

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

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| **Code assigned:** | ***2023.028M*** |  |
| **Short title:** Create one new genus and nine new species in family *Nairoviridae* (family *Bunyavirales*) | | |
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**Author(s) and email address(es)**

|  |  |
| --- | --- |
| Alkhovsky SV, Avšič-Županc T, Bergeron É, Burt F, Ergünay K, Garrison AR, Kuhn JH, Marklewitz M, Mirazimi A, Papa A, Pawęska JT, Postler TS. Spengler JR, Palacios G | salkh@yandex.ru; Tatjana.Avsic@mf.uni-lj.si; exj8@cdc.gov; burtfj@ufs.ac.za; ekoray@hacettepe.edu.tr; aura.r.garrison.civ@health.mil; kuhnjens@mail.nih.gov; marco.marklewitz@finddx.org; Ali.Mirazimi@ki.se; annap.med@gmail.com; januszp@nicd.ac.za; TPostler@iavi.org; JSpengler@cdc.gov; gustavo.palacios@mssm.edu |

**Author(s) institutional address(es) (optional)**

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**Corresponding author**

|  |
| --- |
| Palacios G |

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

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| ICTV *Nairoviridae* Study Group |

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

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**ICTV Study Group votes on proposal**

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| **Study Group** | **Number of members** | | |
| **Votes support** | **Votes against** | **No vote** |
| ICTV *Nairoviridae* Study Group | 13 | 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 |

|  |  |  |
| --- | --- | --- |
| **Taxon name** | **Person from whom the name is derived** | **Permission attached (Y/N)** |
| N/A | N/A | N/A |

**Submission dates**

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| --- | --- |
| Date first submitted to SC Chair | June 23, 2023 |
| 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**

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| N/A |

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

**Name of accompanying Excel module**

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| 2023.028M.N.v1.Nairoviridae\_1ng\_9nsp.xlsx |

**Abstract**

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| We propose the classification of nine novel nairovirids into eight novel orthonairovirus species and one new genus including a new species. |

**Text of proposal**

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| |  | | --- | | The bunyaviral family *Nairoviridae* currently includes seven genera (*Norwavirus*, *Ocetevirus*, *Orthonairovirus*, *Sabavirus*, *Shaspivirus*, *Striwavirus*, and *Xinspivirus*). In 2021, the ICTV *Nairoviridae* Study Group established a species demarcation criterion of <93% identity in the amino acid sequence of the nairovirid RNA-directed RNA polymerase (RdRp) (TaxoProp 2020.027M). A reanalysis of the dataset used of last year’s TaxoProp 2022.015M, complemented with newly described nairovirid sequences, indicated nine viruses should be classified into nine novel species, with one of them included in a new genus (Supplementary Data, Figure 1):  **Novel genus *Sitinavirus*:**  Sìchuān tick nairovirus (proposed abbreviation ScTNV rather than the published STNV, which is already in use for other viruses) was first discovered by high-throughput sequencing (HTS) in unspecified ixodid ticks feeding on giant pandas in Sìchuān Province (四川省), China [[4](#_ENREF_4)]. We propose to establish genus/species *Sitinavirus sichuanense* to classify this virus.  **Novel orthonairovirus species:**   * Āntú virus (proposed abbreviation: ANTV) was first discovered by HTS in ticks (ixodid *Dermacentor silvarum* Olenev, 1931) collected in Āntú County (安图县), Yánbiān Korean Autonomous Prefecture (延边朝鲜族自治州), Jílín Province (吉林省), China [[2](#_ENREF_2)]. We propose to establish species *Orthonairovirus antuense* to classify this virus. * cencurut virus (CENV) was first discovered by HTS in Singapore in Asian house shrews (soricid *Suncus murinus* (Linnaeus, 1766)) and in a nymphal tick (ixodid *Amblyomma helvolum* Koch, 1844) collected from an infected shrew [[3](#_ENREF_3)]. We propose to establish species *Orthonairovirus sunci* to classify this virus. * Gubbo nairovirus (GUBV) was first discovered by HTS in ticks (argasid *Carios vespertilionis* Latreille, 1796) in Snesslinge, Uppland, Sweden [[6](#_ENREF_6)]. We propose to establish species *Orthonairovirus gubboense* to classify this virus. * Lamusara virus (LMSV) was first discovered by RT-PCR in goliath shrews (soricid *Crocidura goliath* Thomas, 1906) sampled around Lambaréné in Gabon [[7](#_ENREF_7)]. We propose to establish species *Orthonairovirus lambarenense* to classify this virus. * Méihuā Mountain virus (MHMV) was first discovered by HTS in ixodid ticks (*Haemaphysalis* *hystricis* Supino, 1897, *Haemaphysalis* *formosensis* Neumann, 1913, *Dermacentor* *taiwanensis* Sugimoto, 1935, and *Rhipicephalus* *microplus* (Canestrini, 1888)) sampled in the Méihuā Mountains (梅花山), Fújiàn Province (福建省), China [[8](#_ENREF_8)]. We propose to establish species *Orthonairovirus meihuashanense* to classify this virus. * orthonairovirus sp. strain YS was first discovered by HTS in an unspecified shrew sampled in China [unpublished]. We propose to establish species *Orthonairovirus sinense* to classify this virus. * pangolin orthonairovirus (PONV) was first discovered by HTS in unspecified pangolins sampled in China [unpublished]. We propose to establish species *Orthonairovirus manidae* to classify this virus. * Wufeng Crocidura attenuata orthonairovirus 1 (proposed abbreviation: WfCAV1) was first discovered by HTS in Asian grey shrews (soricid *Crocidura attenuata* Milne-Edwards, 1872) sampled in China [unpublished]. We propose to establish species *Orthonairovirus crocidurae* to classify this virus. | |

**Supporting evidence**

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Figure 1. The maximum-likelihood phylogenetic tree was inferred using IQtree [[5](#_ENREF_5)]; the numbers on the nodes represent bootstrap values derived from the ultrafast bootstrap algorithm [[1](#_ENREF_1)]. Trees were inferred under the LG+G+I substitution model. Tree branches are proportional to genetic distances between sequences, and the scale bars at the top indicate substitutions per amino acid. For all taxa shown here, the complete genome or complete coding sequence is available on the GenBank nucleotide sequence database. Accession numbers are shown next to the respective virus taxon.

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