

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

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| **Code assigned:** | **2021.019M** |  |
| **Short title:** Create two new species in genus *Nyavirus* and one new species in genus *Formivirus* (*Mononegavirales*: *Nyamiviridae*) | | |
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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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| N/A |

**Submission dates**

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| Date first submitted to SC Chair | May 28, 2021 |
| Date of this revision (if different to above) | September 13, 2021 |

**ICTV-EC comments and response of the proposer**

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| * Paraskevopoulou first initial needs to be changed from N to S   Response: done.   * what are the criteria for species demarcation? those criteria should be explained in the text for clarity   Response: added the following sentence: “Species classified in genera of this family are demarcated based upon their members’ phylogeny and hosts.”   * Read the EC-distributed guidance on species naming document, confirm that proposed species names adhere to the guidance, and confirm that you would like to keep the proposed species names as originally proposed.   Response: Read, confirmed, and confirmed. |

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

**Name of accompanying Excel module**

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| 2021.019M.R.Nyamiviridae\_3nsp |

**Abstract**

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

**Text of proposal**

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| |  | | --- | | We propose the taxonomic classification of three novel nyamivirids in three new species in two established genera in the family *Nyamiviridae.* Species classified in genera of this family are demarcated based upon their members’ phylogeny and hosts.  **Two new species in the genus *Nyavirus***  1) **Sekira virus (SEKRV)** was identified in the RNA virome of a pool of soft ticks (*Argas japonicus* Yamaguti, Clifford and Tipton, 1968) [1]. The ticks had been collected from a nest of an Asian house martin (*Delichon dasypus* (Bonaparte, 1850)) at Mishima, Japan, in 2019. The apparently complete genome of 8,799 nucleotides (GenBank #LC585887) was determined by Illumina HTS and validated by PCR and RACE [1]. The genome has only four ORFs with sequence similarities to the nyavirus N, X, P, and L genes in the order 3’-N-X-P-L-5’, and lacks the M and G genes. SEKRV clusters with the other recognized nyaviruses (MIDWV, NYMV, SNVV, SJCV), and with Jeremy Point virus (JPNV; see below) in a ML phylogenetic tree of the L protein (Figure 1).  2) Jeremy Point nyavirus (JPNV) was identified in the spleen of a common eider (*Somateria mollissima* (Linnaeus, 1758)) collected at Jeremy Point, Cape Cod National Seashore, Massachusetts, USA, in 2013. The complete genome sequence of 12,659 nucleotides (isolate 13-143, GenBank #MN045233) has been determined [2]. The genome encodes eight ORFs in the order 3’-N-X-P-M-P5-P6-G-L-5’. JPNV clusters with all other nyaviruses in an L protein ML phylogenetic tree (Figure 1).  We propose to classify SEKRV in the new species *Nyavirus argatis* and JPNV in the new species *Nyavirus somateriae* after the host genus names (*Argas* and *Somateria*, respectively)  **One new species in the genus *Formivirus***  **Solenopsis invicta virus 15 (SoINV-15)** was identified in the transcriptome of red fire ants (*Solenopsis invicta* Buren, 1972). The coding-complete sequence of 10,128 nucleotides (GenBank #MT860232) has been assembled by mining of SRA data from *S. invicta* ants collected in the USA [3]. The genome encodes five ORFs in the order 3’-N-P-M-G-L-5’. In a L protein amino acid sequence tree, SoINV-15 clustered closest to Formica fusca virus 1 and Formica exsecta virus 4 in the genus *Formivirus* ([3]; Figure 1).  We propose to classify SoINV-15 in the new species *Formivirus solenopsi* 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 bootstrap values (1000 replicates). Proposed new nyamivirids are shown in blue font.

**References**

[1] Kobayashi D, Komatsu N, Faizah AN, Amoa-Bosompem M, Sawabe K, Isawa H (2021) A novel nyavirus lacking matrix and glycoprotein genes from *Argas japonicus* ticks. Virus Res 292, 198254. PMID: **33276024** <https://doi.org/10.1016/j.virusres.2020.198254>

[2] Sebastian AL, Feng KH, Grenier JK, Allison AB (2019) Jeremy Point nyavirus isolate 13-143. GenBank #MN045233.

[3] Xavier CAD, Allen ML, Whitfield AE (2021) Ever-increasing viral diversity associated with the red imported fire ant *Solenopsis invicta* (Formicidae: Hymenoptera). Virology J 18, 5. PMID: **33407622**  PMCID: [PMC7788728](http://www.ncbi.nlm.nih.gov/pmc/articles/pmc7788728/) DOI: [10.1186/s12985-020-01469-w](https://doi.org/10.1186/s12985-020-01469-w)