This Word module should be used for all taxonomic proposals.

Please complete **Part 1** and:

either **Part 3** for proposals to create new taxa or change existing taxa

or **Part 2** for proposals of a general nature.

Submit the completed Word module, together with the accompanying Excel module named in Part 3, to the appropriate ICTV Subcommittee Chair.

For guidance, see the notes written in blue, below, and the help notes in file Taxonomic\_Proposals\_Help\_2018.

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

|  |  |  |
| --- | --- | --- |
| **Code assigned:** | ***2019.008M*** | (to be completed by ICTV officers) |
| **Short title:** Create three new species in the genus *Hartmanivirus* (*Bunyavirales*: *Arenaviridae*) |
|  |
| **Author(s):** |
| Hetzel, Udo; udo.hetzel@uzh.ch Smura, Teemu; teemu.smura@helsinki.fi Hepojoki, Satu; satu.hepojoki@helsinki.fiHepojoki, Jussi; Jussi.hepojoki@helsinki.fi andKuhn, Jens H.; kuhnjens@mail.nih.gov  |
| **Corresponding author with e-mail address:** |
| Hepojoki, Jussi; jussi.hepojoki@uzh.ch; jussi.hepojoki@helsinki.fi |
| **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:** |
| Reviewed by the ICTV *Arenaviridae* Study Group and was voted OK without countervotes. |
|  |
| Date first submitted to ICTV: | 12/10/2018 |
| Date of this revision (if different to above): |       |

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

**Part 3:** **PROPOSED TAXONOMY**

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| **Name of accompanying Excel module:** 2019.008M.A.v2.Hartmanivirus\_3new sp.xlsx |

**Supporting material:**

Six novel hartmaniviruses, Dante Muikkunen virus 1 (DaMV-1), Haartman Institute snake virus 2 (HISV-2), old schoolhouse virus 1 (OScV-1), old schoolhouse virus 2 (OScV-2), veterinary pathology Zurich virus 1 (VPZV-1), and veterinary pathology Zurich virus 2 (VPZV-2), were recently discovered by next-generation sequencing in sampled captive boa constrictors (*Boa constrictor*), some of which were euthanized due to suspected boid inclusion body disease (BIBD) and some apparently healthy, from breeding colonies in Germany and Switzerland. Coding-complete genome sequences (both S and L segments) of these viruses are available from GenBank. None of these viruses have been isolated in culture but all share the hartmanivirus-defining lack of the, otherwise typical, arenavirus Z-encoding open reading frame (Hepojoki *et al*. 2018).

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*. 2015). 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. We therefore performed PASC on the newly discovered hartmaniviruses using the only classified hartmanivirus, Haartman Institute snake virus 1 (HISV-1), as the reference (Tables 1 and 2).

**Table 1: S segment PASC (pairwise genome sequence identity in percent):**

|  |  |  |  |  |  |  |  |
| --- | --- | --- | --- | --- | --- | --- | --- |
|  | HISV-1 | HISV-2 | OScV-1 | OScV-2 | VZPV-1 | VZPV-2 | DaMV-1 |
| HISV-1 | 100.0 |  |  |  |  |  |  |
| HISV-2 | 88.7 | 100.0 |  |  |  |  |  |
| OScV-1 | 62.8 | 63.4 | 100.0 |  |  |  |  |
| OScV-2 | 63.3 | 64.1 | 85.0 | 100 |  |  |  |
| VZPV-1 | 63.9 | 63.4 | 63.3 | 63.9 | 100.0 |  |  |
| VZPV-2 | 64.0 | 62.9 | 62.4 | 63.1 | 85.9 | 100.0 |  |
| DaMV-1 | 66.8 | 67.3 | 63.6 | 62.9 | 63.5 | 64.3 | 100.0 |

**Table 2: L segment PASC (pairwise genome sequence identity in percent):**

|  |  |  |  |  |  |  |  |
| --- | --- | --- | --- | --- | --- | --- | --- |
|  | HISV-1 | HISV-2 | OScV-1 | OScV-2 | VZPV-1 | VZPV-2 | DaMV-1 |
| HISV-1 | 100.0 |  |  |  |  |  |  |
| HISV-2 | 85.4 | 100.0 |  |  |  |  |  |
| OScV-1 | 59.0 | 58.9 | 100.0 |  |  |  |  |
| OScV-2 | 59.0 | 59.3 | 78.0 | 100.0 |  |  |  |
| VZPV-1 | 59.8 | 59.9 | 58.9 | 57.9 | 100.0 |  |  |
| VZPV-2 | 61.2 | 60.0 | 58.5 | 57.1 | 83.8 | 100.0 |  |
| DaMV-1 | 64.9 | 64.3 | 59.5 | 60.4 | 60.7 | 61.0 | 100.0 |

Together, these results indicate that

1. DMaV-1 ought to be assigned to a novel hartmanivirus species, for which the name *Muikkunen hartmanivirus* is proposed;
2. HISV-2 ought to be classified into the existing species *Haartman hartmanivirus* together with HISV-1
3. OScV-1 and OScV-2 ought to be assigned to one novel hartmanivirus species, named *Schoolhouse hartmanivirus*; and
4. VPZV-1 and VPZV-2 ought to be assigned to one novel hartmanivirus species, with proposed name *Zurich hartmanivirus*.

These interpretations are also supported by phylogenetic studies (Figure 1).

Figure 1. Phylogenetic analysis of novel hartmaniviruses. A) Maximum clade credibility tree of the polymerase region of mammarenaviruses (blue), reptarenaviruses (green), hartmaniviruses (red), and antennaviruses (black). The tree was constructed from amino acid alignment using Bayesian MCMC method with LG model of substitution. Posterior probabilities are shown in each node. B) Maximum clade credibility tree of S segment nucleotide sequences of hartmaniviruses. The tree was constructed from Bayesian MCMC method with HKY model of substitution with gamma distributed rate variation among sites and proportion of invariable sites. Posterior probabilities are shown in each node (taken from Hepojoki *et al*. 2018).



Etymology:

* Dante Muikkunen virus, named after the Finnish nickname (Dante Muikkunen) that a three-year-old boy gave to his little sister.
* *Muikkunen hartmanivirus*, named after DaMV-1 and genus *Hartmanivirus*.
* old schoolhouse virus, named after an old schoolhouse where “the BIBD group” in Zurich often meets for discussions about reptarenaviruses and hartmaniviruses.
* *Schoolhouse hartmanivirus*, named after OScV-1 and genus *Hartmanivirus.*
* veterinary pathology Zurich virus, named after the institute where the second HISV-like virus was found.
* *Zurich hartmanivirus*, named after the Swiss city of Zurich and genus *Hartmanivirus.*

| **References:** |
| --- |
| Hepojoki J, Hepojoki S, Smura T, Szirovicza L, Dervas E, Prähauser B, Nufer L, Schraner EM, Vapalahti O, Kipar A, Hetzel U. Characterization of Haartman Institute snake virus-1 (HISV-1) and HISV-like viruses-The representatives of genus *Hartmanivirus*, family *Arenaviridae*. PLoS Pathog. 2018 Nov 14;14(11):e1007415. doi: 10.1371/journal.ppat.1007415. eCollection 2018 Nov. PMID: 30427944.Radoshitzky SR, et al. Past, present, and future of arenavirus taxonomy. Arch. Virol. 2015;160:1851–1874. doi: 10.1007/s00705-015-2418-y. |