

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

|  |  |  |
| --- | --- | --- |
| **Code assigned:** | **2020.027M** |  |
| **Short title:** Create four new genera and 30 new species (*Bunyavirales*: *Nairoviridae*) | | |
|  | | |

**Author(s) and email address(es)**

|  |  |
| --- | --- |
| Marklewitz M, Paraskevopoulou S, Alkhovsky SV, Avšič-Županc T, Bente D, Bergeron É, Burt F, Ergünay K, Garrison AR, Hewson R, Mirazami A, Palacios G, Papa A, Pawęska JT, Sall AA, Spengler J, Di Paola N, Kuhn JH | marco.marklewitz@charite.de;  sofia.paraskevopoulou@charite.de; salkh@yandex.ru; Tatjana.Avsic@mf.uni-lj.si; dabente@UTMB.EDU; exj8@cdc.gov; burtfj@ufs.ac.za; korayergunay@gmail.com; aura.r.garrison.civ@mail.mil; Roger.Hewson@phe.gov.uk; Ali.Mirazimi@ki.se; gustavo.f.palacios.civ@mail.mil; annap.med@gmail.com; januszp@nicd.ac.za; Amadou.SALL@pasteur.sn; wsk7@cdc.gov; nicholas.dipaola.ctr@mail.mil; kuhnjens@niaid.nih.gov |

**Corresponding authors**

|  |
| --- |
| Marklewitz M, Paraskevopoulou S, Di Paola N |

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

|  |
| --- |
| ICTV *Nairoviridae* Study Group |

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

|  |
| --- |
|  |

**Submission dates**

|  |  |
| --- | --- |
| 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**

|  |
| --- |
|  |

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

**Name of accompanying Excel module**

|  |
| --- |
| 2020.027M.R.Nairoviridae\_4ngen\_30nsp.xlsx |

**Abstract**

|  |
| --- |
| We propose the establishment of four new genera (*Norwavirus*, *Ocetevirus*, *Sabavirus*, and *Xinspivirus*) including one new species each, and 26 novel *Orthonairovirus* species in the family *Nairoviridae*. |

**Text of proposal**

|  |  |
| --- | --- |
| |  | | --- | | The bunyaviral family *Nairoviridae* currently includes the two monospecific genera, *Shaspivirus* and *Striwavirus*, as well as genus *Orthonairovirus*, which includes 15 species. Most of the orthonairovirus species have been established for several viruses each, most of which are considered distinct entities in the nairovirid research community. For instance, the species *Hughes orthonairovirus* has been established for Caspiy virus (CASV), Farallon virus (FARV). Great Saltee virus (GRSV), Hughes virus (HUGV), Punta Salinas virus (PSV), Raza virus (RAZAV), Soldado virus (SOLV), and Zirqa virus (ZIRV).  In recent years, various ICTV Study Groups responsible for other bunyaviral families, most notably those responsible for families *Peribunyaviridae* and *Phenuiviridae*, have begun to dissolve these “species complexes” by establishing objective species demarcation criteria based on sequence identity. For instance, species of the peribunyavirid genus *Orthobunyavirus* and the phenuivirid genus *Phlebovirus* are currently discriminated by <96% and <95% identity in the amino-acid sequence of the RNA-directed RNA polymerase (RdRp) of the member viruses.  Here, we propose using the same methodology to dissolve orthonairovirus “species complexes” and to expand the nairovirid taxonomy by new taxa for recently discovered novel viruses. To establish a species demarcation criterion, we analyzed the pairwise amino-acid sequence identities of the RdRp (Supplementary Data) among the classified nairovirids and unclassified, tentative nairovirids. Similar to the approach used for phenuivirids, the naturally occurring diversity of nairovirids has been analyzed by the determination of the intraspecies genetic diversity of Crimean‑Congo hemorrhagic fever (CCHFV), as it represents a well-investigated nairovirid for which numerous complete or coding-complete genomes are available. (At the time of writing, 184 RdRp genes have been completely sequenced.) The analysis of pairwise distances among all available CCHFV strains in their RdRps revealed maximum pairwise and amino acid genetic distances of 6.8%. We therefore propose to define the species demarcation criteria for nairovirids as <93% identity in the amino acid sequence of the RdRp: viruses with <93% sequence identity represent unique species. Application of this criterion results in the expansion of the currently accepted 15 species into a total of 41 species. Furthermore, this analysis, in conjunction with phylogenetic evidence (Figure 1), indicated the need to create four new genera:   1. Genus *Norwavirus*, including species *Grotenhout norwavirus*, is proposed for Grotenhout virus, discovered by high-throughput sequencing (HTS) in a castor bean tick (*Ixodes ricinus* (Linnaeus, 1758) [[6](#_ENREF_6)]. The virus has not been isolated in culture. 2. Genus *Ocetevirus*, including species *Blattodean ocetevirus*, is proposed for Blattodean nairo‑related virus 321, discovered by HTS in a cockroach (*Paratemnopteryx couloniana* (Saussure, 1863)) [[2](#_ENREF_2)]. The virus has not been isolated in culture. 3. Genus *Sabavirus*, including species *South Bay sabavirus*, is proposed for South Bay virus, discovered by HTS in a deer tick (*Ixodes scapularis* Say, 1821) in the U.S. [[5](#_ENREF_5)]. The virus has not been isolated in culture. 4. Genus *Xinspivirus*, including species *Xinzhou xinspivirus*, is proposed for Xīnzhōu spider virus, discovered by HTS in a brown sailor spider (*Neoscona nautica* (L. Koch, 1875)) in China [[3](#_ENREF_3)]. The virus has not been isolated in culture.   **Etymology**   1. All new orthonairovirus species are named after their member viruses; for instance, *Meram orthonairovirus* is named after Meram virus. The one exception is *Congoid orthonairovirus*, which is a new species for a virus previously thought to be CCHFV (species *Crimean-Congo hemorrhagic fever orthonairovirus*) and which is now renamed CCHFV-2. Congoid indicates “similar to” *Crimean-Congo hemorrhagic fever orthonairovirus.* 2. Genus name *Norwavirus* is derived from a contraction of the name of a strain of its member virus, Norway virus. Species *Grotenhout norwavirus* is named after the member virus, Grotenhout virus. 3. Genus name *Ocetevirus* is derived from "Oceania" and "τέμνω" (témno), which means "to cross" in Greek. The host of member virus Blattodean nairo-related virus 321 is a cockroach occurring in Australia with the species name *Paratemnopteryx couloniana*. Species *Blattodean ocetevirus* is named after this virus. 4. Genus name *Sabavirus* is derived from a blend of the name of its member virus, South Bay virus. Species *South Bay sabavirus* is named after this virus. 5. Genus name *Xinspivirus* is derived from a blend of the name of its member virus, Xīnzhōu spider virus. Species *Xinzhou xinspivirus* is named after this virus.   **Supporting evidence**    Figure 1. The maximum-likelihood phylogenetic tree was inferred using IQtree [[4](#_ENREF_4)]; 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.  **References**  1. Hoang DT, Chernomor O, von Haeseler A, Minh BQ, Vinh LS (2018) UFBoot2: improving the ultrafast bootstrap approximation. Mol Biol Evol 35:518-522. PMID: 29077904. PMCID: PMC5850222. doi: 10.1093/molbev/msx281.  2. Käfer S, Paraskevopoulou S, Zirkel F, Wieseke N, Donath A, Petersen M, Jones TC, Liu S, Zhou X, Middendorf M, Junglen S, Misof B, Drosten C (2019) Re-assessing the diversity of negative strand RNA viruses in insects. PLoS Pathog 15:e1008224. PMID: 31830128. PMCID: PMC6932829. doi: 10.1371/journal.ppat.1008224.  3. Li CX, Shi M, Tian JH, Lin XD, Kang YJ, Chen LJ, Qin XC, Xu J, Holmes EC, Zhang YZ (2015) Unprecedented genomic diversity of RNA viruses in arthropods reveals the ancestry of negative-sense RNA viruses. Elife 4:e05378. PMID: 25633976. PMCID: PMC4384744. doi: 10.7554/eLife.05378.  4. Nguyen LT, Schmidt HA, von Haeseler A, Minh BQ (2015) IQ-TREE: a fast and effective stochastic algorithm for estimating maximum-likelihood phylogenies. Mol Biol Evol 32:268-74. PMID: 25371430. PMCID: PMC4271533. doi: 10.1093/molbev/msu300.  5. Tokarz R, Williams SH, Sameroff S, Sanchez Leon M, Jain K, Lipkin WI (2014) Virome analysis of *Amblyomma americanum*, *Dermacentor variabilis*, and *Ixodes scapularis* ticks reveals novel highly divergent vertebrate and invertebrate viruses. J Virol 88:11480-92. PMID: 25056893. PMCID: PMC4178814. doi: 10.1128/jvi.01858-14.  6. Vanmechelen B, Laenen L, Vergote V, Maes P (2017) Grotenhout virus, a novel nairovirus found in *Ixodes ricinus* in Belgium. Genome Announc 5:e00288-17. PMID: 28546475. PMCID: PMC5477388. doi: 10.1128/genomeA.00288-17. | |