

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

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| **Code assigned:** | **2020.025M** |  |
| **Short title:** Create five new species in subfamily *Mammantavirinae* (*Bunyavirales*: *Hantaviridae*) | | |
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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 (authors) |

**ICTV study group comments and response of proposer**

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**Submission dates**

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| Date first submitted to SC Chair | July 31, 2020 |
| Date of this revision (if different to above) | August 28, 2020 |

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

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

**Name of accompanying Excel module**

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| 2020.025M.R.Hantaviridae\_5nsp.xlsx |

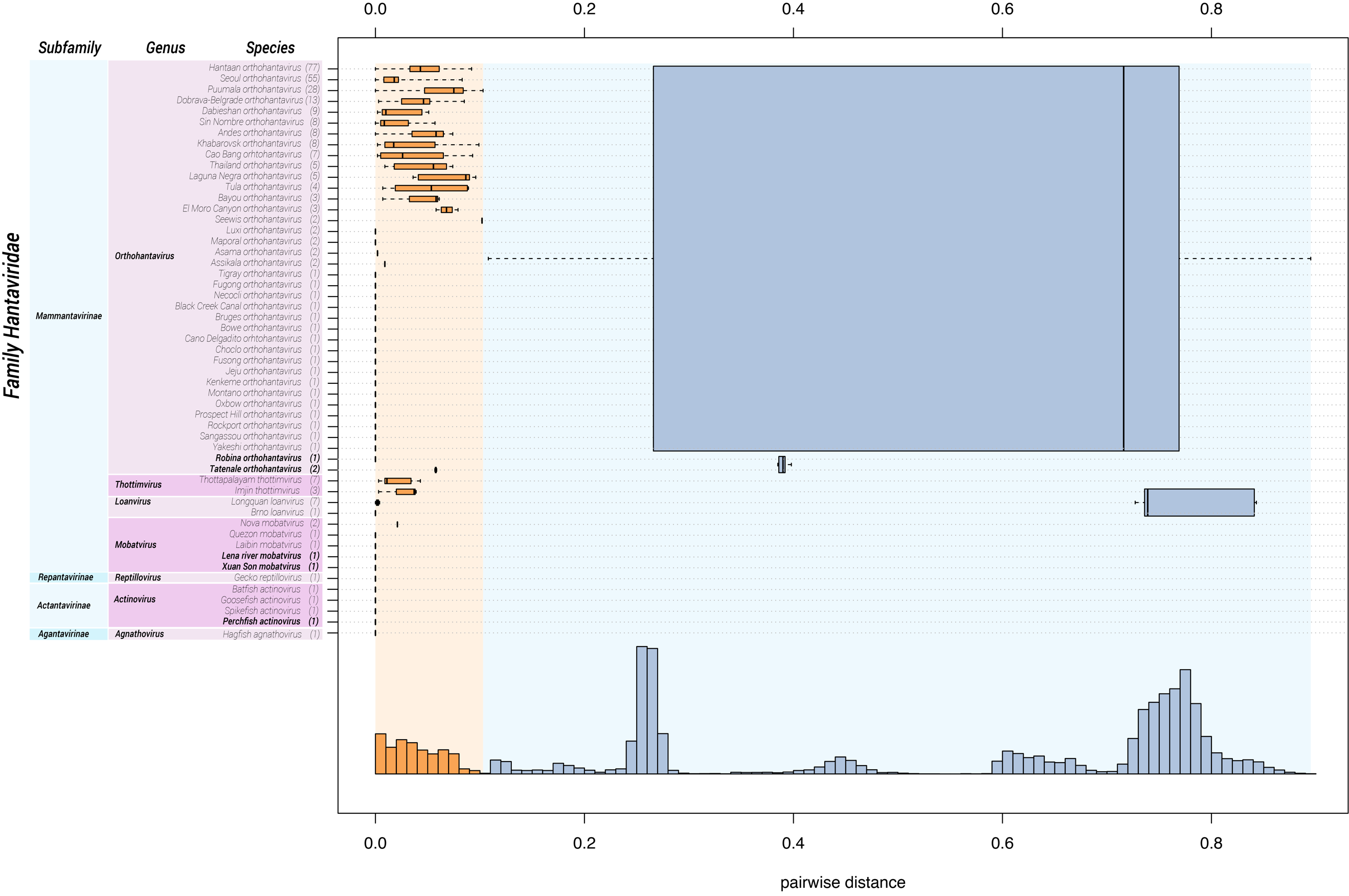
**Abstract**

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| We propose the creation of 5 new species in the family *Hantaviridae:* two in genus *Orthohantavirus*, two in genus *Mobatvirus*, and one in genus *Actinovirus*. |

**Text of proposal**

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| |  | | --- | | DEmARC/Bayesian MCMC analysis was performed with all available full-length hantavirid-like sequences (complete S and M segment sequences were used for the analysis). Briefly, Bayesian phylogenetic analyses were inferred in BEAST v1.10.4 using 20 independent MCMC runs with a chain length of 50,000,000 generations. Tree and log files of independent runs of BEAST were combined using LogCombiner v1.10.4, using a Burn in period of 10%. The Markov chain Monte Carlo analyses were run until effective sample sizes above 200 were obtained. The consensus tree was built with TreeAnnotator v1.10 using the maximum clade credibility method and visualized in Figtree. This consensus tree was used as guide tree for the DEmARC analysis (adapted from version 1.0).  Five hantavirids with complete genome (S, M, and L) sequences were identified as new releases in NCBI GenBank during this analysis, and these viruses were identified to represent 5 new hantavirid species:   * ***Robina orthohantavirus*** for Robina virus isolated from brain tissue of a black flying fox (*Pteropus alecto* Temminck, 1837) trapped near Robina, Queensland, Australia (unpublished). The species is named after the member virus. * ***Tatenale orthohantavirus*** for Tatenale virus isolated from lung tissue of a field vole (*Microtus agrestis* (Linnaeus, 1761)) trapped in North West England in 2013 [[2](#_ENREF_2), [3](#_ENREF_3)]. The virus is named after the historical town Tatenale, and the species is named after the virus. * ***Lena mobatvirus*** for Lena virus isolated from lung tissue of a Laxmann's shrew (*Sorex caecutiens* Laxmann, 1785) caught in 2008 in Khabarovsk, Russia, close to the Lena River [[4](#_ENREF_4)]. The species is named after the member virus. * ***Xuan Son mobatvirus*** for Xuân Sơn virus isolated in 2013 from lung tissue of a Pomona leaf-nosed bat (*Hipposideros Pomona* K. Andersen, 1918) in Vietnam [[1](#_ENREF_1)]. The virus (and consequently species) is named after Xuân Sơn National Park, Phú Thọ Province, Vietnam, where the animal was caught. * ***Perch actinovirus*** for Bern perch virus was isolated from a European perch (*Perca fluviatilis* Linnaeus, 1758) trapped in Switzerland (unpublished). Virus and species are named after the host of the virus. | |

**Supporting evidence**

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**Figure 1:** Intra-family genetic divergence in three-level hierarchical clustering of hantaviruses by DEmARC (version 1.0). Levels 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.

**References**

1. Arai S, Nguyen ST, Boldgiv B, Fukui D, Araki K, Dang CN, Ohdachi SD, Nguyen NX, Pham TD, Boldbaatar B, Satoh H, Yoshikawa Y, Morikawa S, Tanaka-Taya K, Yanagihara R, Oishi K (2013) Novel bat-borne hantavirus, Vietnam. Emerg Infect Dis 19:1159-61. PMID: 23763849. PMCID: PMC3713973. doi: 10.3201/eid1907.121549.

2. Chappell JG, Tsoleridis T, Onianwa O, Drake G, Ashpole I, Dobbs P, Edema W, Kumi-Ansah F, Bennett M, Tarlinton RE, Ball JK, McClure CP (2020) Retrieval of the complete coding sequence of the UK-endemic Tatenale orthohantavirus reveals extensive strain variation and supports its classification as a novel species. Viruses 12:454. PMID: 32316655. PMCID: PMC7232349. doi: 10.3390/v12040454.

3. Pounder KC, Begon M, Sironen T, Henttonen H, Watts PC, Voutilainen L, Vapalahti O, Klempa B, Fooks AR, McElhinney LM (2013) Novel hantavirus in wildlife, United Kingdom. Emerg Infect Dis 19:673-5. PMID: 23750506. PMCID: PMC3647411. doi: 10.3201/eid1904.121057.

4. Yashina LN, Kartashov MY, Wang W, Li K, Zdanovskaya NI, Ivanov LI, Zhang YZ (2019) Co-circulation of distinct shrew-borne hantaviruses in the far east of Russia. Virus Res 272:197717. PMID: 31422116. doi: 10.1016/j.virusres.2019.197717.