

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

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| **Code assigned:** | **2021.041M** |  |
| **Short title:** Create five new species in genera *Auricularimonavirus*, *Botrytimonavirus* and *Sclerotimonavirus* (*Mononegavirales*: *Mymonaviridae*) | | |
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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 Fungal and Protist Viruses Subcommittee Chair and Deputy Chair, ICTV Animal dsRNA and ssRNA- Viruses Subcommittee Chair; ICTV *Mymonaviridae* 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 | May 28, 2021 |
| Date of this revision (if different to above) |  |

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

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

**Name of accompanying Excel module**

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| 2021.041M.A.v1.Mymonaviridae\_5nsp |

**Abstract**

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| We create one new species in genus *Auricularimonavirus*, one in genus *Botrytimonavirus*, and three in genus *Sclerotimonavirus* of the mononegaviral family *Mymonaviridae*. |

**Text of proposal**

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| |  | | --- | | The monjiviricete family *Mymonaviridae* currently includes nine genera. Genera *Auricularimonavirus*, *Botrytimonavirus*, and *Sclerotimonavirus* include one, three and eleven 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 five novel species in genera *Auricularimonavirus*, *Botrytimonavirus*, and *Sclerotimonavirus* (Table 1), and one new virus can be assigned to an established species of genus *Botrytimonavirus* (Table 2). The phylogenetic analysis and alignment of selected viruses are shown in Figures 1 and 2.  The proposed species are named *Auricularimonavirus bondarzewiae*, *Botrytimonavirus alphabotrytidis, Sclerotimonavirus alphabotrytidis, Sclerotimonavirus betabotrytidis*,and *Sclerotimonavirus cryphonectriae*.  32% L protein amino acid sequence identity is proposed as a genus rank demarcation threshold. This demarcation can support most genera.  The demarcation criteria for species (80%) and genus demarcation (32%) in the family *Mymonaviridae* also are supported by the result of phylogenetic analysis. | |

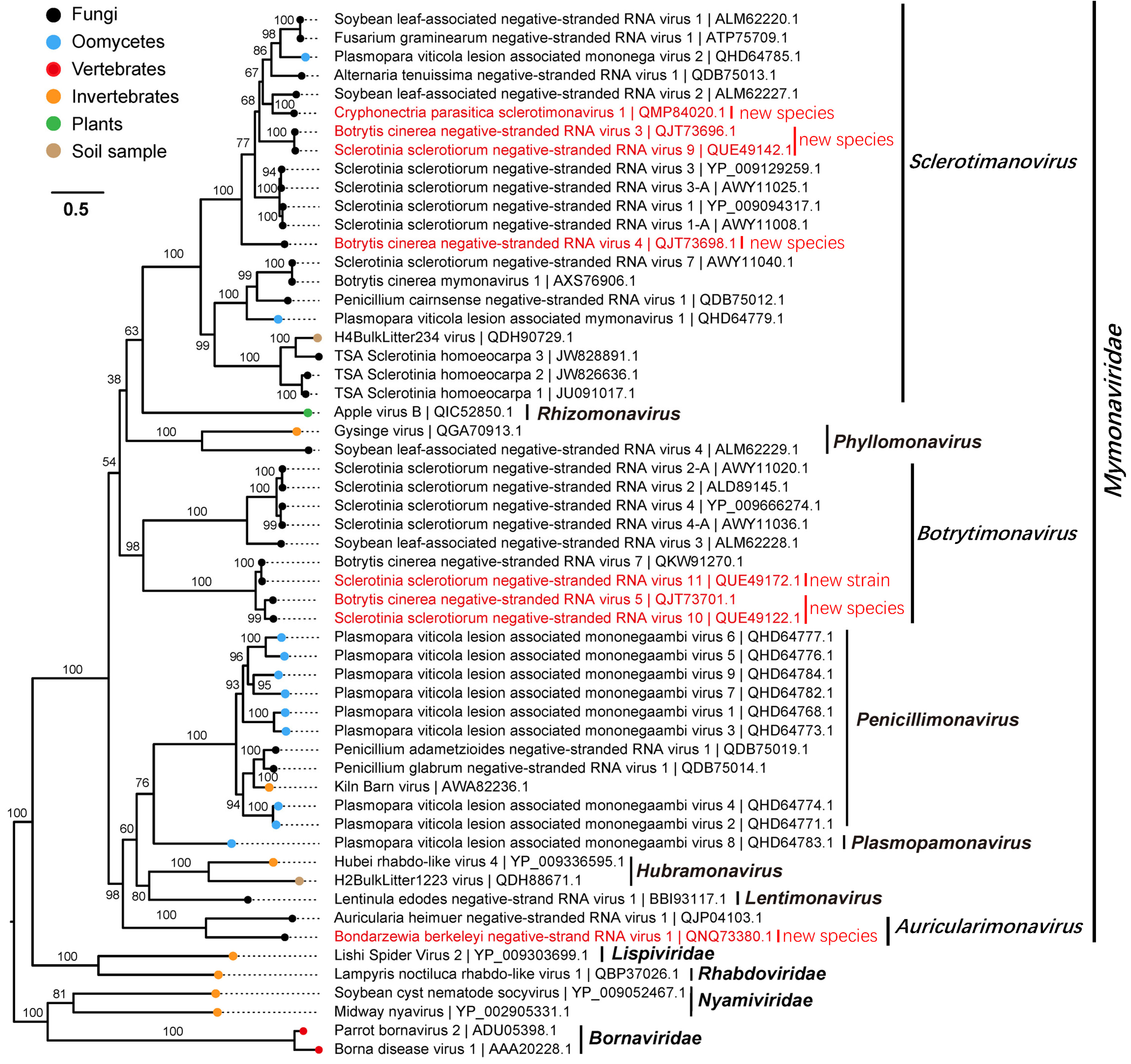
**Supporting evidence**

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

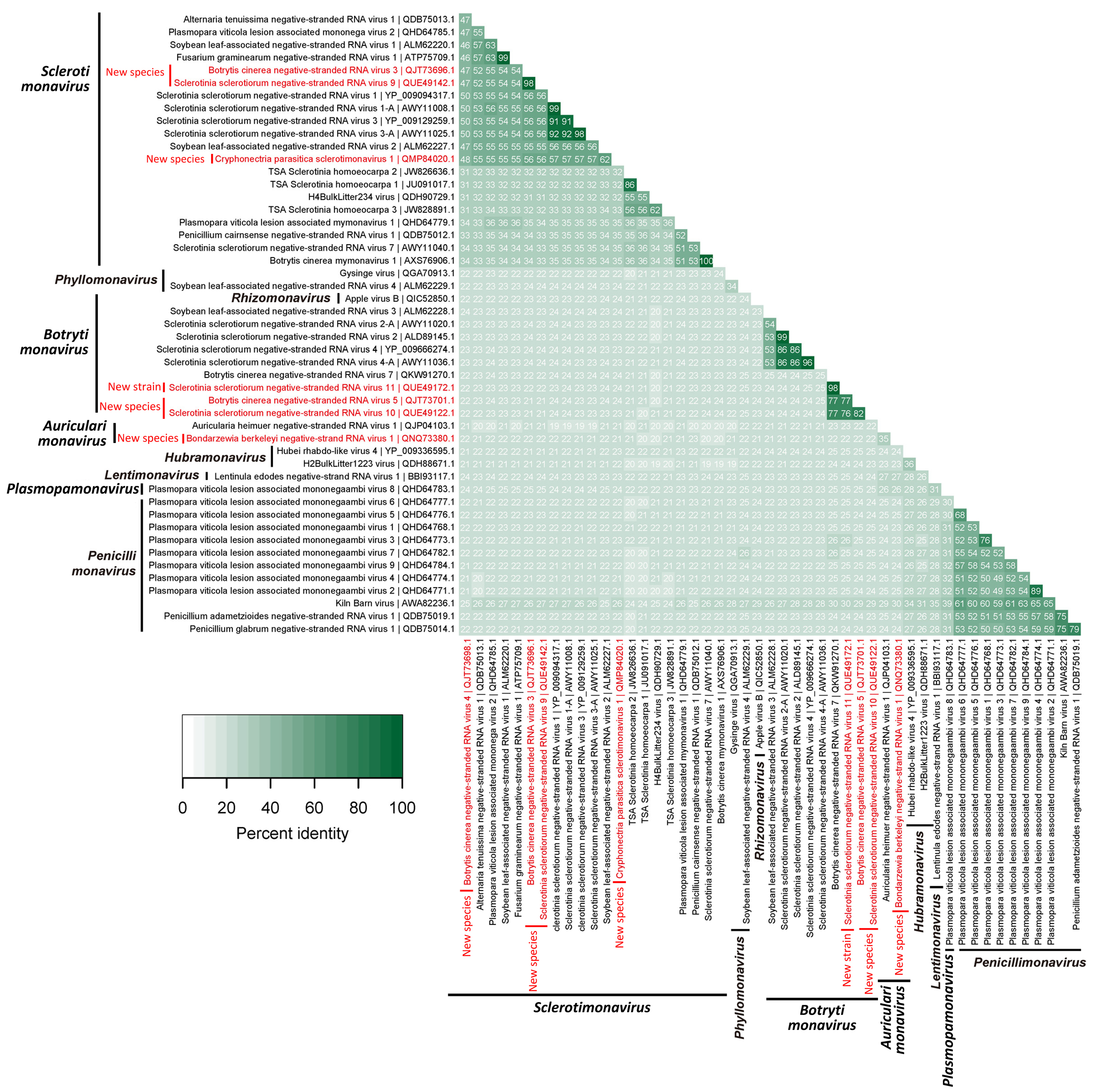
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| --- | --- | --- | --- | --- | --- |
| Genus name | New species name | Newly identified virus | Accession number(P/N) | Host | Reference |
| *Auricularimonavirus* | *Auricularimonavirus bondarzewiae* | Bondarzewia berkeleyi negative-strand RNA virus 1 | QNQ73380.1 | Fungi, *Bondarzewia berkeleyi* | 1 |
| *Botrytimonavirus* | *Botrytimonavirus alphabotrytidis* | Botrytis cinerea negative-stranded RNA virus 5 | QJT73701.1 | Fungi, *Botrytis cinerea* | 2 |
| Sclerotinia sclerotiorum negative-stranded RNA virus 10 | QUE49122.1 | Fungi, *Sclerotinia sclerotiorum* | 3 |
| *Sclerotimonavirus* | *Sclerotimonavirus alphabotrytidis* | Botrytis cinerea negative-stranded RNA virus 3 | QJT73696.1 | Fungi, *Botrytis cinerea* | 2 |
| Sclerotinia sclerotiorum negative-stranded RNA virus 9 | QUE49142.1 | Fungi, *Sclerotinia sclerotiorum* | 3 |
| *Sclerotimonavirus betabotrytidis* | Botrytis cinerea negative-stranded RNA virus 4 | QJT73698.1 | Fungi, *Botrytis cinerea* | 2 |
| *Sclerotimonavirus cryphonectriae* | Cryphonectria parasitica sclerotimonavirus 1 | QMP84020.1 | Fungi, *Cryphonectria parasitica* | 4 |

**Table 2** Newly identified mymonavirid assignable to an established species

|  |  |  |  |  |  |
| --- | --- | --- | --- | --- | --- |
| Genus name | Established species name | Newly identified virus | Accession number(P/N) | Host | Reference |
| *Botrytimonavirus* | *Botrytimonavirus botrytidis* | Sclerotinia sclerotiorum negative-stranded RNA virus 11 | QUE49172.1 | Fungi, *Sclerotinia sclerotiorum* | 3 |

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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) [[5](#_ENREF_10)] 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.

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**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. Vaino EJ and Sutela S (2020) Mixed infection by a partitivirus and a negative-sense RNA virus related to mymonaviruses in the polypore fungus Bondarzewia berkeleyi. Virus Research 286: 198079. doi.org/10.1016/j.virusres.2020.198079.
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5. 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.