

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

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| **Code assigned:** | ***2022.011M*** |  |
| **Short title:** Create two new species in the genus *Hartmanivirus* (*Arenaviridae*) | | |
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**Author(s) and email address(es)**

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**Corresponding author**

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| Hepojoki J |

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

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| ICTV *Arenaviridae* Study Group |

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

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| Approved. |

**ICTV Study Group votes on proposal**

Study Group Chair(s) please report voting by Study Group members on the proposal prior to final submission to the Subcommittee Chair.

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| --- | --- | --- | --- |
| **Study Group** | **Number of members** | | |
| **Votes support** | **Votes against** | **No vote** |
| ICTV *Arenaviridae* Study Group | 15 | 0 | 0 |

**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)** |
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**Submission dates**

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| --- | --- |
| Date first submitted to SC Chair | May 27, 2022 |
| 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**

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| 2022.011M.N.v1.Hartmanivirus\_2nsp.xlsx |

**Abstract**

Please provide a concise summary of your taxonomic proposal (maximum 150 words).

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| We propose the establishment of two novel hartmanivirus species: *Hartmanivirus quadrati* to accommodate big electron-dense squares virus 1 (BESV-1) and *Hartmanivirus unni* to accommodate Universidad Nacional virus 1 (UnNV-1). Complete coding genome sequences were obtained for both viruses using high-throughput sequencing and *de novo* genome assembly from *Boa constrictor* snakes captured in Costa Rica. Both viruses were isolated through inoculation of cultured cells with tissue homogenate or blood from *B. constrictor* with boid inclusion body (BIBD) signs. Inoculated cell cultures exhibited a co-infection with the novel hartmaniviruses and reptarenavirus(es). PAirwise Sequence Comparison (PASC) is the basis of the proposed classification. For BESV-1, PASC analysis of both L and S segments supports establishment of a novel species based on current Study Group criteria. However, for UnNV-1, PASC analysis showed that L and S segment are 77.75% and 75.61%, respectively, identical to the closest relative. According to species demarcation criteria the L segment would belong to the same species established for Haartman Institute snake virus 1 (HISV-1; *Haartman hartmanivirus* [proposed to be renamed *Hartmanivirus haartmani* in a separate proposal) (>76% identical at nt level) but based on the S segment identity we propose classification into a new species (< 80% identical at nt level). |

**Text of proposal**

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| |  | | --- | | We identified two pairs of novel hartmanivirus segments while performing a high-throughput sequencing study of *Boa Constrictor* (Linneus, 1785) snakes sampled in Costa Rica (Alfaro-Alarcón and Hetzel et al. 2022). For both viruses, we obtained complete coding sequence for both genomic segments. As described (<https://www.biorxiv.org/content/10.1101/2022.04.25.489483v1.full.pdf>, page 8), the viruses were isolated by inoculating *B. constrictor* kidney-derived I/1Ki cells (described in Hetzel et al. 2013) with tissue homogenate or blood from an infected boa constrictor. Analysis of the cell culture supernatant using NGS indicated that both culture isolations resulted in a co-culture of hartmaniviruses with reptarenavirus(es) (or a swarm of reptarenavirus segments, for details on the reptarenavirus segments see Table 1 on pages 38 and 39 of <https://www.biorxiv.org/content/10.1101/2022.04.25.489483v1.full.pdf>). The sequences have been deposited to GenBank: Universidad Nacional virus 1 (UnNV-1), S and L segment, GenBank accessions MW091473 and MW091472, respectively; big electron-dense squares virus 1 (BESV-1), S and L segment, GenBank accessions OM456563 and OM456564, respectively. Following the recommendation by ICTV *Arenaviridae* Study Group for the classification of novel arenaviruses (Radoshitzky et al. 2015), the sequences were compared to those of previously identified arenaviruses using the PAirwise Sequence Comparison (PASC) tool (<https://www.ncbi.nlm.nih.gov/sutils/pasc/viridty.cgi?textpage=overview>). To further verify the result, the nucleotide sequences were compared in a separate alignment, which allowed generation of distance matrices for both L and S segments.    **The PASC results:**  Universidad Nacional virus 1 (UnNV-1), L segment, MW091472      Universidad Nacional virus 1 (UnNV-1), S segment, MW091473      Big electron-dense squares virus 1 (BESV-1), L segment, GenBank accession OM456564      Big electron-dense squares virus 1 (BESV-1), S segment, GenBank accession OM456563      **Distance matrices for L and S segments:**  L segment nucleotide identities among hartmaniviruses. AHeV=andere Heimat virus, HISV=Haartman Institute snake virus, OScV=old schoolhouse virus, VPZV=veterinary pathology Zurich virus, DaMV=Dante Muikkunen virus, UnNV=Universidad Nacional virus, BESV=big electron-dense squares virus.    S segment nucleotide identities among hartmaniviruses. AHeV=andere Heimat virus, HISV=Haartman Institute snake virus, OScV=old schoolhouse virus, VPZV=veterinary pathology Zurich virus, DaMV=Dante Muikkunen virus, UnNV=Universidad Nacional virus, BESV=big electron-dense squares virus.    Of the identified segment pairs, those belonging to BESV-1 fulfill the nucleotide difference criteria required for classification into a novel hartmanivirus species (virus shares less than 80% nucleotide sequence identity in the S segment and less than 76% identity in the L segment, Radoshitzky et al., 2015). However, for UnNV-1, the L segment nucleotide sequence is 77.75% identical to Haartman Institute snake virus 1, which would prevent classification into a novel species. On the other hand, the S segment of the virus fulfills the criteria for classification into a novel species (i.e., is less than 80% identical to the closest “relative”). Because of the novel segment combination and the fact that the S segment fulfills and the L segment is close to fulfilling the species demarcation criteria, we propose the classification of UnNV-1 into a novel species in the genus *Hartmanivirus*. | |

**Supporting evidence**

N/A

**References**

Alejandro Alfaro-Alarcón, Udo Hetzel, Teemu Smura, Francesca Baggio, Juan Alberto Morales, Anja Kipar, Jussi Hepojoki. Boid Inclusion Body Disease (BIBD) Is Also a Disease of Wild Boa Constrictors. bioRxiv 2022.04.25.489483; doi: https://doi.org/10.1101/2022.04.25.489483

Hetzel U, Sironen T, Laurinmäki P, Liljeroos L, Patjas A, Henttonen H, Vaheri A, Artelt A, Kipar A, Butcher SJ, Vapalahti O, Hepojoki J. Isolation, identification, and characterization of novel arenaviruses, the etiological agents of boid inclusion body disease. J Virol. 2013 Oct;87(20):10918-35. doi: 10.1128/JVI.01123-13. Epub 2013 Aug 7. PMID: 23926354; PMCID: PMC3807292.

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