This form should be used for all taxonomic proposals. Please complete all those modules that are applicable.

For guidance, see the notes written in blue and the separate document “Help with completing a taxonomic proposal”

Please try to keep related proposals within a single document.

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

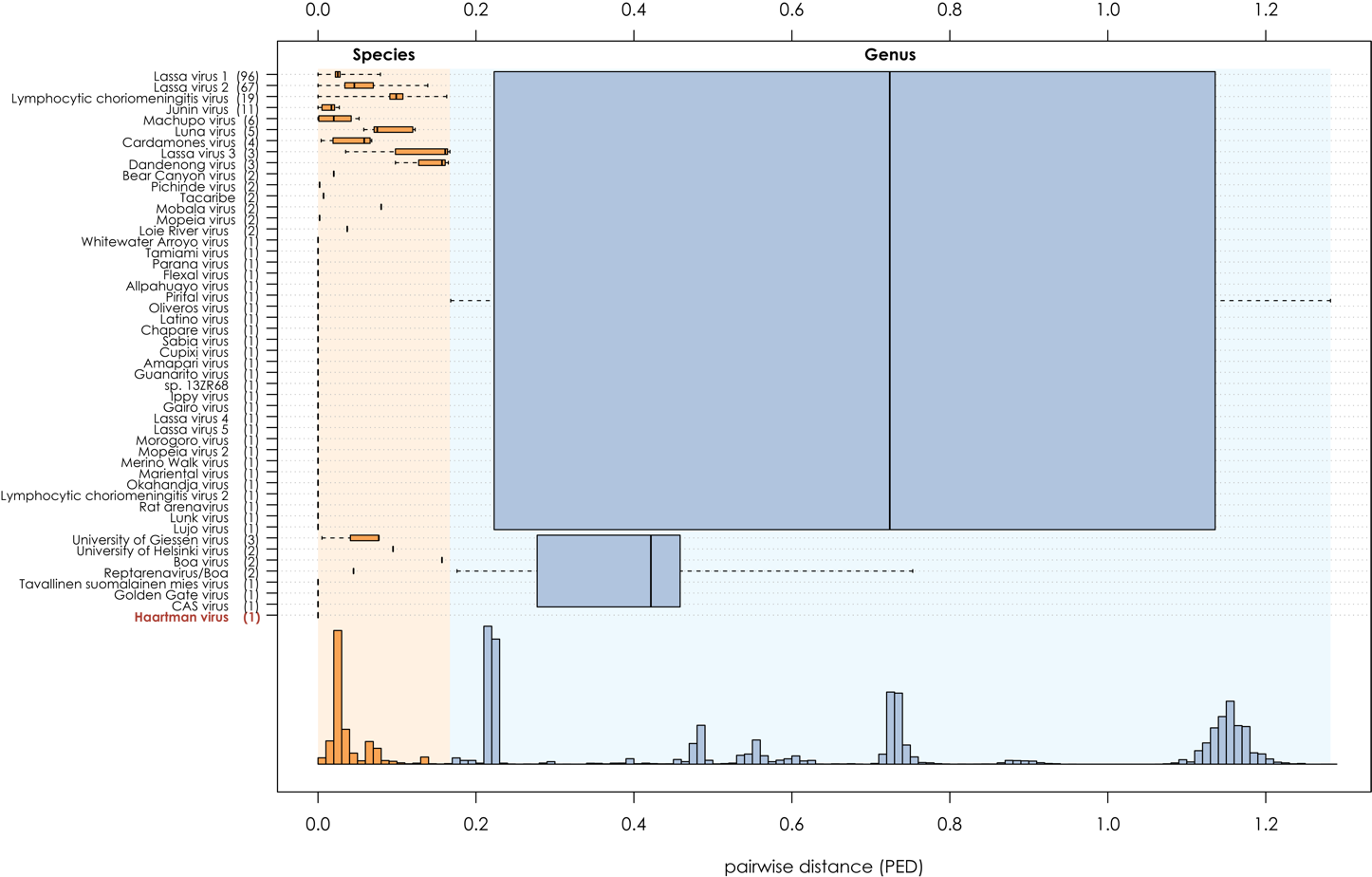
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| --- | --- | --- | --- | --- | --- |
| **Code assigned:** | ***2017.001M*** | | | | (to be completed by ICTV officers) |
| **Short title: One (1) new genus including one (1) new species in the family *Arenaviridae*** | | | | | |
| **Modules attached**  (Modules 1, 4 and either 2 or 3 are required. | | **1**  **2  3  4** | | | |
| **Author(s):** | | | | | |
| Jussi Hepojoki  Pertteli Salmenperä  Tarja Sironen  Udo Hetzel  Yegor Korzyukov  Anja Kipar  Olli Vapalahti  Piet Maes  and the ICTV *Arenaviridae* Study Group:  Buchmeier, Michael J., m.buchmeier@uci.edu  Charrel, Rémi, remi.charrel@univ-amu.fr  Clegg, Christopher S., cleggjcs@yahoo.fr  de la Torre, Juan Carlos, juanct@scripps.edu  DeRisi, Joseph L., joe@derisilab.ucsf.edu  Emonet, Sébastien, sebastien.emonet@irba.fr  Gonzalez, Jean-Paul, jpgonzalez2808@gmail.com  Kuhn, Jens H., kuhnjens@mail.nih.gov  Lukashevich, Igor S., isluka01@louisville.edu  Peters, Clarence J., cj.cj.peters@gmail.com  Radoshitzky, Sheli R., sheli.r.radoshitzky.ctr@mail.mil  Romanowski, Victor, vromanowski@gmail.com  Salvato, Maria S., msalvato@ihv.umaryland.edu  Stenglein, Mark D., mark.stenglein@colostate.edu | | | | | |
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| **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) | | | **ICTV *Arenaviridae* Study Group** | | |
| **ICTV Study Group comments (if any) and response of the proposer:** | | | | | |
|  | | | | | |
|  | | | | | |
| Date first submitted to ICTV: | | | | June 8, 2017 | |
| Date of this revision (if different to above): | | | |  | |

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

**Part 2**: **PROPOSED TAXONOMY**

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| Haartman Institute snake virus (HISV) was discovered by next-generation sequencing (NGS) in a captive German boa constrictor (*Boa constrictor*) in Helsinki, Finland (snake #11 in Hetzel *et al*.). HISV was isolated in boid I/1K cells (Hetzel *et al*.) and its genome was completely sequenced and deposited into GenBank (Hepojoki *et al*. published and personal communication). After the initial report (Hepojoki *et al*.), a pure preparation of HISV (initially existing in a mixture with University of Helsinki virus 2 [UHV-2]) was produced and re-analyzed by NGS. Based on NGS and sequencing of the L and S segment termini, the HISV genome is complete in terms of ORF/coding regions (unpublished data/manuscript in preparation). The genomic termini of both L and S segments of HISV form “arenavirus-like” panhandles, suggesting that no additional ORFs exist (unpublished data/manuscript in preparation). Furthermore, since NGS of cell-culture produced virus did not provide evidence for existence of a third segment, HISV seems to lack a gene encoding the Z protein (unpublished data/manuscript in preparation). HISV can be grown in clean cell culture i.e. without co-infecting “helper” reptarenaviruses (unpublished data/manuscript in preparation).  The ICTV *Arenaviridae* Study Group has recommended the use of the PAirwise Sequence Comparison (PASC) tool (<https://www.ncbi.nlm.nih.gov/sutils/pasc/viridty.cgi?textpage=overview>) for the assessment of novel arenaviruses (Radoshitzky *et al*.). Cut-off values chosen for classifying arenaviruses belonging to the same species using this tool are >80% and >76% nucleotide sequence identity in the S and L segments, respectively. Cut-off values chosen for classifying arenaviruses belonging to the same genus using this tool are >29-40% and >30-35% nucleotide sequence identity in the S and L segments, respectively. We therefore performed PASC on HISV. The closest PASC hit for the HISV L segment is Amaparí virus (*Amapari mammarenavirus*, GenBank AY924389.1) with 18.53% pairwise identity (i.e. less than 30-35%), thereby justifying the creation of a novel genus and species.  C:\Users\kuhnjens\Desktop\HISV L.JPG  The closest PASC hit for the HISV S segment is Lassa virus (*Lassa mammarenavirus*, GenBank #AB627952.1) with 18.25% pairwise identity (i.e. less than 29-40%), confirming the need for a new mammarenavirus genus and species.  C:\Users\kuhnjens\Desktop\S.JPG  To further confirm the taxonomic position of HISV, Bayesian phylogenetic analyses were inferred in BEAST2 employing 6 independent MCMC runs with a chain length of 50,000,000 generations using concatenated coding-complete arenavirus genomes (polymerase+glycoprotein+nucleocapsid). Tree and log files of independent runs of BEAST were combined using LogCombiner 2.4.5, employing a Burn-in period of 10%. The Markov chain Monte Carlo analyses were run until effective sample sizes above 200 were obtained. A consensus tree was built with TreeAnnotator 2.4.5 using the maximum clade credibility method and visualized in FigTree v1.4.0 (Figure 3).    **Figure 3**: Maximum clade credibility summary tree representations estimated from concatenated polymerase, glycoprotein and nucleocapsid amino acid sequences. 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. The tree is drawn to scale, with branch lengths expressed in the number of substitutions per site. *Arenaviridae* species are presented in blue, genera in purple, and putative new taxa in beige. The HISV branch is highlighted in red.  The establishment of a new genus is further substantiated by DEmARC analysis (version 1.0, Figure 4). Several PED thresholds (clustering cost of zero, CC=0 and monophyletic clustering under these thresholds in the Bayesian maximum clade credibility summary tree) were identified and represent clear thresholds for *Arenaviridae* species and genera delimitation (0.17 for species and 1.3 for genus). |
| **Name of accompanying spreadsheet: 2017.001M.N.v1.Hartmanivirus** |

Please display the taxonomic changes you are proposing on the accompanying spreadsheet module 2017\_TP\_Template\_Excel\_module. Submit both this and the spreadsheet to the appropriate ICTV Subcommittee Chair.



**Figure 4**: Intra-family genetic divergence using hierarchical clustering by DEmARC (version 1.0). Levels are defined by strict PED thresholds. The number of sequences in the identified clusters are shown in brackets. All identified clusters have a clustering cost of zero and correspond to monophyletic groups in the MCMC tree of Figure 3. 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 (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

**Part 4:** **APPENDIX**: supporting material

| additional material in support of this proposal |
| --- |
| **References:** |
| [Arenavirus Coinfections Are Common in Snakes with Boid Inclusion Body Disease.](https://www.ncbi.nlm.nih.gov/pubmed/26041290)  Hepojoki J, Salmenperä P, Sironen T, Hetzel U, Korzyukov Y, Kipar A, Vapalahti O.  J Virol. 2015 Aug;89(16):8657-60. doi: 10.1128/JVI.01112-15. Epub 2015 Jun 3.  PMID: 26041290  [Isolation, identification, and characterization of novel arenaviruses, the etiological agents of boid inclusion body disease.](https://www.ncbi.nlm.nih.gov/pubmed/23926354)  Hetzel U, Sironen T, Laurinmäki P, Liljeroos L, Patjas A, Henttonen H, Vaheri A, Artelt A, Kipar A, Butcher SJ, Vapalahti O, Hepojoki J.  J Virol. 2013 Oct;87(20):10918-35. doi: 10.1128/JVI.01123-13. Epub 2013 Aug 7.  PMID: 23926354  [Past, present, and future of arenavirus taxonomy.](https://www.ncbi.nlm.nih.gov/pubmed/25935216)  Radoshitzky SR, Bào Y, Buchmeier MJ, Charrel RN, Clawson AN, Clegg CS, DeRisi JL, Emonet S, Gonzalez JP, Kuhn JH, Lukashevich IS, Peters CJ, Romanowski V, Salvato MS, Stenglein MD, de la Torre JC.  Arch Virol. 2015 Jul;160(7):1851-74. doi: 10.1007/s00705-015-2418-y.  PMID: 25935216 |