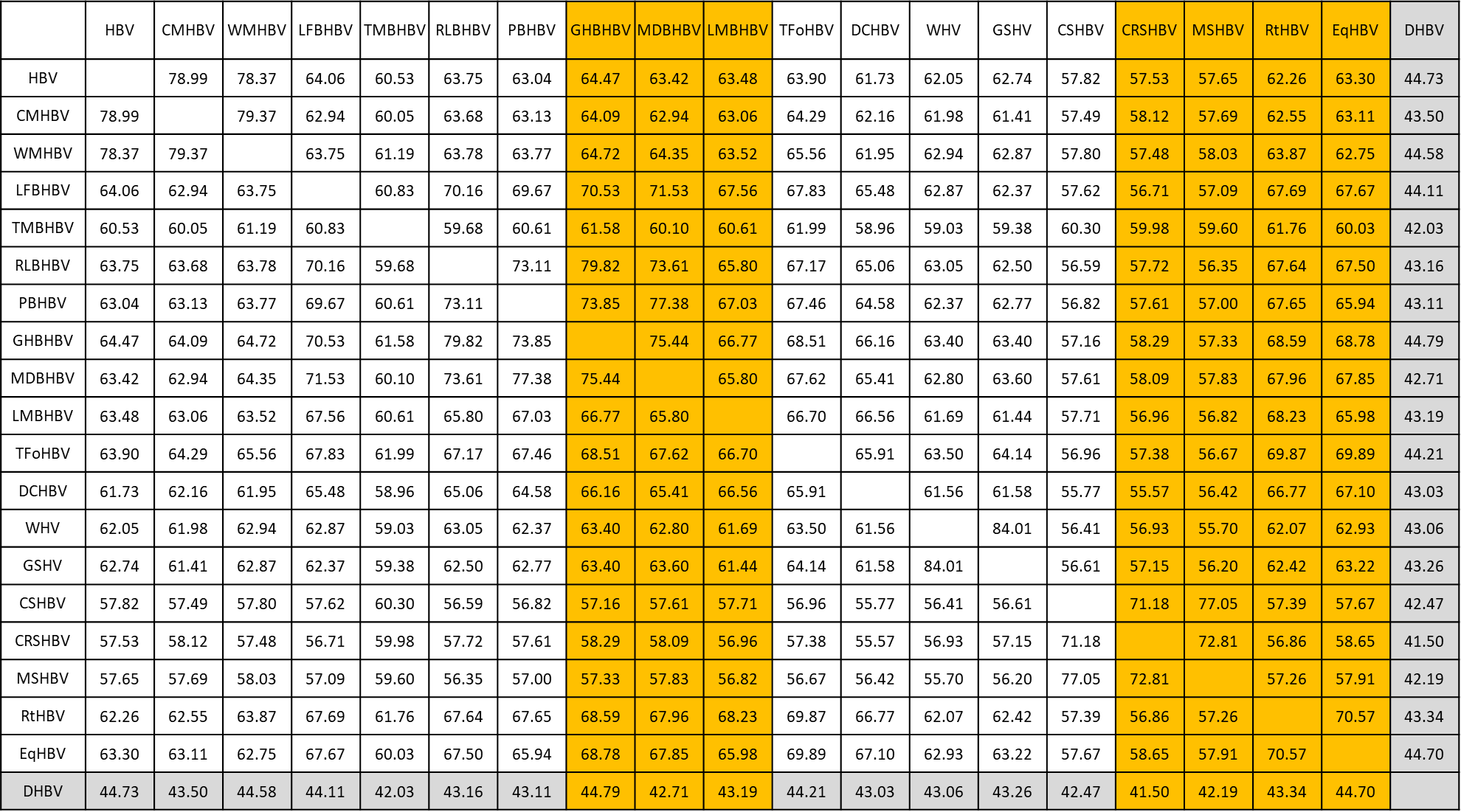
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| Here we propose: **(1) Binominal naming** of all currently ICTV-assigned viral species of the family Hepadnaviridae to; (**2)** Introduction of **7 new species** in the genus Orthohepadnavirus and **2 new species** in the genus Avihepadnavirus. The transformation of **known viral species** to binominal names was done for the known genera: Orthohepadnavirus (12 species), Avihepadnavirus (3), Herpetohepadnvirus (1), Metahepadnavirus (1), Parahepadnavirus (1). The introduction of the **7 new species** in the genus Orthohepadnavirus and **2 new species** in the genus Avihepadnavirus was done according to the species demarcation criteria in the family Hepadnaviridae of more than 20% nucleotide sequence divergence of complete genomes (including information on cross-infectivity, if available). More than 20% nucleotide sequence divergence of complete genomes (and Genbank listed) was fulfilled for all new virus species. Genus **Orthohepadnavirus** contains now **19 recognized virus species** and the genus **Avihepadnavirus** **5 recognized virus species**. There was no change within the other genera. |

**Text of proposal**

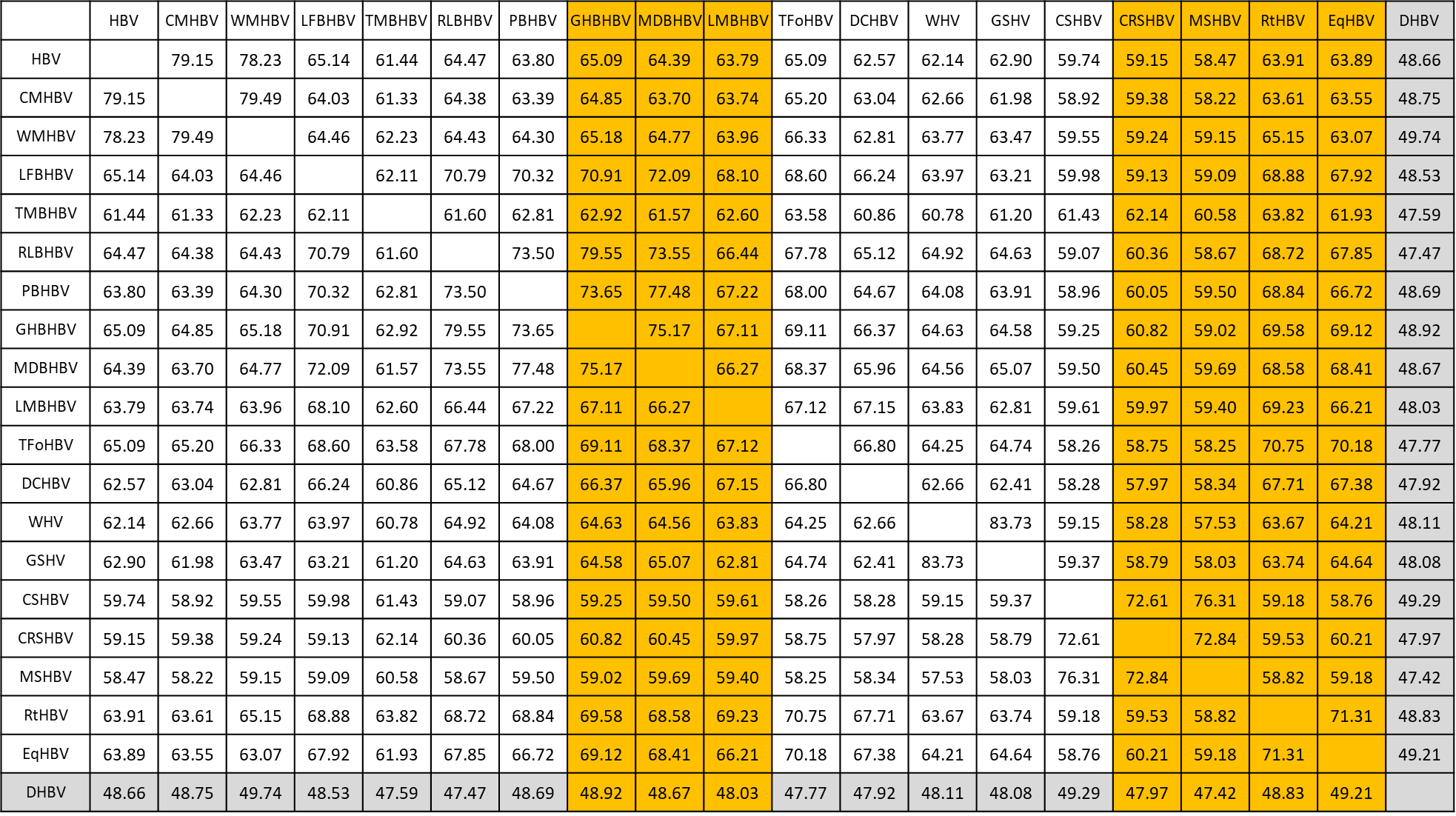
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Renaming of all currently ICTV-assigned viral species of Hepadnaviridae**  The transformation of known species to binominal names was done for the known Genera: Orthohepadnavirus (12 species), Avihepadnavirus (3), Herpetohepadnvirus (1), Metahepadnavirus (1), Parahepadnavirus (1). The description of the chosen binominal names is indicated in the accompanying Excel-Sheet.  **2. Introduction of 7 new species in the genus Orthohepadnavirus and 2 new species in the order Avihepadnavirus (all complete virus genomes and GenBank listed).**  The species demarcation criteria in the genera Orthohepadnavirus and Avihepadnavirus is more than 20% nucleotide sequence divergence of complete genomes and was fulfilled for all new virus species. The description of the chosen binominal names is indicated in the accompanying Excel-Sheet.  **2.1. New species in the genus Orthohepadnavirus**  2.1.1. ***Orthohepadnavirus magniferrequini*** from “Bat Hepatitis B virus isolate Jiyuan-Rf-11”, GenBank: KY962687 from the bat species *Rhinolophus ferrumequinum,* trivial name “Greater Horseshoe Bat”. (Nie et al., Virology 514, 88-97 (2018). The virus was named “Greater Horseshoe Bat Hepatitis B Virus”, abbreviation: **GHBHBV**.  The virus has 57-79% nucleotide sequence identity to all other Orthohepadnavirus species.  2.1.2. ***Orthohepadnavirus myominrhinus***from “Bat Hepatitis B virus isolate Guizhou-Md-295”, GenBank: KY9662683 from the bat species *Myotis davidii,* trivial name “David's Myotis” (Nie et al., Virology 514, 88-97 (2018). The virus was named “Myodav bat hepatitis B virus”. Virus abbreviation: **MDBHBV**.  The virus has 57-77% nucleotide sequence identity to all other Orthohepadnavirus species.  2.1.3. ***Orthohepadnavirus magnimyotis*** from “Longquan Myotis chinensis orthohepadnavirus 1 isolate LQB\_ZhongShu” GenBank: OM030297 from the bat species *Myotis chinensis*, trivial name. “Large Myotis” via direct submission to GenBank. The virus was named: “Large myotis bat hepatitis B virus”, Virus abbreviation: **LMBHBV**.  The virus has 57-68% nucleotide sequence identity to all other Orthohepadnavirus species.  2.1.4. ***Orthohepadnavirus soricicoronati*** from “Crowned shrew hepatitis B virus isolate GF2139” GenBank: MK345465 from the shrew species *Sorex coronatus*, trivial name: “Crowned shrew” (Rasche et al., 2019). The virus was named: “Crowned shrew hepatitis B virus”, Virus abbreviation: **CRSHBV**.  The virus has 55-72% nucleotide sequence identity to all other Orthohepadnavirus species.  2.1.6. ***Orthohepadnavirus soriciodoris*** from “Musk shrew hepatitis B virus isolate CIV-304” GenBank: MK345463 from the shrew species *Crocidura olivieri*, trivial name: “Musk shrew” (Rasche et al., 2019). The virus was named: “Musk shrew hepatitis B virus”, Virus abbreviation: **MSHBV**.  The virus has 55-77% nucleotide sequence identity to all other Orthohepadnavirus species.  2.1.6. ***Orthohepadnavirus bassarisci*** from “Ringtail hepadnavirus isolate CO-09/924” GenBank: MZ393519 from the ringtail species *Bassariscus astutus*, trivial name: “Ringtail” (Jo et al., 2021). The virus was named: “Ringtail hepatitis B virus”, Virus abbreviation: **RtHBV**.  The virus has 57-70% nucleotide sequence identity to all other Orthohepadnavirus species.  2.1.7. ***Orthohepadnavirus equidae*** from “Equine hepatitis B virus isolate doneky86” GenBank: MT134309 from the donkey species *Equus asinus*, trivial name: “domestic donkey” (Rasche et al., 2021). The virus was named: “Equine hepatitis B virus”, Virus abbreviation: **EqHBV**, because the virus species was also found in zebras (*Equus quagga*).  The virus has 57-70% nucleotide sequence identity to all other Orthohepadnavirus species.  **Genus Orthohepadnavirus**  Now 19 recognized virus species in 7 animal orders  Primates: 3; Chiroptera: 7; Artiodactyla: 1, Perissodactyla: 1, Carnivora: 2, Rodentia: 2, Eulipotyphla:3  **Overview of the genus Orthohepadnavirus**   |  |  |  |  |  | | --- | --- | --- | --- | --- | | **No** | **Species name** | **Virus** | **New** | **Host order** | | 1 | *Orthohepadnavirus hominoidei* | HBV chHBV giHBV goHBV orHBV | - | Primates | | 2 | *Orthohepadnavirus sapaji* | CMHBV | - | Primates | | 3 | *Orthohepadnavirus lagothricis* | WMHBV | - | Primates | |  |  |  |  |  | | 4 | *Orthohepadnavirus longidigiti* | LFBHBV | - | Chiroptera | | 5 | *Orthohepadnavirus tabernarii* | TMBHBV | - | Chiroptera | | 6 | *Orthohepadnavirus rotundifolii* | RLBHBV, HSBHBV | - | Chiroptera | | 7 | *Orthohepadnavirus pomi* | PBHBV | - | Chiroptera | | 8 | *Orthohepadnavirus magniferrequini* | GHBHBV | new | Chiroptera | | 9 | *Orthohepadnavirus myominrhinus* | MDBHBV | new | Chiroptera | | 10 | *Orthohepadnavirus magnimyotis* | LMBHBV | new | Chiroptera | |  |  |  |  |  | | 11 | *Orthohepadnavirus philantombae* | TFoHBV | - | Artiodactyla | | 12 | *Orthohepadnavirus equidae* | EqHBV | new | Perissodactyla | |  |  |  |  |  | | 13 | *Orthohepadnavirus felisdomestici* | DCHBV | - | Carnivora | | 14 | *Orthohepadnavirus bassarisci* | RtHBV | new | Carnivora | |  |  |  |  |  | | 15 | *Orthohepadnavirus marmotae* | WHV | - | Rodentia | | 16 | *Orthohepadnavirus sciuri* | GSHV (ASHV) | - | Rodentia | |  |  |  |  |  | | 16 | *Orthohepadnavirus soricisinensis* | CSHBV | - | Eulipotyphla | | 18 | *Orthohepadnavirus soricicoronati* | CRSHBV | new | Eulipotyphla | | 19 | *Orthohepadnavirus soriciodoris* | MSHBV | new | Eulipotyphla | |  |  |  |  |  |   Still unclassified: ASHV, Arctic Squirrel hepatitis B Virus. It is not yet clear, if this virus belongs to WHV or GSHV species.  **2.2. New species in the genus Avihepadnavirus**  2.2.1. ***Avihepadnavirus psittaduorum*** from “Parrot hepatitis B virus isolate P902”, GenBank: JX274018 from the parrot species *Platycercus elegans,* trivial name “Crimson rosella”. (Piasecki et al., Virology 438 (2), 98-105 (2013)). The virus was named “Parrot hepatitis B virus 2”, abbreviation: PHBV2.  The virus has 73-78% nucleotide sequence identity to all other Avihepadnavirus species.  2.2.1. ***Avihepadnavirus bonicursoris*** from “Tinamou hepatitis B virus isolate 160050”, GenBank: KY977507 from the bird species *Eudromia elegans,* trivial name “elegant-crested tinamou”. (Jo et al., EID, 2013). The virus was named “Elegant-crested tinamou hepatitis B virus”, abbreviation: ETHBV.  The virus has 73-76% nucleotide sequence identity to all other Avihepadnavirus species.  **Genus Avihepadnavirus**  Now 5 recognized virus species in 4 animal orders  Anseriformes: 1; Pelecaniformes: 1; Psittaciformes: 2; Tinamiformes: 1  **Overview of the genus Avihepadnavirus**   |  |  |  |  |  |  | | --- | --- | --- | --- | --- | --- | | **No** | **Species name** | **Virus** | **New** | **Host order** |  | | 1 | *Avihepadnavirus anatigruidae* | DHBV SHGHBV SGHBV CHBV RGHBV | - | Anseriformes |  | | 2 | *Avihepadnavirus ciconiardeae* | HHBV STHBV | - | Pelecaniformes |  | | 3 | *Avihepadnavirus psittaunius* | PHBV1 | - | Psittaciformes |  | | 4 | *Avihepadnavirus psittaduorum* | PHBV2 | new | Psittaciformes |  | | 5 | *Avihepadnavirus bonicursoris* | ETHBV | new | Tinamiformes |  |   **Genus Herpetohepadnavirus (no changes)**  1 recognized virus species in 1 animal order:  Anura: 1   |  |  |  |  |  |  | | --- | --- | --- | --- | --- | --- | | **No** | **Species name** | **Virus** | **New** | **Host order** |  | | 1 | *Herpetohepadnavirus nanoranae* | TFHBV | - | Anura |  | |  |  |  |  |  |  |   **Genus Metahepadnavirus (no changes)**  1 recognized virus species in 1 animal order  Perciformes: 1   |  |  |  |  |  |  | | --- | --- | --- | --- | --- | --- | | **No** | **Species name** | **Virus** | **New** | **Host order** |  | | 1 | *Metahepadnavirus lepomi* | BGHBV | - | Perciformes |  | |  |  |  |  |  |  |   **Genus Parahepadnavirus (no changes)**  1 recognized virus species in 1 animal order  Cypriniformes: 1   |  |  |  |  |  |  | | --- | --- | --- | --- | --- | --- | | **No** | **Species name** | **Virus** | **New** | **Host order** |  | | 1 | *Parahepadnavirus osdeorsi* | WSHBV | - | Cypriniformes |  | |  |  |  |  |  |  |   The following species will not be included at this time, but will be when the full GenBank accession number and documentation is available in the near future (this was discussed in a phone call with Chris Lauber on 05/31/2023).  **Notes from the current ICTV website Hepadnaviridae:**  **See:** [**https://ictv.global/report/chapter/hepadnaviridae/hepadnaviridae**](https://ictv.global/report/chapter/hepadnaviridae/hepadnaviridae)  **Genus Herpetohepadnavirus**  Metagenomic sequencing has identified two exogenous hepadnaviruses genetically similar to herpetohepadnavirus (Lauber et al., 2017). One was isolated from a skink (*Saproscinus basilikus*) and designated skink hepatitis B virus (SkHBV), and another from liver from a spiny lizard (*Sceloporus adleri*) and designated spiny lizard hepatitis B virus (SLHBV-1).   |  |  |  | | --- | --- | --- | | **Virus name** | **Accession number** | **Virus abbreviation** | | skink hepatitis B virus | # | SkHBV | | spiny lizard hepatitis B virus | # | SLHBV-1 |   **Genus Metahepadnavirus**  Apart from BGHBV, there are additional virus isolates that may represent three tentative species in the genus. These viruses were identified from teleost fish samples by metagenomic sequencing. These three viruses are: icefish metahepadnavirus (IMDV) from the muscle of crocodile icefish (*Chionodraco hamatus*), Astatotilapia metahepadnavirus (AMDV) from Astatotilapia (*Astatotilapia* sp.) and tetra metahepadnavirus (TMDV) from the eye-surface of Mexican tetra (*Astyanax mexicanus*) (Lauber et al., 2017).   |  |  |  | | --- | --- | --- | | **Virus name** | **Accession number** | **Virus abbreviation** | | Astatotilapia metahepadnavirus | # | AMDV | | icefish metahepadnavirus | # | IMDV | | tetra metahepadnavirus | # | TMDV |   Virus names and virus abbreviations are not official ICTV designations.  #GenBank accession number not available, but the sequence can be obtained from the alignment file associated with Figure 4. *Hepadnaviridae* and provided in the Resources section of this Report.  **Genus Parahepadnavirus**  A virus, CSKV, infecting the Coho salmon (*Oncorhynchus kisutch*) was identified by metagenomic sequencing of the complete genome of the Coho salmon (NC\_034179). However this genome is incomplete, and the regions corresponding to the C-terminal part of the polymerase and the core region are missing. The genome was identified from kidney tissue (Lauber et al., 2017). | |

**Supporting evidence**

**A**

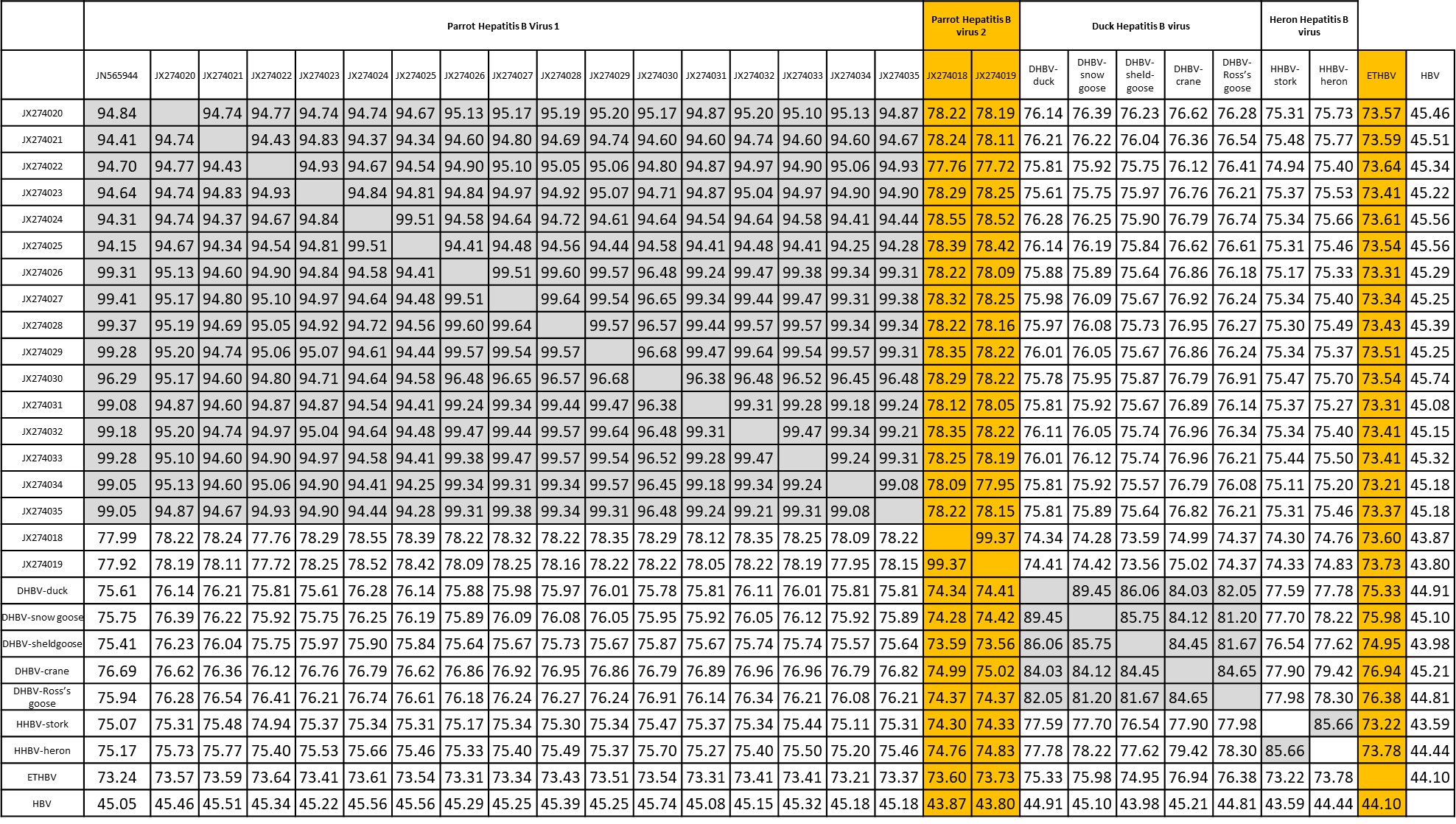


**B**

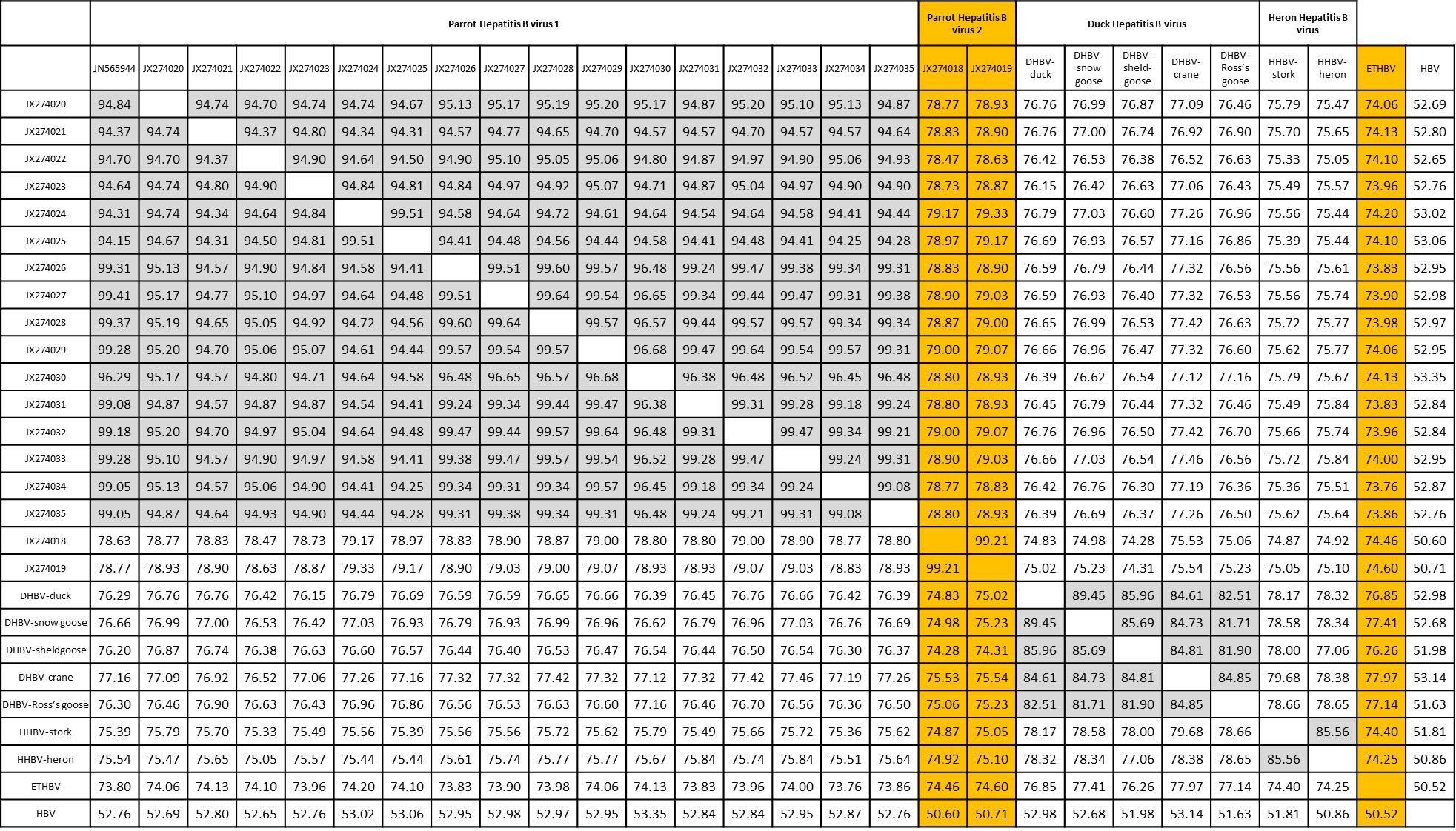
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**Figure 1: Nucleotide identity between the complete genomes of the viral species belonging to the genus Orthohepadnavirus.** Known (white) and new (orange) species of the genus Orthohepadnavirus are listed. The identity matrix (% identity on full genomes) was done with **(A)** MEGA11 and following parameters: boostrap method (1000 bootstraps) p-distance model incl. transitions and transversions, uniform rates of transitions/transversions, pairwise deletion for gaps using MAFFT-(L-INS-i)-Algorithm for alignment, Geneious. **(B)** MEGA11 using the MUSCLE-Algorithm for alignment using MEGA11 with same parameters as (A). All new species meet the criteria of more than 20% nucleotide sequence divergence of complete genomes (GenBank listed) with both algorithm. As shown in the previous ICTV report, WHV and GSHV share 84 % identity, but are regarded as different species, since WHV could not infect the host of GSHV (ground squirrels). ASHV still remains unassigned. The isolate HSBHBV (Horseshoe bat hepatitis B virus) clusters with the master species Roundleaf bat hepatitis B virus (RLBHBV) with a difference of about 20% and is not considered a separate species, as agreed upon in the last ICTV report. The DHBV (grey) of the genus Avihepadnavirus is listed as an outgroup.

**A**



**B**

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**Figure 2: Nucleotide identity between the complete genomes of the viral species belonging to the genus Avihepadnavirus.** Known (white) and new (orange) species of the genus Avihepadnavirus are listed. The identity matrix (% identity on full genomes) was done with **(A)** MEGA11 and following parameters: boostrap method (1000 bootstraps) p-distance model incl. transitions and transversions, uniform rates of transitions/transversions, pairwise deletion for gaps using MAFFT-(L-INS-i)-Algorithm for alignment, Geneious. **(B)** MEGA11 using the MUSCLE-Algorithm for alignment using MEGA11 with same parameters as (A). All new species meet the criteria of more than 20% nucleotide sequence divergence of complete genomes (GenBank listed) with both algorithm. New Parrot virus isolates (Piasecki et al., 2013) cluster either together with previously classified PHBV1 (Piasecki et al., 2012; grey), or form a new species designated “Parrot Hepatitis B virus 2” (PHBV2) The “Elegant-crested tinamou hepatitis B virus” (ETHBV) showed >20 % difference to other species of the genus Avihepadnavirus. ETHBV was not able to infect Peking duck embryos via allantoic cavity or by intravenous infection (Jo et al., 2017). The HBV of the genus Orthohepadnavirus is listed as an outgroup.

**References**

Jo WK, Alfonso-Toledo JA, Salas-Rojas M, Almazan-Marin C, Galvez-Romero G, García-Baltazar A, Obregón-Morales C, Rendón-Franco E, Kühne A, Carvalho-Urbieta V, Rasche A, Brünink S, Glebe D, Aguilar-Setién Á, Drexler JF. Natural co-infection of divergent hepatitis B and C virus homologues in carnivores. Transbound Emerg Dis. 2022 Mar;69(2):195-203. doi: 10.1111/tbed.14340. Epub 2021 Oct 19. PMID: 34606685

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