

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

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| **Code assigned:** | ***2022.016M*** |  |
| **Short title:** Create one new species in genus *Formivirus* and one new species in genus *Orinovirus* (*Mononegavirales*: *Nyamiviridae*) | | |
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**Author(s) and email address(es)**

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**Corresponding author**

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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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| Approved. |

**ICTV Study Group votes on proposal**

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| --- | --- | --- | --- |
| **Study Group** | **Number of members** | | |
| **Votes support** | **Votes against** | **No vote** |
| OCTV *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)** |
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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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| 2022.016M.N.v1.Nyamiviridae\_2nsp.xlsx |

**Abstract**

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| *Nyamiviridae* is a family of viruses in the order *Mononegavirales* for viruses with unsegmented or segmented, negative-sense RNA genomes. Two novel unsegmented invertebrate-infecting nyamivirids were discovered recently and their complete or coding-complete genome sequences determined. This proposal aims to taxonomically classify these two viruses in two new species in the nyamivirid genera *Formivirus* and *Orinovirus*, respectively. |

**Text of proposal**

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| |  | | --- | | We propose the taxonomic classification of two novel nyamivirids in two new species in two established genera. Species classified in genera of this family are demarcated based upon their members’ phylogeny and hosts.  **One new species in the genus *Orinovirus***  **Sanya nyamivirus 1 (SaNyV-1)** was identified in the metagenome of the *Paederus fuscipes* Curtis, 1826 beetle (Coleoptera) sampled in a rice field in China [1]. The complete genome of 9,925 nucleotides (GenBank #MZ209903) was assembled from Illumina HTS data and contains 3’ and 5’ UTRs. The genome encodes five ORFs in the order 3’-1–2–3–4–L-5’. The SaNyV-1 L protein amino acid sequence is 63.8% identical to that of the unclassified orino-related virus OKIAV84, 55.5% to Orinoco virus (genus *Orinovirus*), 36.3% to Formica fusca virus 4 (genus *Formivirus*) and 33.6% to Nyamanini virus (genus *Nyamivirus*). In a phylogenetic tree of L protein amino acid sequences, SaNyV-1 clusters closely with Orinoco virus (Figure 1).  We propose to classify SaNyV-1 in the new species *Orinovirus sanyae* in the genus *Orinovirus*.  **One new species in the genus *Formivirus***  **Xiāngshān nyami-like virus (XNyV)** was identified in the metagenome of wild insect pollinators in Xiāngshān Park (香山公园), Beijing, China [2]. The coding-complete genome of 9,797 nucleotides (GenBank #OK491485) of isolate “Novel\_9” was assembled from Illumina insect metagenome data. The genome encodes five ORFs in the order 3’-1–2–3–4–L -5’. The closest relative of XNyV is orino-related virus OKIAV85 (genus *Formivirus*) with 63.5% amino acid sequence identity in the L protein. In phylogenetic ML analysis inferred from conserved RdRp amino acid sequences, XNyV clustered closest with hymenopteran orino-related OKIAV85 (species *Formivirus gorytis*), in a larger cluster including the other recognized formiviruses, Formica fusca virus 1 (FfV-1) (species *Formivirus* *angliae*), Formica exsecta virus 4 (FeV-4) (species *Formivirus finnoniae*), hymenopteran orino-related virus OKIAV87 (species *Formivirus chalbii*) and Solenopsis invicta virus 15 (species *Formivirus solenopsi*) (Figure 1).  We propose to classify XNyV in the new species *Formivirus pollinis*.  **Other related viruses**  In a NCBI BlastN search, the SaNyV-1 genome nucleotide sequence is 98% identical to the 8,234 nucleotides partial genome sequence of Hángzhōu nyamivirus 1 (MZ209713). Based on NCBI metadata, both sequences originated from the same source material and Hángzhōu nyamivirus 1 should be considered as an additional isolate of SaNyV-1.  Ixodes ricinus orinovirus-like virus 1 (IROV-1) was identified by HTS in the metagenome of a pool of castor bean ticks (ixodid *Ixodes ricinus* (Linnaeus, 1758)) from Croatia [3]. The coding-complete genome contains 10,148 nucleotides [3] and encodes six ORFs in the order 3’–N–2–3–4–G–L-5’. The provided sequencing project code PRJNA802541 is not recognized by NCBI and a GenBank accession number for the IROV-1 genome sequence is not currently available. This virus can therefore not be formally classified at this point. According to the peer-reviewed publication [3], the IROV-1 L protein amino acid sequence is 42% identical to that of hymenopteran orino-related virus OKIAV85 (genus *Formivirus*). In a ML phylogenetic tree of the RdRp fragment, IROV-1 clustered with the formiviruses Formica fusca virus 1 and Formica exsecta virus 4. Once the sequence can be verified, IROV-1 should be classified in a new species in the genus *Formivirus*. | |

**Supporting evidence**

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**Figure 1.** Phylogenetic relationships of established and proposed nyamivirids. The maximum likelihood phylogenetic tree is based on a MAFFT 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 (1000 replicates). Proposed new nyamivirids are shown in blue font.

**References**

[1] Feng G (2021) Sanya nyamivirus 1 isolate QCYXYSY225, complete genome. GenBank #MZ209903

[2] Li N, Huang Y, Li W, Xu S (2022) Virome analysis reveals diverse and divergent RNA viruses in wild insect pollinators in Beijing, China. Viruses 14, 227. <https://doi.org/10.3390/v14020227> PMID: [35215821](https://pubmed.ncbi.nlm.nih.gov/35215821/?utm_source=gquery&utm_medium=referral&utm_campaign=CitationSensor?otool=None)

[3] 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>