

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

|  |  |  |
| --- | --- | --- |
| **Code assigned:** | ***2022.014M*** |  |
| **Short title:** Establishment of thirteen new species in genera *Auricularimonavirus*, *Hubranonavirus,* *Lentimonavirus*, *Penicilliumonavirus*, *Plasmopamonavirus* and *Sclerotimonavirus* in family *Mymonaviridae* (*Mononegavirales*) | | |
|  | | |

**Author(s) and email address(es)**

|  |  |
| --- | --- |
| Jiang D, Ayllón MA, Marzano S-Y, Kondo H, Turina M | Daohongjiang@mail.hzau.edu.cn; mariaangeles.ayllon@upm.es; shinyi.marzano@usda.gov;  hkondo@okayama-u.ac.jp; massimo.turina@ipsp.cnr.it |

**Author(s) institutional address(es) (optional)**

|  |
| --- |
| Huazhong Agricultural University [DJ]  Universidad Politécnica de Madrid (UPM) [MAA]  United States Department of Agriculture, Agricultural Research Service [SYLM]  Okayama University [HK]  Institute for Sustainable Plant Protection, CNR [MT] |

**Corresponding author**

|  |
| --- |
| Jiang D |

**List the ICTV Study Group(s) that have seen this proposal**

|  |
| --- |
| ICTV *Mymonaviridae* Study Group |

**ICTV Study Group comments and response of proposer**

|  |
| --- |
| Approved. |

**ICTV Study Group votes on proposal**

|  |  |  |  |
| --- | --- | --- | --- |
| **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**

|  |  |
| --- | --- |
| 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**

|  |
| --- |
|  |

**Part 2:** **NON-TAXONOMIC PROPOSAL**

**Text of proposal**

|  |
| --- |
|  |

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

**Name of accompanying Excel module**

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

**Abstract**

|  |
| --- |
| 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*. |

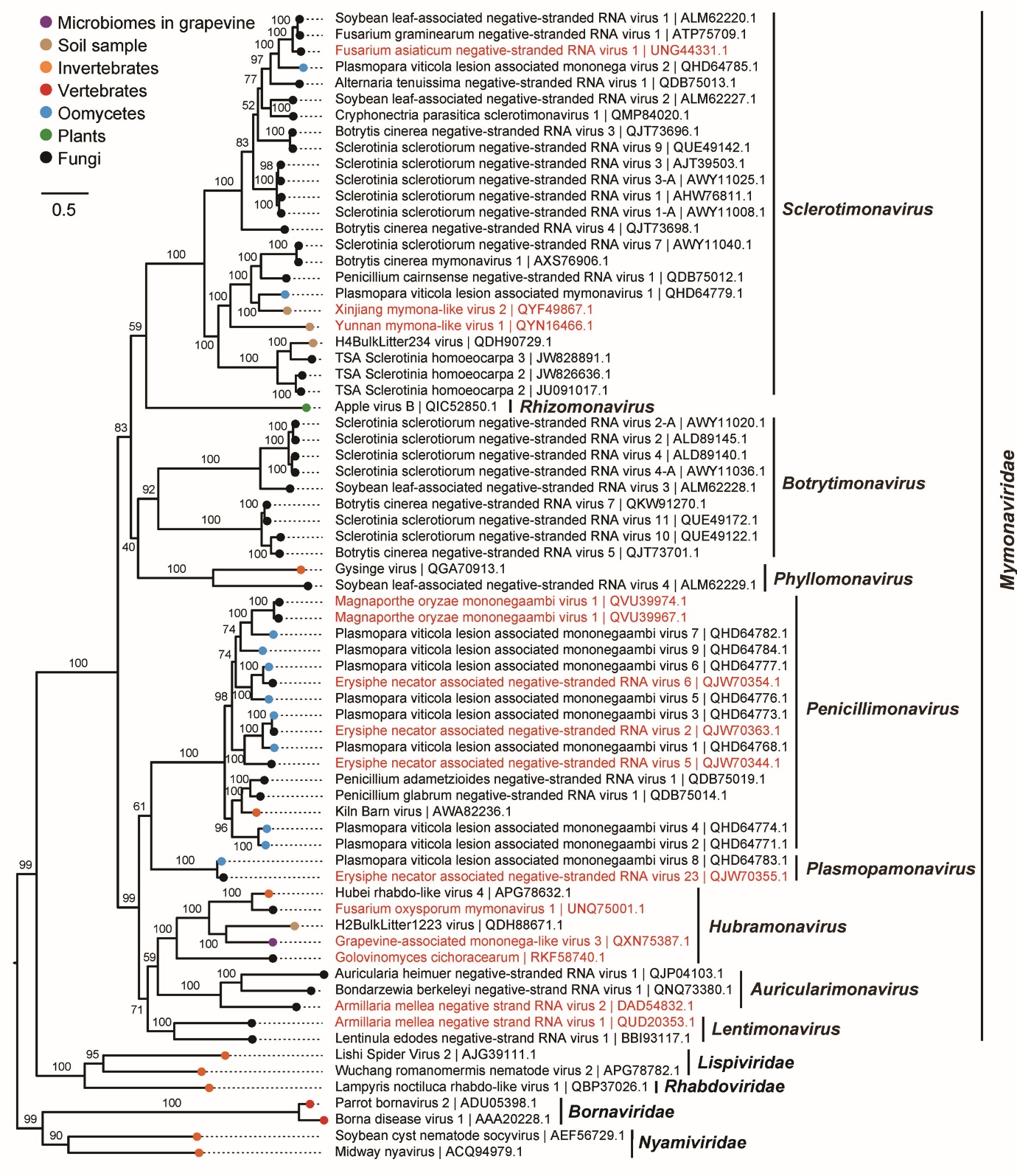
**Text of proposal**

|  |  |
| --- | --- |
| |  | | --- | | 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. | |

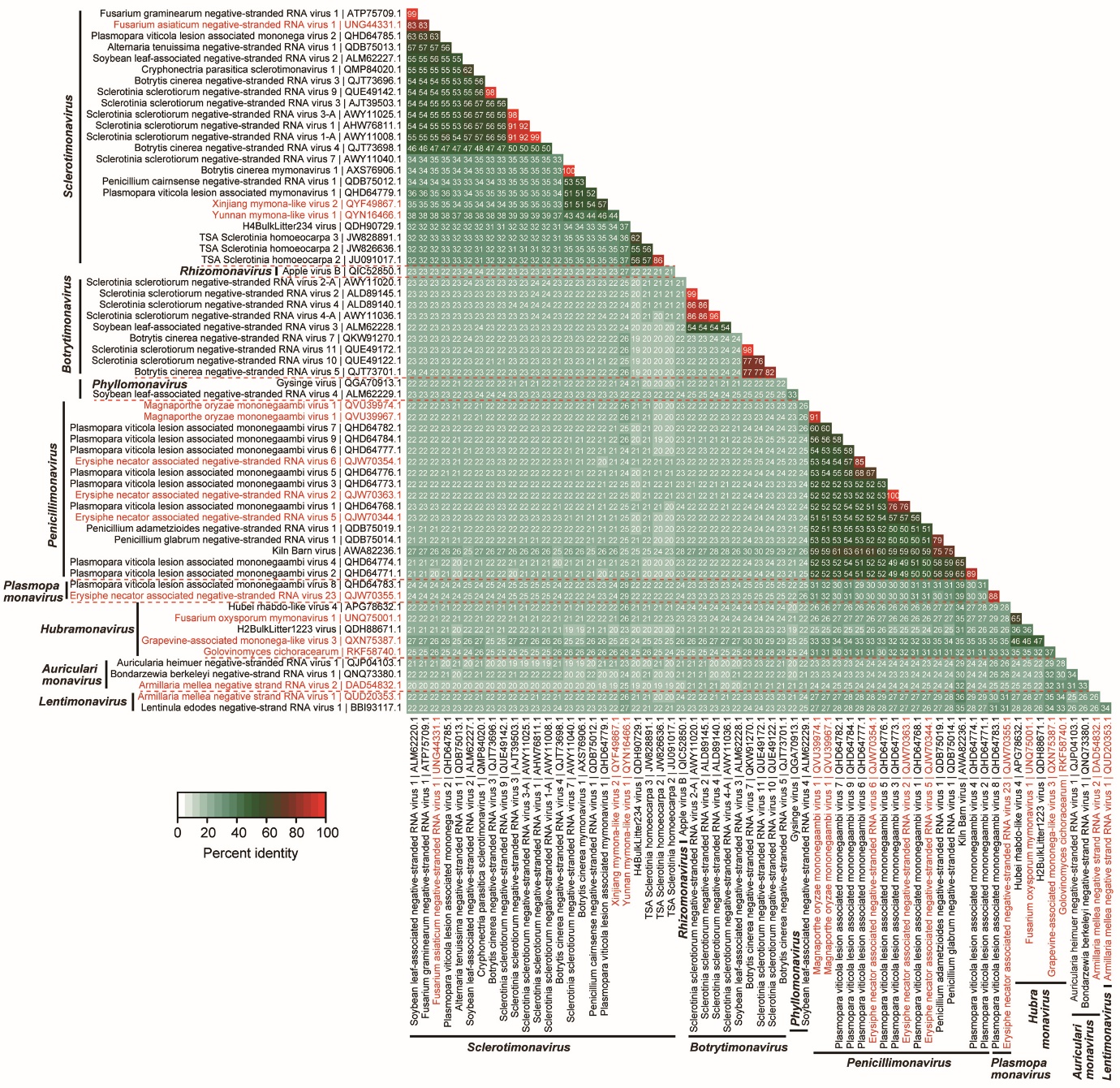
**Supporting evidence**

**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 |

****

**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**

1. Linnakoski R, Sutela S, Coetzee MPA, Duong TA, Pavlov IN, Litovka YA, Wingfield HJ, Vainio EJ (2021) Armillaria root rot fungi host single-stranded RNA viruses. Scientific Reports 11(1):7336. doi: 10.1038/s41598-021-86343-7.
2. Wang J, Li C, Song P, Qiu R, Song R, Li X, Ni Y, Zhao H, Liu H and Li S (2022) Molecular and biological characterization of the first mymonavirus identified in Fusarium oxysporum. Frontier in Microbiology 13:870204. doi.org/10.3389/fmicb.2022.870204
3. Nerva L, Garcia JF, Favaretto F, Giudice G, Moffa L, Sandrini M, Cantu D, Zanzotto A, Gardiman M, Velasco R, Gambino G, Chitarra W (2022) The hidden world within plants: metatranscriptomics unveils the complexity of wood microbiomes. Journal of Experimental Botany 73(8):2682-2697. doi: 10.1093/jxb/erac032.
4. Wu Y, Ma X, Pan Z, Kale SD, Song Y, King H, Zhang Q, Presley C, Deng X, Wei CI, Xiao S (2018) Comparative genome analyses reveal sequence features reflecting distinct modes of host-adaptation between dicot and monocot powdery mildew. BMC Genomics 19(1):705. doi: 10.1186/s12864-018-5069-z.
5. Chen, Yan-Mei and Chen, Yan-Mei and Sadiq, Sabrina and Tian, Jun-Hua and Chen, Xiao and Lin, Xian-Dan and Shen, Jin-Jin and Chen, Hao and Hao, Zong-Yu and Yang, Wei-Di and Zhou, Zhuo-Cheng and Wu, Jun and Li, Feng and Wang, Hong-Wei and Xu, Qi-Yi and Wang, Wen and Gao, Wen-Hua and Holmes, Edward C. and Zhang, Yong-Zhen, RNA Virome Composition Is Shaped by Sampling Ecotype. http://dx.doi.org/10.2139/ssrn.3934022
6. Nguyen LT, Schmidt HA, von Haeseler A, Minh BQ (2015) IQ-TREE: a fast and effective stochastic algorithm for estimating maximum-likelihood phylogenies. Mol Biol Evol 32:268-74. doi: 10.1093/molbev/msu300.