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:** | ***2017.015M*** | | | | (to be completed by ICTV officers) |
| **Short title: Two (2) new species in the genus *Reptarenavirus* (*Arenaviridae*) and renaming of three (3) species** | | | | | |
| **Modules attached**  (Modules 1, 4 and either 2 or 3 are required. | | **1**  **2  3  4** | | | |
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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:** | | | | | |
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|  | | | | | |
| 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:** |
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**Part 2**: **PROPOSED TAXONOMY**

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| --- |
|  |
| **Name of accompanying spreadsheet: 2017.015M.N.v1.Reptarenavirus\_2sp3ren** |

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.

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

The genus *Reptarenavirus* (*Arenaviridae*) was established in 2015 to accommodate highly divergent snake arenaviruses. The genus includes three species for Golden Gate virus (*Alethinophid 1 reptarenavirus*), CAS virus (*Alethinophid 2 reptarenavirus*) and ROUT and University of Helsinki viruses (*Alethinophid 3 reptarenavirus*) (TP 2014.011a-dV, “Create a new genus, *Reptarenavirus*, comprising three new species in the family *Arenaviridae*”) ([1-3](#_ENREF_1)). Discovery of new reptarenaviruses has since accelerated considerably ([4-9](#_ENREF_4)). Reptarenaviruses appear to reassort their S and L genomic segments rather frequently ([9](#_ENREF_9)) and non-equimolar ratios of divergent S and L segments can often be found in the same infected snake individual ([9](#_ENREF_9)). There is currently no consensus on how to address these viruses taxonomically. However, at least four novel reptarenaviruses, Tavallinen suomalainen mies virus 2 (TSMV-2) and University of Giessen viruses 1–3 (UGV-1–3) ([4](#_ENREF_4)), are classifiable by the reptarenavirus classification standards established in TP 2014.011a-dV because their S and L genomic segments are unique and have not been found in reassortants.

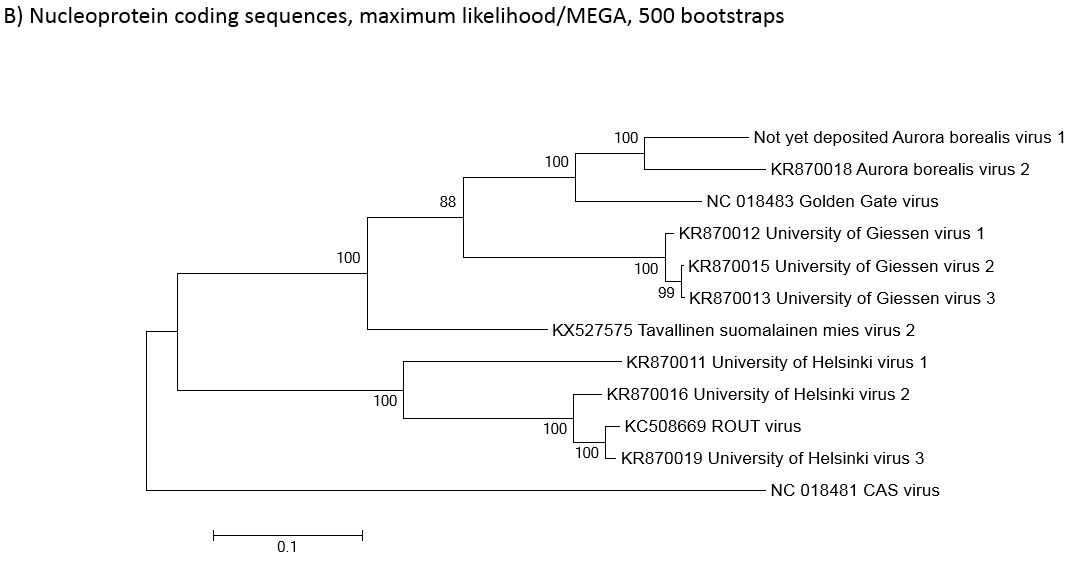
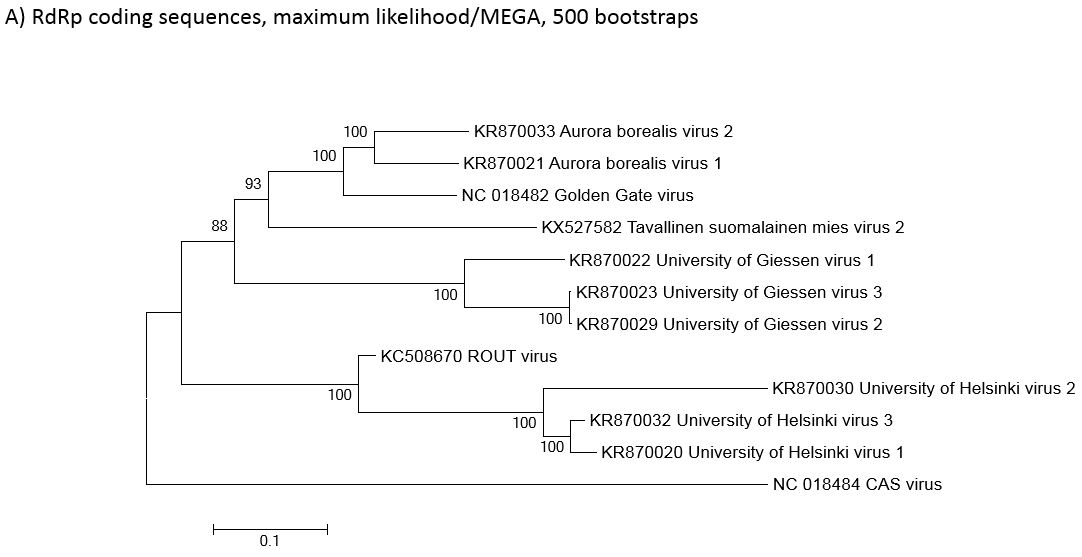
The ICTV *Arenaviridae* Study Group has recommended the use of the PAirwise Sequence Comparison (PASC) tool (<https://www.ncbi.nlm.nih.gov/sutils/pasc/viridty.cgi?textpage=overview>) for the assessment of novel arenaviruses ([1](#_ENREF_1)). Cut-off values chosen for classifying reptarenaviruses belonging to the same species using this tool are >80% and >76% nucleotide sequence identity in the S and L segments, respectively. We therefore performed PASC on TSMV-2 and UGV-1–3.

The closest PASC hit for the TSMV-2 L segment is Golden Gate virus (*Alethinophid 1 reptarenavirus*, GenBank #JQ717263) with 71% pairwise identity (i.e. less than 76%), thereby justifying the creation of a novel species. The closest PASC hit for the TSMV-2 S segment is Golden Gate virus (*Alethinophid 1 reptarenavirus*, GenBank #JQ717264) with 75% pairwise identity (i.e. less than 80%), thereby justifying the creation of a novel species.

UGV-1-3 cluster tightly together. The closest PASC hit for the UGV-1 L segment is Golden Gate virus (*Alethinophid 1 reptarenavirus*, GenBank #JQ717263) with 68% pairwise identity (i.e. less than 76%), thereby justifying the creation of a novel species for all three viruses. The closest PASC hit for the UGV-1 S segment is Golden Gate virus (*Alethinophid 1 reptarenavirus*, GenBank #JQ717264) with 75% pairwise identity (i.e. less than 80%), thereby justifying the creation of a novel species for all three viruses.

Phylogenetic analysis of the reptarenavirus RNA-dependent RNA polymerase (RdRp) and nucleoprotein (NP) coding sequences confirm the PASC results (Figure 1A and 1B).

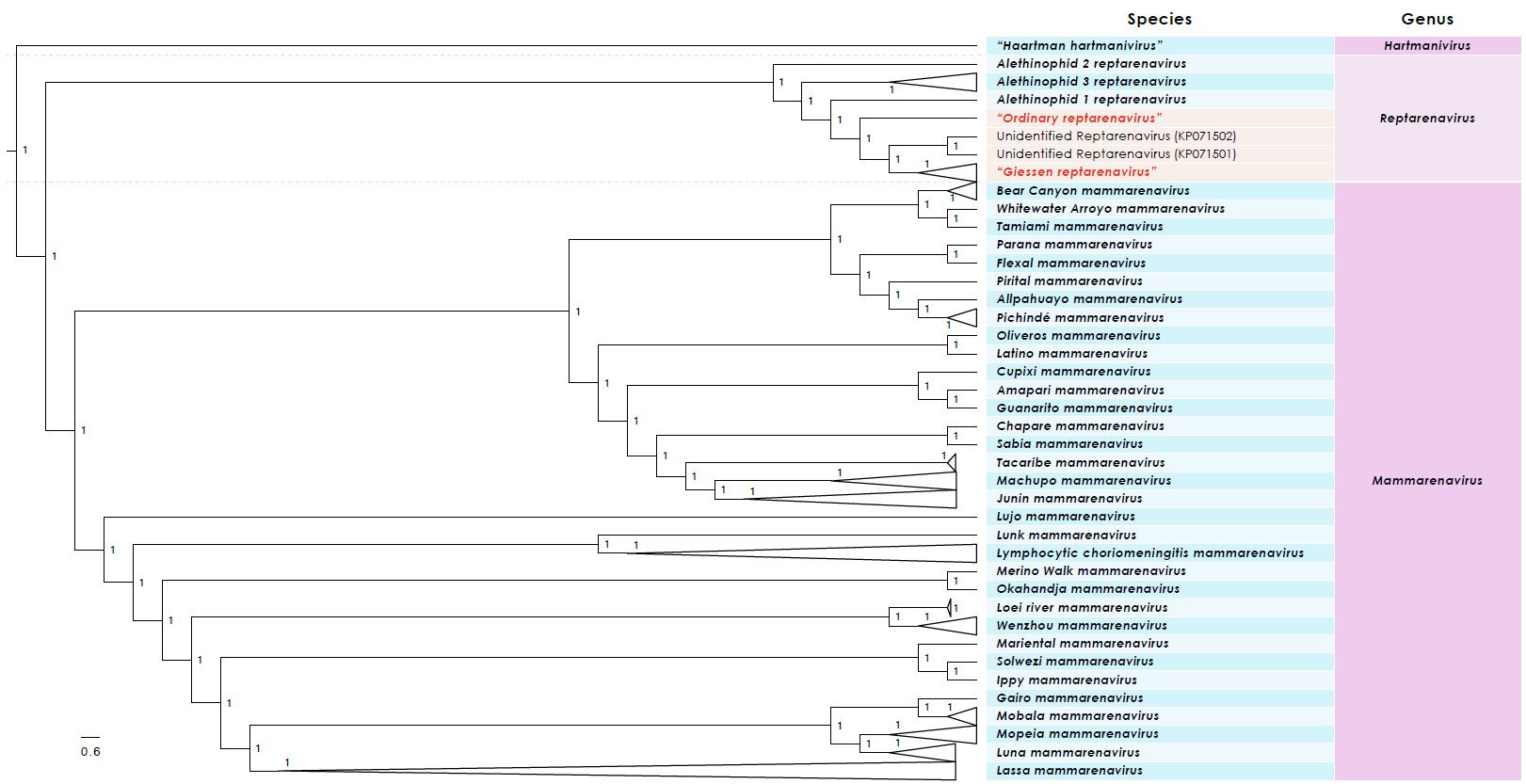
Figure 1



To further confirm the taxonomic position of TSMV-2 and UGV–3, 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 reptarenavirus 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 2). Once again, the results of this analysis are in accordance with those above and indicate the need for two novel reptarenavirus species.

Figure 2

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.



We propose to classify TSMV-2 in a new species “*Ordinary reptarenavirus*” [Finish “Tavallinen” = usual, ordinary] and UGV-1–3 in a new species “*Giessen reptarenavirus*” [after the virus name, which is named after a town]. Furthermore, we propose to change the current species names *Alethinophid 1–3 reptarenavirus* to “*Golden reptarenavirus*”, “*California reptarenavirus*”, and “*Rotterdam reptarenavirus*” to more closely mimic mammarenavirus species names and to avoid future numbering conflicts.

| **References:** |
| --- |
| 1. **Radoshitzky SR, Bao 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.** 2015. Past, present, and future of arenavirus taxonomy. Arch Virol **160:**1851-1874.  2. **Stenglein MD, Sanders C, Kistler AL, Ruby JG, Franco JY, Reavill DR, Dunker F, Derisi JL.** 2012. Identification, characterization, and in vitro culture of highly divergent arenaviruses from boa constrictors and annulated tree boas: candidate etiological agents for snake inclusion body disease. MBio **3:**e00180-00112.  3. **Bodewes R, Kik MJ, Raj VS, Schapendonk CM, Haagmans BL, Smits SL, Osterhaus AD.** 2013. Detection of novel divergent arenaviruses in boid snakes with inclusion body disease in The Netherlands. J Gen Virol **94:**1206-1210.  4. **Hepojoki J, Salmenpera P, Sironen T, Hetzel U, Korzyukov Y, Kipar A, Vapalahti O.** 2015. Arenavirus Coinfections Are Common in Snakes with Boid Inclusion Body Disease. J Virol **89:**8657-8660.  5. **Aqrawi T, Stohr AC, Knauf-Witzens T, Krengel A, Heckers KO, Marschang RE.** 2015. Identification of snake arenaviruses in live boas and pythons in a zoo in Germany. Tierarztl Prax Ausg K Kleintiere Heimtiere **43**.  6. **Bodewes R, Raj VS, Kik MJ, Schapendonk CM, Haagmans BL, Smits SL, Osterhaus AD.** 2014. Updated phylogenetic analysis of arenaviruses detected in boid snakes. J Virol **88:**1399-1400.  7. **Abba Y, Hassim H, Hamzah H, Ibrahim OE, Ilyasu Y, Bande F, Mohd Lila MA, Noordin MM.** 2016. In vitro isolation and molecular identification of reptarenavirus in Malaysia. Virus Genes.  8. **Hellebuyck T, Pasmans F, Ducatelle R, Saey V, Martel A.** 2015. Detection of arenavirus in a peripheral odontogenic fibromyxoma in a red tail boa (Boa constrictor constrictor) with inclusion body disease. J Vet Diagn Invest **27:**245-248.  9. **Stenglein MD, Jacobson ER, Chang LW, Sanders C, Hawkins MG, Guzman DS, Drazenovich T, Dunker F, Kamaka EK, Fisher D, Reavill DR, Meola LF, Levens G, DeRisi JL.** 2015. Widespread recombination, reassortment, and transmission of unbalanced compound viral genotypes in natural arenavirus infections. PLoS Pathog **11:**e1004900. |