

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

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| **Code assigned:** | **2020.024M** |  |
| **Short title:** Create one new species in the genus *Nyavirus* and four new species in one new genus *Formivirus* (*Mononegavirales*: *Nyamiviridae*) | | |
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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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**Submission dates**

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| Date first submitted to SC Chair | July 28, 2020 |
| Date of this revision (if different to above) | November 23, 2020 |

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

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| All text edits proposed by the ICTV-EC have been incorporated into this revised proposal. GenBank accession numbers for all new sequences have now been assigned and are provided. |

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

**Name of accompanying Excel module**

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| 2020.024M.R.Nyamiviridae\_1ngen\_5nsp |

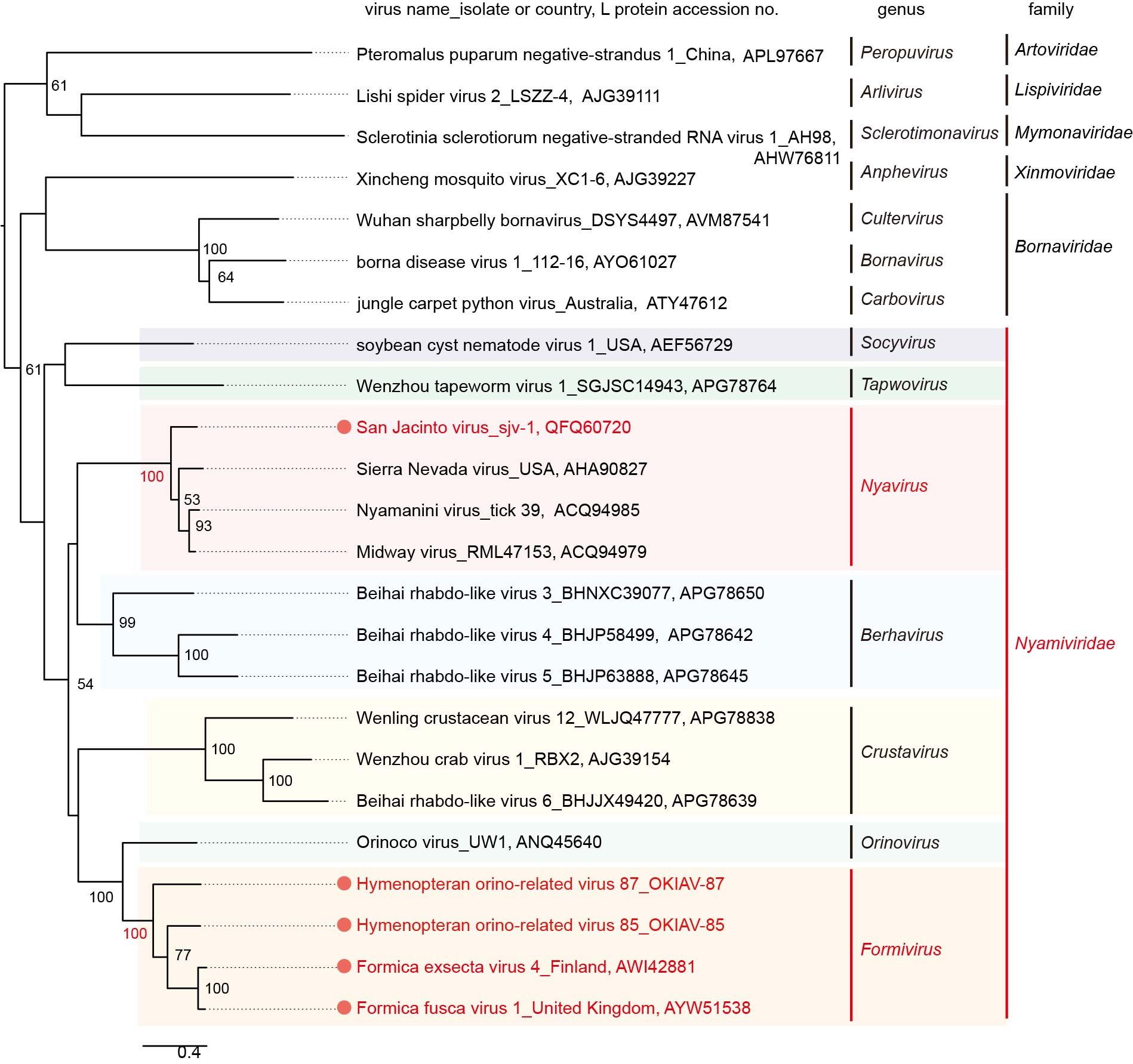
**Abstract**

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| We propose the taxonomic placement of five viruses into five new species in the family *Nyamiviridae:* One new species in the established genus *Nyavirus,* and four new species in a new genus, *Formivirus*. The two viruses infecting ants of different species and two hymenopteran viruses form a well-supported monophyletic phylogenetic cluster (new genus *Formivirus*), divergent from Orinoco virus in the established *Orinovirus* genus that forms a sister clade. |

**Text of proposal**

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| |  | | --- | | 1. **Create one new species in the genus *Nyavirus*, family *Nyamiviridae***   The genus *Nyavirus* currently includes three species, one for each of the following: Nyamanini virus (NYAV), Midway virus (MIDWV), and Sierra Nevada virus (SNVV) [1]. We propose the creation of a fourth species named *Jacinto nyavirus* for **San Jacinto virus** (SJCV). SJCV was isolated from the brains of dead birds in Harris County, Texas in 2013. Experimentally infected Vero E6 cells showed large virus particles that were either spherical (320-800 nm diameter) or pleomorphic and elongated (ranging from 350 x 540 nm to 280 x 1120 nm and 3280 x 1275 nm). Large numbers of virions were seen at the cell surface [1]. No cross-reaction with other nyaviruses occurred in complement fixation tests [1].  The coding-complete genome (missing the exact 3’ and 5’ ends) of the DO-200 isolate is 13,295 nucleotides long (MK971153) and encodes 7 open reading frames (ORFs) in the order 3’-N-X-P-M-G-P6-L-5’ [2]. SJCV has a unique genome organization compared to other classified nyaviruses in that it encodes a small ORF, P6, between the G and L ORFs. This ORF has significant amino-acid sequence identity to the N-terminal domain of L protein and may have arisen by gene duplication. L protein amino-acid sequence identities with NYAV, MIDWV, and SNVV are 62.4–82.4% [1]. Genome sequence identity with these nyaviruses is 66.4–67.4%. Based on ML trees generated from complete L‑protein sequences, SJCV cluster phylogenetically with the other nyaviruses [1] (Figure 1).   1. **Create new genus *Formivirus*,including four new species, in the family *Nyamiviridae***   Two novel mononegaviruses that phylogenetically cluster with members of the family *Nyamiviridae* were recently discovered in ants of two species: Formica fusca virus 1 (FfusV-1) and Formica exsecta virus 4 (FeV-4) [3, 4]. Also, two novel nyamivirids were identified in hymenopteran insects and named hymenopteran orino‑related virus 85 (HORV-85) and hymenopteran orino-related virus 87 (HORV‑87) [5]. All four viruses are phylogenetically related to Orinoco virus, genus *Orinovirus*, family *Nyamiviridae*, but form a well-supported distinct lineage separated from Orinoco virus. We propose creation of the new genus *Formivirus* and classification of these four viruses in four new species (one in each) within this new genus.  **Viruses to be assigned, genome organization, phylogeny, and sequence relationships**  **Formica fusca virus 1** (FfusV-1) was discovered in a *Formica fusca* ant transcriptomic dataset [3]. The FfusV-1 complete genome (MH477287) is comprised of 9,851 nucleotides and encodes five ORFs in the order 3’-N-P-M-G-L-5’. The FfusV-1 genome nucleotide sequence is 71% identical to that of Formica exsecta virus 4 (FeV-4). Blast-P analysis of the L protein reveals 81.4% amino-acid sequence identity with the L protein of FeV-4, 47.6% with hymenopteran orino-related virus 87 (see below) and 39.1% with orinoco virus L protein. We propose classification of FfusV-1 in the new species *Fusca formivirus.*  **Formica exsecta virus 4** (FeV-4) was identified in a *Formica exsecta* ant [4]. The FeV‑4 complete genome (MF287670) is comprised of 9,866 nucleotides and encodes five ORFs in the order 3’-N-P-M-G-L-5’. We propose classification of FeV-4 in the new species *Exsecta formivirus*.  **Hymenopteran orino-related virus 85** (HORV-85; strain OKIAV85) was discovered in the transcriptome shotgun assembly (TSA) of a sand wasp (*Gorytes laticinctus*) collected in Germany in 2011 [5]. The near-complete genome sequence (9,813 nucleotides) has been determined (MW039259), including complete coding sequences but incomplete 3' and 5' termini [5, 6]. We propose assigning hymenopteran orino-related virus 85 to the new species *Gorytes formivirus.*  **Hymenopteran orino-related virus 87** (HORV-87; strain OKIAV87) was discovered in the TSA of a blue mud dauber wasp (*Chalybion californicum*) collected in Tennessee, United States in 2011 [5]. The near-complete genome sequence (9,703 nucleotides) has been determined (MT153386), including complete coding sequences but incomplete 3' and 5' termini [5, 6]. The L protein amino-acid sequence of OKIAV87 is 47.6% identical to that of FfusV‑1. We propose assigning hymenopteran orino-related virus 87 to the new species *Chalybion formivirus.*  **Derivation of the genus name**  *Formivirus* is derived from *Formica,* the ant genus name associated with the ant in which the type member was discovered.  **Type species**  *Fusca formivirus* is designated as the type species of the genus because the complete genome sequence of its member virus is known, and this virus is the best characterized of the formiviruses. | |

**Supporting evidence**

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**Figure 1.** Phylogenetic maximum-likelihood tree of mononegavirus L polymerase protein sequences highlighting Nyamiviridae and its genera. Amino-acid sequences were aligned using MAFFT version 7, and then the alignment was filtered using Gblocks 0.91b. The resulting alignment was used to generate a phylogenetic tree using PhyML 3.0 with the best-fit model LG + G + I +F. The colors indicate the different mononegavirus families and nyamivirus genera. Numbers at the nodes indicate bootstrap support over 50% (100 replicates) [taken from [1]].

**References**

[1] Dietzgen RG, Jiang D, Kondo H, Kuhn JH, Vasilakis N (2019) *Nyamiviridae*. <https://talk.ictvonline.org/ictv-reports/ictv_online_report/negative-sense-rna-viruses/mononegavirales/w/nyamiviridae>

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[6] Käfer S et al. (2019) Data from: Re-assessing the diversity of negative strand RNA viruses in insects, v9, Dataset <https://doi.org/10.5061/dryad.87vt6hm>