

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

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| **Code assigned:** | ***2022.015M*** |  |
| **Short title:** Four new species in family *Nairoviridae* (*Bunyavirales*) | | |
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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 *Nairoviridae* Study Group |

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

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| Approved. |

**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**

|  |  |
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| **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)** |
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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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| 2022.015M.N.v1.Nairoviridae\_4nsp.xlsx |

**Abstract**

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| We propose the classification of three novel orthonairoviruses (Sōnglǐng virus, Sulina virus, and Yezo virus) and one novel norwavirus (Běijí nairovirus) into four novel nairovirid species. |

**Text of proposal**

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| |  | | --- | | The bunyaviral family *Nairoviridae* currently includes six monospecific genera (*Norwavirus*, *Ocetevirus*, *Sabavirus*, *Shaspivirus*, *Striwavirus*, and *Xinspivirus*) and genus *Orthonairovirus*, which includes 41 species. 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 in TaxoProp 2020.027M, complemented with newly described nairovirid sequences, indicated four viruses should be classified into four novel species (Supplementary Data, Figure 1):  **Novel norwavirus species:**  Běijí nairovirus (BJNV) was first discovered by HTS in taiga ticks (ixodid *Ixodes persulcatus* (Schulze, 1930)) sampled in Běijí (北极镇), Hēilóngjiāng Province (黑龙江省), China [[4](#_ENREF_4)]. Gakugsa tick virus, found in taiga ticks sampled in Gakugsa (Гакугса), Republic of Karelia (Республика Карелия), Russia (unpublished; GenBank #MN542362, MN542363), should be considered a strain of BJNV. We propose to establish species *Norwavirus beijiense* to classify this virus.  [Norway nairovirus 1, detected by HTS in castor bean ticks sampled in Tofte, Viken, Norway [[6](#_ENREF_6)], and Pustyn virus, detected by HTS in castor bean ticks sampled in Pustyn’ (Пустынь), Russia (unpublished: Genbank # KT007142, KT007143) should be considered strains of the classified Grotenhout virus (GRHV; genus *Norwavirus*).]  **Novel orthonairovirus species:**   * Sōnglǐng virus (SGLV) was isolated from febrile patients sampled in Sōnglǐng District (松岭区), Hēilóngjiāng Province (黑龙江省), China [[3](#_ENREF_3)]. We propose to establish species *Orthonairovirus songlingense* to classify this virus. * Sulina virus (SULV) was discovered by high-throughput sequencing (HTS) in castor bean ticks (ixodid *Ixodes ricinus* (Linnaeus, 1758)) sampled around Sulina, Northern Dobruja (Dobrogea de Nord), Romania [[7](#_ENREF_7)]. We propose to establish species *Orthonairovirus sulinaense* to classify this virus. * Yezo virus (YEZV) was isolated from a febrile human patient sampled in Hokkaidō (北海道), Japan [[2](#_ENREF_2)]. We propose to establish species *Orthonairovirus yezoense* to classify this virus. | |

**Supporting evidence**

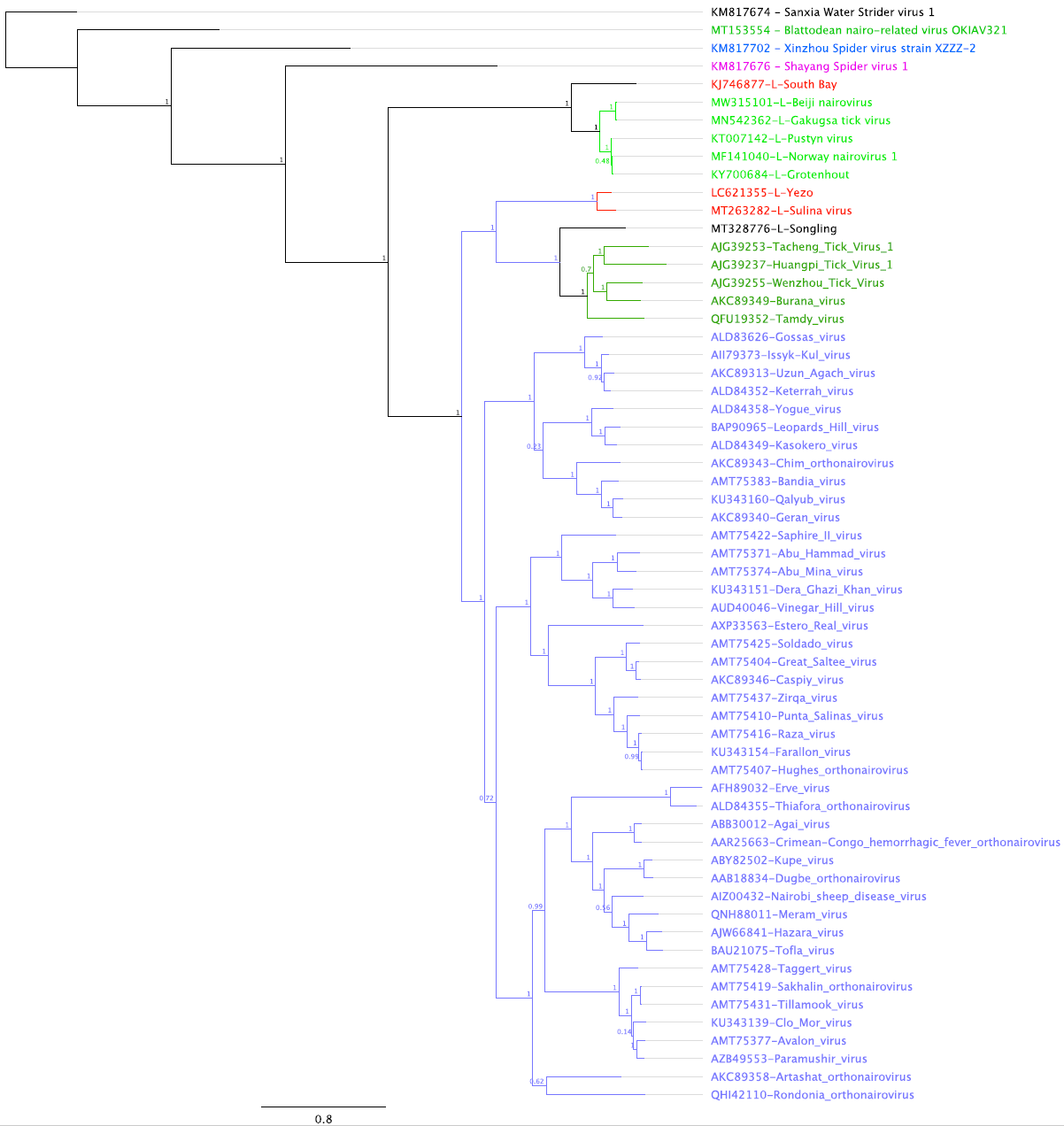
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Figure 1. The maximum-likelihood phylogenetic tree was inferred using IQtree [[5](#_ENREF_5)]; the numbers on the nodes represent bootstrap values derived from the ultrafast bootstrap algorithm [[1](#_ENREF_1)]. Trees were inferred under the LG+G+I 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.

**References**

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