

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

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| **Code assigned:** | ***2022.014M*** |  |
| **Short title:** Establishment of thirteen new species in genera *Auricularimonavirus*, *Hubranonavirus,* *Lentimonavirus*, *Penicilliumonavirus*, *Plasmopamonavirus* and *Sclerotimonavirus* in family *Mymonaviridae* (*Mononegavirales*) | | |
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**List the ICTV Study Group(s) that have seen this proposal**

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| ICTV *Mymonaviridae* 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 *Mymonaviridae* Study Group | 5 | 0 | 0 |

**Authority to use the name of a living person**

|  |  |
| --- | --- |
| **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)** |
|  |  |  |

**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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| 2022.014M.N.v1.Mymonaviridae\_13nsp.xlsx |

**Abstract**

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| We propose the establishment of one new species in genus *Auricularimonavirus*, three in genus *Hubranonavirus*, one in genus *Lentimonavirus*, four in genus *Penicilliumonavirus*, one in genus *Plasmopamonavirus* and thee in genus *Sclerotimonavirus*, all in mononegaviral family *Mymonaviridae*. |

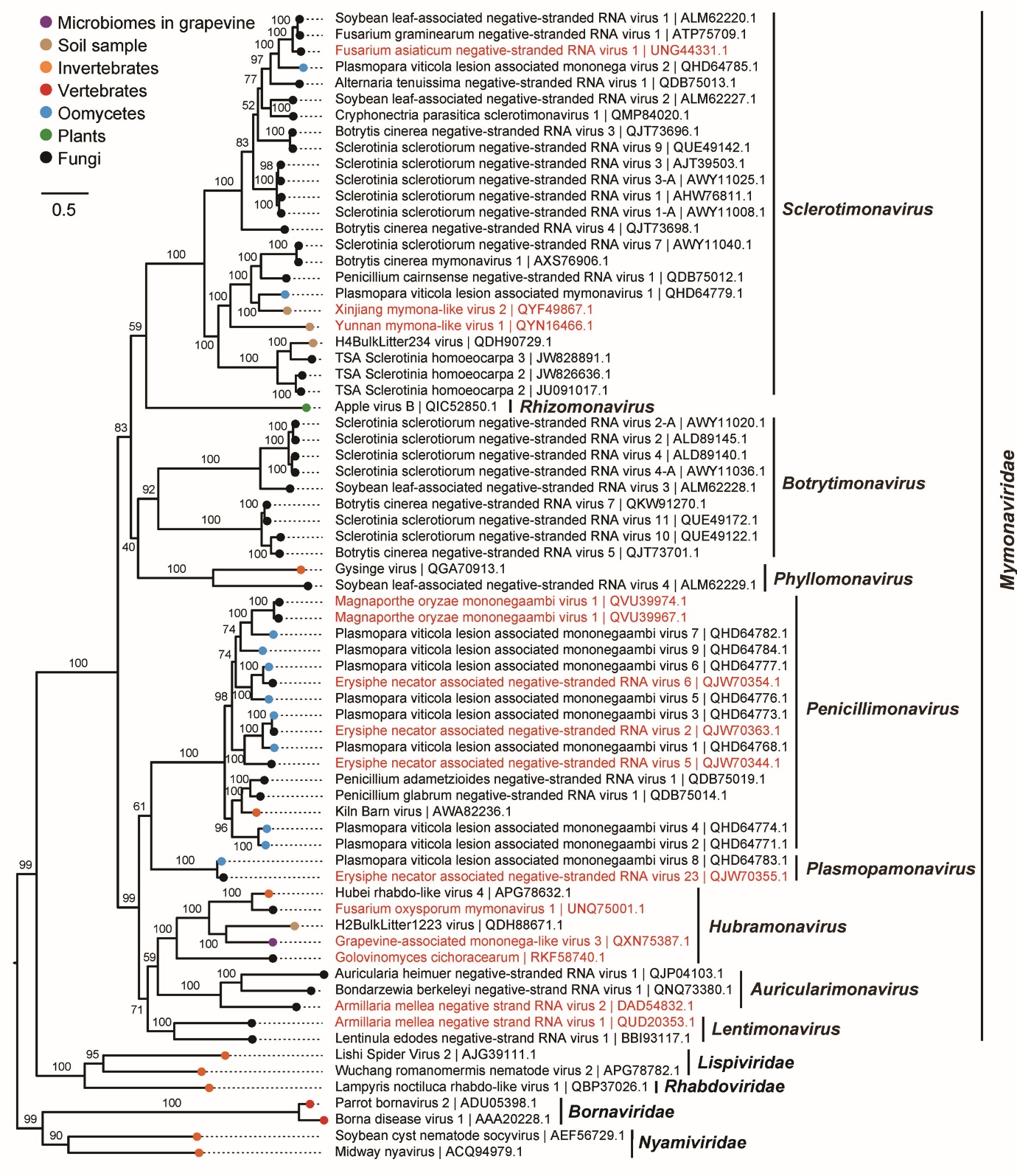
**Text of proposal**

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| |  | | --- | | The monjiviricete family *Mymonaviridae* currently includes nine genera. Genera *Auricularimonavirus*, *Hubramonavirus*, *Lentimonavirus*, *Penicillimonavirus*, *Plasmopamonavirus and Sclerotimonavirus* include two, two, one, ten, one and fourteen species, respectively. We searched the NCBI database for novel mymonavirids and found that, based upon available coding-complete genome sequences, several novel viruses should be classified into a total of thirteen novel species in *genera* *Auricularimonavirus*, *Hubramonavirus*, *Lentimonavirus*, *Penicillimonavirus*, *Plasmopamonavirus* and *Sclerotimonavirus* (Table 1). The phylogenetic analysis and alignment of selected viruses are shown in Figures 1 and 2. 32% L protein amino acid sequence identity is proposed as a genus rank demarcation threshold. The demarcation criteria for species (80%) and genus demarcation (32%) in the family *Mymonaviridae* also are supported by the result of phylogenetic analysis. | |

**Supporting evidence**

**Table 1** Newly proposed species of the family *Mymonaviridae*

|  |  |  |  |  |  |
| --- | --- | --- | --- | --- | --- |
| Genus name | New species name | Newly identified virus | Accession number | Host | Reference |
| *Auricularimonavirus* | *Auricularimonavirus armillariae* | Armillaria mellea negative strand RNA virus 2 | BK014417 | Fungi, *Armillaria mellea* | 1 |
| *Hubramonavirus* | *Hubramonavirus fusarii* | Fusarium oxysporum mymonavirus 1 | OM049502 | Fungi, *Fusarium oxysporum* | 2 |
| *Hubramonavirus vitis* | Grapevine-associated mononega-like virus 3 | MW648481 | Grapevine associated | 3 |
| *Hubramonavirus golovinomycesae* | Golovinomyces cichoracearum GcM3\_contig\_4635 | MCBQ01018032 | *Golovinomyces cichoracearum* | 4 |
| *Lentimonavirus* | *Lentimonavirus armillariae* | Armillaria mellea negative strand RNA virus 1 | MW423801 | Fungi, *Armillaria mellea* | 1 |
| *Penicillimonavirus* | *Penicillimonavirus magnaporthe* | Magnaporthe oryzae mononegaambi virus 1 | MW752165 | Fungi, *Magnaporthe oryzae* | NCBI:txid2838328 |
| Magnaporthe oryzae mononegaambi virus 1 | MW752172 | Fungi, *Magnaporthe oryzae* | NCBI:txid2838328 |
| *Penicillimonavirus alphaerysiphe* | Erysiphe necator associated negative-stranded RNA virus 2 | MN617061 | Fungi, *Erysiphe necator* | NCBI:txid2737064 |
| *Penicillimonavirus betaerysiphe* | Erysiphe necator associated negative-stranded RNA virus 5 | MN617042 | Fungi, *Erysiphe necator* | NCBI:txid2737072 |
| *Penicillimonavirus gammaerysiphe* | Erysiphe necator associated negative-stranded RNA virus 6 | MN617052 | Fungi, *Erysiphe necator* | NCBI:txid2737073 |
| *Plasmopamonavirus* | *Plasmopamonavirus erysiphe* | Erysiphe necator associated negative-stranded RNA virus 23 | MN617053 | Fungi, *Erysiphe necator* | NCBI:txid2737068 |
| *Sclerotimonavirus* | *Sclerotimonavirus asiafusarii* | Fusarium asiaticum negative-stranded RNA virus 1 | MZ969066 | Fungi, *Fusarium asiaticum* | NCBI:txid2921215 |
| *Sclerotimonavirus xinjiangense* | Xinjiang mymona-like virus 2 | MW897041 | Soil associated | 5 |
| *Sclerotimonavirus yunnanense* | Yunnan mymona-like virus 1 | MW897022 | Soil associated | 5 |

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**Figure 1** Phylogenetic tree of the expanded and reorganized family *Mymonaviridae*. A maximum likelihood phylogenetic tree was constructed based on the multiple amino acid sequence alignment of the RNA-directed RNA polymerase (RdRp) using IQ-TREE (version 1.6.11) [1] with the best-fit model “LG+F+R6”. The tree was midpoint-rooted for clarity of presentation and 1,000 bootstrap replicates were performed. Nguyen L-T, Schmidt HA, von Haeseler A, Minh BQ. IQ-TREE: a fast and effective stochastic algorithm for estimating maximum-likelihood phylogenies. Mol Biol Evol. 2015; 32:268-274. Viruses classified in families *Lispiviridae*, *Rhabdoviridae*, *Nyamiviridae*, and *Bornaviridae* were used as outgroups. Newly identified viruses are written in red.



**Figure 2** Matrix diagram of amino acid identities of L proteins among members of the expanded and reorganized family *Mymonaviridae*. The percent identity matrix was created via multiple sequence alignment using Clustal Omega. Percent identity matrices were converted to heat map plots using a custom R script. Newly identified viruses are written in red.

**References**

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