

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

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| **Code assigned:** | ***2023.029M*** |  |
| **Short title:** Create 7 new species in the family *Nyamiviridae* (*Mononegavirales*) |
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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 *Nyamiviridae* 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 *Nyamiviridae* Study Group | 5 | 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 |

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| --- | --- | --- |
| **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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| 2023.029M.N.v1.Nyamiviridae\_7nsp.xlsx |

**Abstract**

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| We propose the creation of one new species in the genus *Formivirus*, one new species in the genus *Nyavirus*, one new species in the genus *Tapwovirus* and four new species in the genus *Berhavirus*, in the mononegaviral family *Nyamiviridae*. |

**Text of proposal**

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| **One new species in the genus *Formivirus***Ixodes ricinus orinovirus-like virus (IROV1) isolate CT8 was identified by high throughput sequencing (HTS) in the metagenome of a pool of ixodid castor bean ticks (*Ixodes ricinus* (Linnaeus, 1758)) in Croatia [1]. The coding-complete (CC) genome contains 10,148 nucleotides (GenBank #ON684369) and has six ORFs in the order 3'-N-2-3-4-G-L-5'. The IROV 1 L protein amino acid sequence is 42% identical to that of hymenopteran orino-related virus OKIAV85 (genus *Formivirus*). In an ML phylogenetic tree of the RdRp, IROV1 clustered with the formiviruses Formica fusca virus 1 and Formica exsecta virus 4. We propose to classify IROV 1 in the new species *Formivirus ixodis*.**One new species in the genus *Nyavirus***Toure virus (TOUV) isolate DAKAnD 4611 was isolated from liver tissue of murid northern savanna gerbils (*Gerbilliscus kempi* (Wroughton, 1906)) in Senegal in 1968. The CC genome contains 12,117 nucleotides (GenBank #OL774864) and has six ORFs in the order 3'-N-2-P-M-G-L-5'. The TOUV genome has highest nucleotide sequence identity with that of known nyaviruses. The TOUV L protein amino acid sequence is about 60% identical to that of the nyaviruses Midway virus, Nyamanini virus, Sierra Nevada virus, San Jacinto virus, and Jeremy Point virus in a Blast P analysis. In an ML phylogenetic tree of the RdRp, TOUV clustered with the known nyaviruses. We propose to classify TOUV in the new species *Nyavirus gerbillisci*.**One new species in the genus *Tapwovirus***Taeniapi virus (TNPV) was discovered by mining of HTS data of taeniid rabbit tapeworms (*Taenia pisiformis* Bloch 1780) [2]. The CC genome consists of two segments, RNA 1 of 5,981 nucleotides encoding the L protein (GenBank #BK059762) and RNA 2 of 4,742 nucleotides has four ORFs in the order 3'-1-2-3-G-5' (GenBank #BK059763). In a Blast P search, the TNPV L protein amino acid sequence is 79.6% identical to that of Wēnzhōu tapeworm virus 1 (WTV1). In ML phylogenetic trees of the L protein [2, figure S7], TNPV clusters with the only known tapwovirus WTV1. We propose to classify TNPV in the species *Tapwovirus taeniae*.**Four new species in the genus *Berhavirus*****Girado virus 1, 2 and 3** were discovered by mining of HTS data of a dugesiid triclad (*Girardia dorotocephala* (Woodworth, 1897)) [2]. The girado virus 1 (GiV1) CC genome consists of 11,626 nucleotides (GenBank #BK059719) has seven ORFs in the order 3'-1-2-3-4-5-L-7-5'. The girado virus 2 (GiV2) CC genome consists of 11,839 nucleotides (GenBank #BK059720) and has five ORFs in the order 3'-1-2-3-4-L-5'. The girado virus 3 (GiV3) CC genome consists of 11,534 nucleotides (GenBank #BK059721) and has five ORFs in the order 3'-1-2-3-4-L-5'. In Blast P searches, the L protein amino acid sequence of GiV1 was 59% identical to that of GiV2 and 57% identical to that of GiV3. GiV2 and GiV3 L protein sequences were 75% identical. GiV1, 2, and 3 L protein sequences were 33–35% identical to that of the established berhavirus Běihǎi rhabdo-like virus 3. In ML phylogenetic trees of the L protein [2, figure S7], GiV1 and GiV2 clustered closely together and formed a subclade with GiV3 within viruses of the genus *Berhavirus*. We propose to classify GiV1, GiV2, and GiV3 in the new species *Berhavirus alphagirardiae*, *Berhavirus betagirardiae* and *Berhavirus gammagirardiae*, respectively.**Macroli virus (MacrV)** was discovered by mining of HTS data of a macrostomid flatworm (*Macrostomum lignano* Ladurner, Schärer, Salvenmoser, & Rieger, 2005) [2]. The MacrV CC genome consists of 8,517 nucleotides (GenBank #BK059722) and has four ORFs in the order 3'-1-2-3-L-5'. In Blast P searches, the MacrV L protein amino acid sequence was 38% identical to that of the established berhavirus Běihǎi rhabdo-like virus 3. In ML phylogenetic trees of the L protein [2, figure S7], MacrV clustered with Běihǎi rhabdo-like virus 3 and with the other established berhaviruses, including the newly proposed dirado1–3 viruses. We propose to classify MacrV in the new species *Berhavirus macrostomi*. |

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**Supporting evidence**

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**Figure 1.** Phylogenetic relationships of established and proposed nyamivirids. The maximum likelihood phylogenetic tree is based on a MASFFT alignment of the L protein amino acid sequences using the E-INS-I algorithm and was inferred with the IQ-TREE software and the LG substitution model. Numbers on branch nodes represent ultrafast bootstrap values (1,000 replicates). New nyamivirids are shown in blue font.

**References**

[1] Sameroff S, Tokarz R, Vucelja M, Jain K, Oleynik A, Boljfetic M, Bjedov L, Yates RA, Margaletic J, Oura CLA, Lipkin WI, Krajinovic LC, Marcotic A (2022) Virome of *Ixodes ricinus*, *Dermacentor reticulans*, and *Haemaphysalis concinna* ticks from Croatia. Viruses 14, 929. <https://doi.org/10.3390/v14050929>

[2] Dheilly NM, Lucas P, Blanchard Y, Rosario K (2022) A world of viruses nested within parasites: Unraveling viral diversity within parasitic flatworms (Platyhelminthes). Microbiol Spectrum 10, 3. <http://doi.org/10.1128/spectrum.00138-22>.