

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

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| **Code assigned:** | ***2023.035M*** |  |
| **Short title:** Reevaluate and reorganize family *Hantaviridae* (order *Bunyavirales*) | | |
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**Author(s) and email address(es)**

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

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| ICTV *Hantaviridae* Study Group |

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

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**ICTV Study Group votes on proposal**

|  |  |  |  |
| --- | --- | --- | --- |
| **Study Group** | **Number of members** | | |
| **Votes support** | **Votes against** | **No vote** |
| ICTV *Hantaviridae* Study Group | 7 | 0 | 0 |

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

|  |  |
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| **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)** |
| N/A | N/A | N/A |

**Submission dates**

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| Date first submitted to SC Chair | June 23, 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**

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| N/A |

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

**Name of accompanying Excel module**

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| 2023.035M.N.v1.Hantaviridae\_reorg.xlxs |

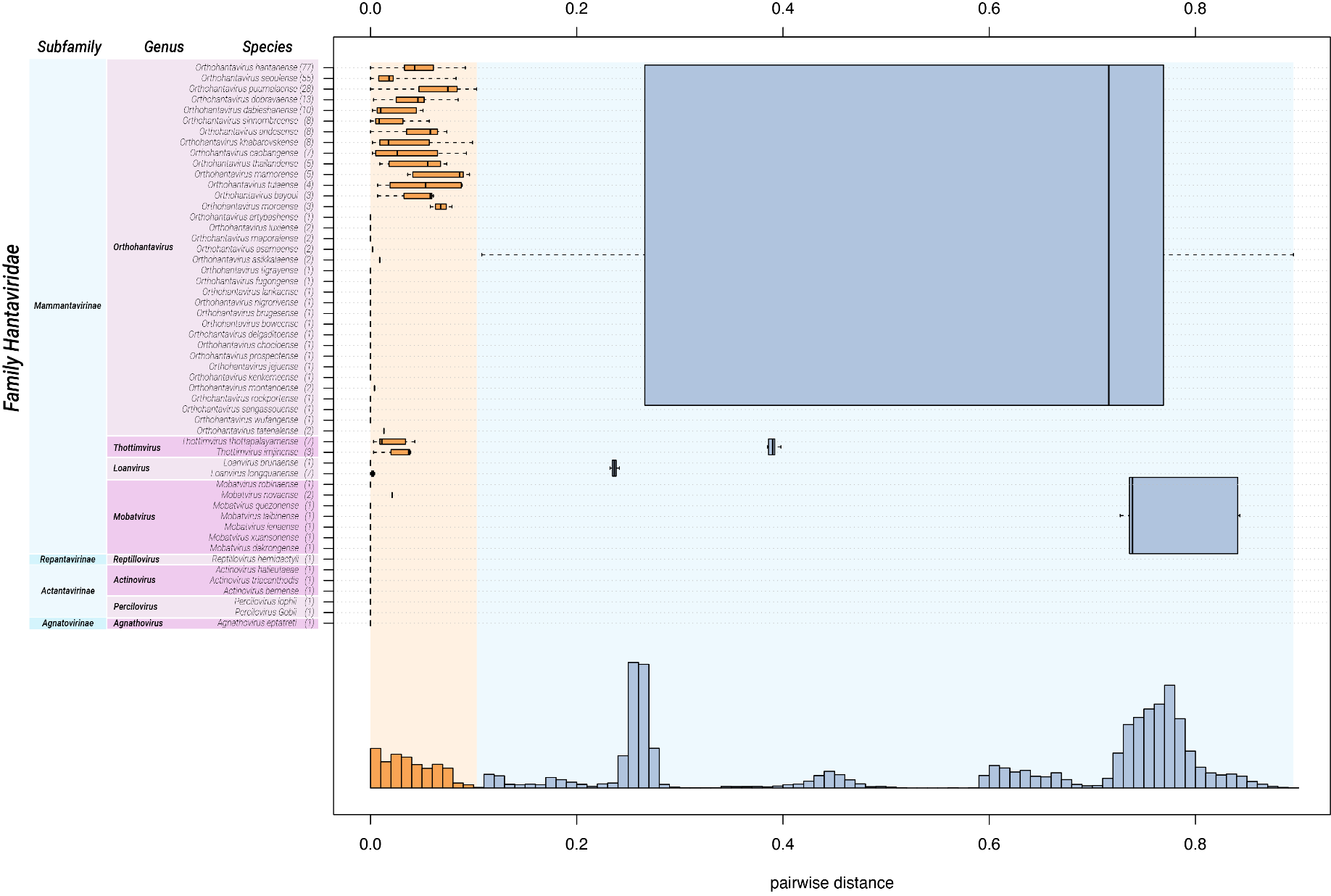
**Abstract**

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| We propose to abolish five established hantavirid species not represented by fully-sequenced viruses; to rename two species after fully sequenced viruses representing them; to establish three new orthohantavirus species for previously unclassified fully sequenced viruses; to move one species from genus *Orthohantavirus* to genus *Mobatvirus*; to establish one new genus with one new species for a novel fish hantavirid and to move one species from genus *Actinovirus* into this new genus; and to remove several “viruses” (isolates of classified viruses) from the ICTV Virus Metadata Resource (VMR) as previously outlined in [7]. |

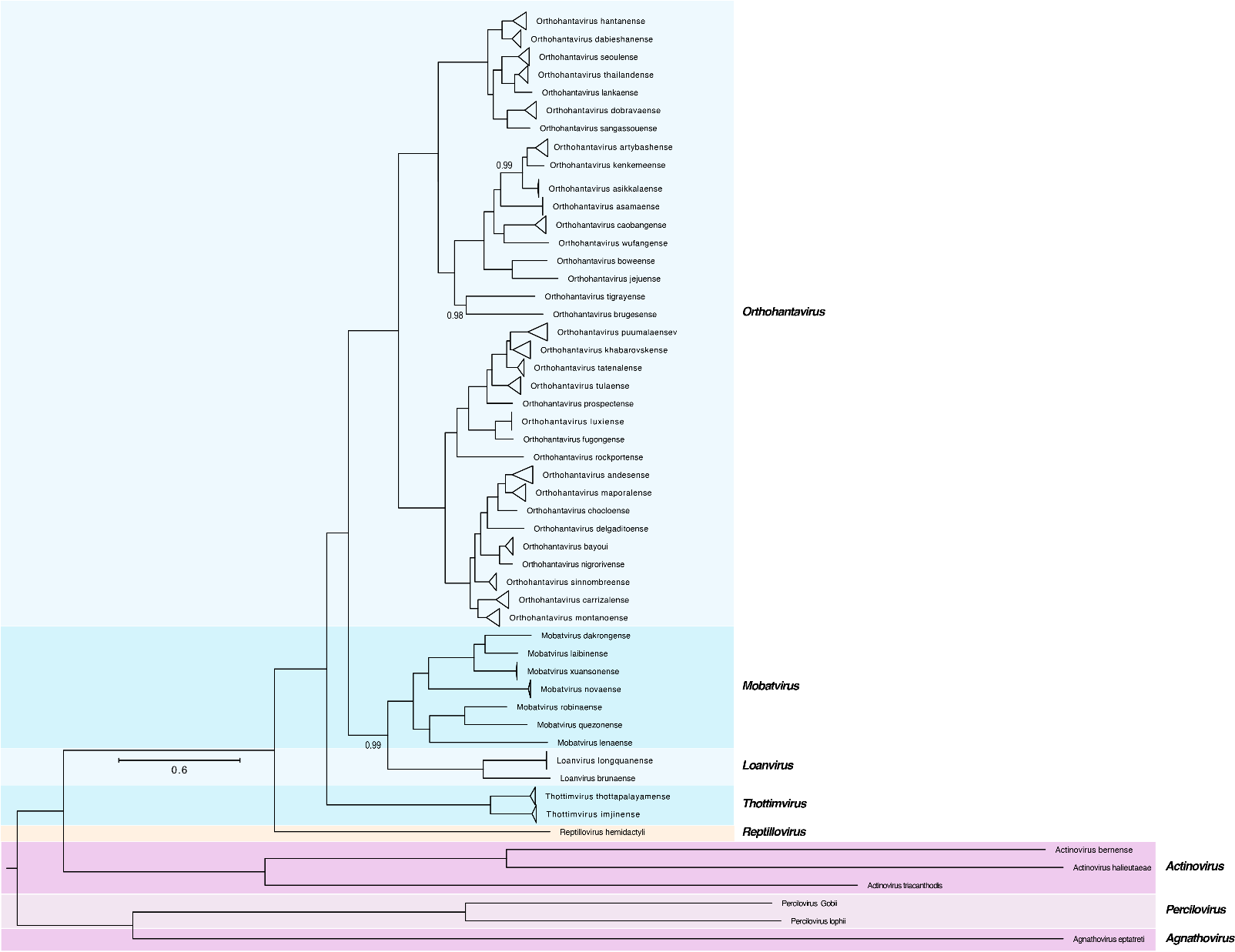
**Text of proposal**

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| |  | | --- | | In 2017, the International Committee on Taxonomy of Viruses (ICTV) permitted official virus classification based only on genomic sequence information as long as that information is coding-complete (i.e., covers all open reading frames) or near-complete (i.e., lacks only very few terminal or internal nucleotide that are difficult to resolve) [11]. Soon after, the ICTV made it a requirement to provide coding-/near-complete genome sequence information via GenBank deposition for exemplar viruses of novel species [10, 12]. However, this decision was prospective, i.e., it applied only to classification of newly discovered or previously unclassified viruses into new taxa. Viruses classified by the ICTV prior to the 2017 decision remained classified even with, in some cases, the complete absence of genomic sequence information. This situation contradicts the ICTV’s goal to “…categorize the multitude of known viruses into a single classification scheme that reflects their evolutionary relationships, i.e., their individual phylogenies” [5, 12].  We recently evaluated the taxonomy of bunyaviral family *Hantaviridae* considering coding-/near-complete genome sequence information [7]. Based on this evaluation, we propose:   1. To abolish the following five orthohantavirus species due to the absence of coding-complete sequence information for their exemplar viruses:  * *Orthohantavirus* *fusongense*; * *Orthohantavirus* *necocliense*; * *Orthohantavirus* *oxbowense*; * *Orthohantavirus* *seewisense*; and * *Orthohantavirus* *yakeshiense*.  1. To remove (“declassify”) the following nine non-exemplar viruses from established species (and the ICTV VMR) due to the absence of coding-complete sequence information for their exemplar viruses (and to consider these “virus” names potential isolates of the remaining exemplar viruses):  * Adler virus (ADLV) from *Orthohantavirus tulaense*; * Castelo dos Sonhos virus (CASV), Lechiguanas virus (LECV = LECHV), and Orán virus (ORNV) from *Orthohantavirus andesense*; * El Moro Canyon virus (ELMCV) from *Orthohantavirus moroense*; * gōu virus (GOUV) from *Orthohantavirus seoulense*; * Laguna Negra virus (LANV) from *Orthohantavirus negraense*; * Liánghé virus (LHEV) from *Orthohantavirus caobangense*; * Serang virus (SERV) from *Orthohantavirus thailandense*;  1. To rename the following two species which currently have confusing names due to the removal of previously name-giving viruses:  * *Orthohantavirus moroense* → *Orthohantavirus carrizalense* (after Carrizal virus [CARV]); and * *Orthohantavirus negraense* → *Orthohantavirus mamorense* (after Rio Mamoré virus [RIOMV]).   Coding-/near-complete genome sequence information is available for several currently unclassified hantavirids [7]:   1. A potential new mobatvirus:  * Đakrông virus [2].  1. Potential new orthohantaviruses:  * Artybash virus [1]; * Jīngmén Rattus norvegicus orthohantavirus 1 [Unpublished]; * Juquitiba virus [Unpublished]; * Lanka virus [9]; * Limestone Canyon virus [Unpublished]; * Monongahela virus [13]; * Rusne virus [3]; * Traemmersee virus [6]; * Ussuri virus [Unpublished]; * Wēnzhōu Niviventer niviventer orthohantavirus 1 [Unpublished]; * Wùfēng Chodsigoa smithii orthohantavirus 1 [Unpublished]; * Xìnyì virus [4];  1. A potential new thottimvirus:  * Wēnzhōu Suncus murinus thottimvirus 1 [Unpublished].  1. A potential new actinovirus:  * Luposicya lupus actinovirus [Unpublished].   To determine the taxonomic placement of these viruses, we re-performed family-wide DivErsity pArtitioning by hieRarchical Clustering (DEmARC) analysis as originally established for this family by the ICTV *Hantaviridae* Study Group [8].  Briefly, all publicly available coding-complete hantavirus genomes (last update June 23, 2023) were downloaded from NCBI GenBank. For each of the sequences the three hantavirus protein (N, M and L) amino acid sequences were deduced and used to construct a concatenated multiple alignment. For this, the sequences of each of the proteins were separately aligned with MAFFT v7.453 (Katoh and Standley, 2013) and trimmed with TrimAl v1.4.rev15 (Capella-Gutièrrez et al, 2009), after which the 3 multiple sequence alignments were concatenated. Bayesian phylogenetic analyses were inferred in BEAST v.1.10.4 (Suchard et al, 2018) using the LG+R10 substitution model and using MCMC with a chain length of 100,000,000 generations using the concatenated (S-M-L) alignment. The Markov chain Monte Carlo analysis was run until an effective samples size higher than 200 was obtained (allowing a burn-in period of 10%). A consensus tree was built with TreeAnnotator v1.10.4 using the maximum clade credibility method. This consensus tree was used as input for DEmARC to calculate a pairwise patristic distance matrix. This matrix was then used to calculate subfamily, genera, and species demarcation.  This analysis (Figures 1 and 2) yielded the following results:   * Đakrông virus represents a new mobatvirus species * Artybash virus, Lanka virus, and Wùfēng Chodsigoa smithii orthohantavirus 1 represent novel orthohantavirus species * Robina virus, currently classified in species *Orthohantavirus robinaense* is a mobatvirus and hence needs to be reclassified as *Mobatvirus robinaense* * “Jīngmén Rattus norvegicus orthohantavirus 1” is an isolate of Seoul virus (and hence the name “Jīngmén Rattus norvegicus orthohantavirus 1” should not be used anymore) * “Juquitiba virus” is an isolate of Andes virus (and hence the name “Juquitiba virus” should not be used anymore). Furthermore, we here discourage the use of the names “Ape Aimé–Itapúa virus”, “Araraquara virus”, “Araucaria virus”, “Bermejo virus”, “Buenos Aires virus”, “Cajuru virus”, “Central Plata virus”, “Hu39694 virus”, “Itapúa virus”, “Jaborá virus”, “Lechiguanas virus”, “Maciel virus”, “Ñeembucu virus”, “Orán virus”, “Paranoá virus”, “Pergamino virus”, and “Tunari virus”, all of which are, based on the available limited sequence information, isolates of Andes virus * "Limestone Canyon virus” is an isolate of Montaño virus (and hence the name “Limestone Canyon virus” should not be used anymore) * Luposicya lupus actinovirus forms a new genus/species (proposed name *Percilovirus gobii*) within subfamily *Actantavirinae* together with Goosefish agnatovirus * Goosefish agnatovirus will moved to the genus *Percilovirus* by moving/renaming *Actinovirus* *lophii* as *Percilovirus* *lophii* * “Monongahela virus” is an isolate of Sin Nombre virus (and hence the name “Monongahela virus” should not be used anymore) * “Rusne virus” is an isolate of Tatenale virus (and hence the name “Rusne virus” should not be used anymore) * “Traemmersee virus” is an isolate of Tatenale virus (and hence the name “Traemmersee virus” should not be used anymore) * “Ussuri virus” is an isolate of Puumala virus (and hence the name “Ussuri virus” should not be used anymore) * “Wēnzhōu Niviventer niviventer orthohantavirus 1” is an isolate of Dabieshan virus (and hence the name “Wēnzhōu Niviventer niviventer orthohantavirus 1” should not be used anymore) * “Wēnzhōu Suncus murinus thottimvirus 1” is an isolate of Thottapalayam virus (and hence the name “Wēnzhōu Suncus murinus thottimvirus 1” should not be used anymore) * “Xìnyì virus” is an isolate of Cao Bằng virus (and hence the name “Xìnyì virus” should not be used anymore) | |

**Supporting evidence**



**Figure 1 (see Supplementary File 1 for original size)**: Intra-family genetic divergence in three-level hierarchical clustering of hantaviruses by DEmARC (version 1.4). Ranks are defined by the three strongest PED thresholds. The number of viruses in the identified clusters are shown in brackets. All identified clusters correspond to monophyletic groups. Box-and-whisker graphs were used to plot distributions of distances between viruses from the same species (orange), and between viruses from different species but the same genus, and between viruses from different genera but the same family (blue). The boxes span from the first to the third quartile and include the median (bold line), and the whiskers (dashed lines) extend to the extreme values. The corresponding part of the PED distribution is shown below.

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**Figure 2 (see Supplementary File 2 for original size)**: Overview of the revised *Hantaviridae* taxonomy matched with a Bayesian maximum clade credibility summary tree. Numbers next to selected nodes indicate the posterior support, which can be interpreted as the probability of the clade being true given the data, the model, and the parameter priors. Only posterior values lower than 1 are shown. The tree is drawn to scale, with branch lengths expressed in the number of substitutions per site.

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