

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

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| **Code assigned:** | **2021.003F** |  |
| **Short title:** Create 100 new species and four new genera (*Cryppavirales*: *Mitoviridae*) | | |
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**List the ICTV Study Group(s) that have seen this proposal**

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| *Mitoviridae* SG, Fungal and Protist Viruses Subcommittee Chair |

**ICTV study group comments and response of proposer**

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| Alphabetically listed authors Botella, Nibert, and Vainio constitute the *Mitoviridae* SG at present and have developed this proposal as a team. Author Manny assisted with the analyses. |

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

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| --- | --- |
| **Is any taxon name used here derived from that of a living person (Y/N)** | N |

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| --- | --- | --- |
| **Taxon name** | **Person from whom the name is derived** | **Permission attached (Y/N)** |
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**Submission dates**

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| --- | --- |
| Date first submitted to SC Chair | May 21, 2021 |
| Date of this revision (if different to above) | September 16, 2021 |

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

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| Proposer comment: A draft proposal was sent to SC Chair Sejo Sabanadzovic on April 10, 2021. He suggested a number of edits, which have been incorporated into the proposal submitted here.  **EC comment**: Address typos in the Excel file.  **Response**: Done. |

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

**Name of accompanying Excel module**

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| 2021.003F.R.Mitoviridae\_100nsp\_4ngen.xlsx |

**Abstract**

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| We propose to establish 100 new species and 4 new genera in family *Mitoviridae*. The 100 new species will be assigned to the 4 new genera, which we propose to name *Unuamitovirus*, *Duamitovirus*, *Triamitovirus*, and *Kvaramitovirus*. At present, there are 5 recognized species in family *Mitoviridae*, assigned to genus *Mitovirus*. We propose to transfer those 5 species into the new genera and to abolish genus *Mitovirus*. We lastly propose to rename those 5 species to conform with the newly proposed binomial format devised for the 100 new species. |

**Text of proposal**

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| |  | | --- | | **New species and species demarcation criteria.** Family *Mitoviridae* was first recognized in 2019 as being a separate taxon from family *Narnaviridae*. It currently comprises a single genus, *Mitovirus*, and 5 species from fungal hosts. New species in this genus were most recently recognized in 2002. In the intervening 18+ years, a large number of viruses putatively assignable to family *Mitoviridae* have been reported in journal articles and/or have had their partial, coding-complete, or complete genome sequences deposited in GenBank. For example, a recent search of GenBank with the term “Mitoviridae [organism]” identified 2402 accessions.  Obviously then, there is a large backlog of viruses that need to be evaluated as possibly representing new species in this family, and this proposal represents a first attempt at managing this backlog in a systematic fashion. This proposal was developed by the *Mitoviridae* Study Group (SG), which was newly formed in 2020.  SG members have agreed to the following set of criteria that any virus would need to meet to be considered to represent a new species in this proposal. These criteria may change in future years but were adopted for this year’s proposal. The criteria are:  1) The viral genome sequence must be deposited in GenBank in an appropriate manner (e.g., Third-Party Annotation if appropriate) and must be already annotated in GenBank as a (putative) member of family *Mitoviridae*. We additionally set the end of 2020 as the cut-off date for sequences that we would consider for this year’s proposal.  2) The viral genome sequence must be described in a publication with a DOI number.  3) The viral genome sequence must be, or appear to be, complete or coding complete.  4) The host species for the virus must be assigned in a sufficiently convincing manner as judged by SG members.  5) The viral genome sequence must not be derived, or appear to be possibly derived, from a mixture of distinct host isolates or individuals.  6) For viral genome sequences assembled from high-throughput sequencing reads, and not validated in full by Sanger sequencing, read numbers, RPKM values, and/or coverage depth values for the assembled sequence must be specified, or the read data must be available at NCBI such that these values can be determined by SG members.  7) Viral genome sequences that share <70% amino acid sequence identity will be considered to represent different virus species regardless of whether assigned to the same or different host species.  8) Viral genome sequences assigned to the same host species will be considered to represent the same virus species if they share >70% amino acid sequence identity. An exception would be allowed (i.e., assignment to different virus species) if sequences that share >70% amino acid sequence identity are stably maintained in a simultaneous manner within the same host.  9) Viral genome sequences that share >70% amino acid sequence identity, but are assigned to different host species, will be considered to represent different virus species  Criteria 7–9 are proposed to represent new **species demarcation criteria** for family *Mitoviridae*. Species demarcation criteria for genus *Mitovirus* were most recently described in 2011 in the ICTV 9th Report [1]: “*Species demarcation criteria have not been precisely defined. However, amino acid sequence identities of putative RdRp proteins between the different mitovirus species so far defined are less than 40%. Amino acid sequence identities of putative RdRp proteins between strains of the same mitovirus species are greater than 90%.*”  Based on detailed sequence analyses of the mitoviruses proposed here to represent 100 new species (Table 1), SG members have agreed that the species demarcation criteria previously devised for genus *Mitovirus* are inadequate, and we therefore propose to replace them for the whole of family *Mitoviridae* with criteria 7–9 listed above. Members of all 100 new species proposed here meet these newly proposed demarcation criteria, as evidenced by their host assignments (Table 1) and pairwise sequence identity scores (not shown here in full due to the size of the 105×105 matrix but summarized in Table 2).  All of the mitoviruses representing the 100 newly proposed species, as well as the 5 recognized species, share the same genome organization and coding strategy, and also fall within a reasonably small range of genome and encoded protein lengths (Table 1). Each of the genomes encompasses a single long open reading frame (ORF). This ORF encodes a protein with homologies and identifiable motifs shared with other RNA-dependent RNA polymerases (RdRps). The reported genome lengths range between 2151 and 4955 nt (median, 2735 nt), and the encoded protein (RdRp) lengths range between 636 and 1137 aa (median, 757 aa). Most but not all of these sequences require application of translation table 4 (mold, etc., genetic code) for translating the full-length RdRp, due to the presence of internal UGA codons encoding tryptophan as expected for transcripts in fungal mitochondria [2]. Most of these viruses have been identified in fungal host species, but a few have been recently identified in plant host species in a manner that appears robust [3,4]. For the plant mitoviruses, translation table 1 (standard genetic code), in which UGA is a stop codon, is sufficient for translating the full-length RdRp, due to the lack of internal UGA codons as expected for transcripts in plant mitochondria.  **New genera.** Phylogenetic trees that have appeared in journal articles and/or have been newly generated for the purposes of this proposal suggest that there are at least two distinguishable clades of viruses within family *Mitoviridae*, which might represent at least two genera. A review by Hillman and Cai [5], for example, identified these as Clade I (including recognized species *Ophiostoma mitovirus 4*, *Ophiostoma mitovirus 5*, and *Ophiostoma mitovirus 6*; representative viruses labeled OpnoMV4–6 in Figures 1–3) and Clade II (including recognized species *Cryphonectria mitovirus 1* and *Ophiostoma mitovirus 3a*; representative viruses labeled CrpaMV1 and OpnoMV3a in the figures). In fact, in that review, a cluster of two viruses (Glomus sp. RF1 small virus and Tuber excavatum virus; labeled RhclMv1 and TuexMV1 in the figures here), branching at the base of Clade I, can be seen to have poor bootstrap support (31%), suggesting the possibility of a third clade. Indeed, those three clades evident in the Hillman and Cai review [5] and corroborated by the trees in this proposal represent 3 of the 4 new genera that we propose here. The fourth new genus that we propose here is represented by a single virus (Ophiostoma mitovirus 7; labeled OpnoMV7 in the figures), which was not included in the Hillman and Cai review [5] because it was not reported until soon afterwards [6].  To corroborate published findings that appear to support the creation of several new genera in family *Mitoviridae*, we generated a series of phylogenetic trees using different collections of virus sequences, several different programs for multiple sequence alignment, and several different methods and programs for tree inference. For virus sequences, at a minimum, we used a collection of 111 sequences representing the 100 newly proposed and 5 recognized mitovirus species, plus 6 outgroup viruses from a recently identified clade of viruses from mostly arthropod samples [7] that might warrant identification as a sister to family *Mitoviridae* within order *Cryppavirales,* class *Howeltoviricetes*.Additionally, we used two larger sequence collections that included viruses that are annotated in GenBank as putative members of family *Mitoviridae* but that we have declined to propose as new species in this year’s proposal based on our set of 9 criteria described above. One of these larger collections totaled 205 sequences and the other 297. The 205 collection did not include sequences from the soil metagenome study of Starr et al. [8] whereas the 297 collection did so. We analyzed these larger sequence collections in an effort to confirm that the clades and putative genera identified when using the 111 collection were corroborated when additional sequences of putative mitoviruses were included. For multiple sequence alignments, we used several different programs but settled on MAFFT-L-INS-i, MUSCLE, and Clustal Omega as ones that provided a good balance between conserved and gap-free positions vs. overall length. For tree inference, we used several different programs employing distance, maximum likelihood, or Bayesian methods and settled on FastME (distance), IQ-TREE (maximum likelihood), and MrBayes (Bayesian) for comparisons. Model testing via ModelFinder or SMS was additionally used to identify top-scoring substitution models for each multiple sequence alignment prior to their use in tree inference.  Examples of the trees we generated via preceding approaches are shown in Figures 1–3. From initial work with the 111 collection, we identified a number of clades that are consistently represented in different trees. Based on these findings, as well as findings from the 205 and 297 collections, SG members have identified 4 such clades, whose name labels for the 111 viruses are color-coded in the figures as orange, blue, green, and magenta, plus gray for the outgroup viruses. The name label for each virus has the same color in the different trees and figures, allowing one to discern whether any of the viruses are jumping between clades in the different trees (they are not). The branches within each identified clade are also color-coded. Figure 1 shows results for the 111 collection, after aligning their sequences with MAFFT-L-INS-i (A), MUSCLE (B), or Clustal Omega (C) and inferring each tree with IQ-TREE (find and apply best model option). The consistently identified clades are made readily evident by the color-coding strategy and are well supported by the indicated branch support values. The varying branch points of the green and magenta clades (the latter represented by the single virus labeled OpnoMV7 in Figure 1) contributed to SG members agreeing to identify these as distinct clades. We therefore propose these 4 clades, not including the outgroup viruses, to represent 4 new genera in family *Mitoviridae*.  In Figure 2, we show analyses with the 205 collection of viruses. In this case, the same alignment program—MAFFT—but different tree inference programs—FastME (A), IQ-TREE (B), and MrBayes (C)—were used for generating the illustrated results. Notable features in this case are that the same 4 clades (orange, blue, green, and magenta), plus no new clades, remain readily discernible, with strong branch support values, despite the addition of 94 putative mitoviruses (name labels in black). Additionally, in this case, the tree topologies are remarkably similar, despite the use of different tree inference programs. Figure 3 shows that very similar results (same 4 clades, plus no new clades) were obtained with the 297 collection (alignment via MAFFT, tree inference via IQ-TREE (find and apply best model option); name labels of the 92 additional putative mitoviruses in dark red). In both Figure 2 and Figure 3, it is also noteworthy, though somewhat difficult to discern through the crowded name labels, that a few additional viruses are affiliated with the magenta clade, which is represented by the single virus OpnoMV7 in the 111 collection. This observation bolsters our conclusion that OpnoMV7 is the prototype of a legitimately distinct genus of mitoviruses. For clarity, clade assignments for the 94+92=186 putative mitoviruses added to Figure 2 and/or Figure 3 are also indicated in Table 3. A number of these putative mitoviruses seem destined to be the subjects of future taxonomic proposals from the *Mitoviridae* SG or others.  Viruses constituting different genera in the same family can sometimes be distinguished based on wholly or mostly nonoverlapping ranges of sequence identity scores from global pairwise comparisons via Needle, etc. We attempted this approach for the 105 viruses representing newly proposed or previously recognized species in family *Mitoviridae* as discussed above. Unfortunately, we found that the lowermost sequence identity scores among viruses within each of the proposed genera containing >1 species in this case overlapped many of the uppermost sequence identity scores among viruses from the other proposed genera (summarized in Table 2). This simple approach therefore did not contribute to defining quantitative criteria that could be useful for distinguishing viruses in the different genera. Limited efforts using more conserved portions of the viral genomes for repeating this type of analysis similarly failed. Other features such as host taxonomy, genome length, or protein length also failed to define criteria that could be useful for distinguishing viruses in the different genera. As a consequence, we are relying on the results of phylogenetic analyses for identifying the 4 consistently appearing clades of viruses that we are assigning to represent the 4 newly proposed genera.  For the two clades represented by larger numbers of viruses at present (orange and blue in Figures 1–3), one can discern particular subclades of viruses that appear to be present in most or all trees. These subclades might represent subgenera that could be proposed in the future or might represent new genera into which the currently proposed genera could be subdivided in the future. Based on observations from the different trees and especially the trees from IQ-TREE and MrBayes that are expected to be more reliable, however, SG members have agreed that proposing 4 new genera strikes the most appropriate balance at present between lumping and splitting the 100 newly proposed and 5 recognized species in family *Mitoviridae*.  **New names: genera.** SG members have agreed to use a serial format for naming the newly proposed genera in family *Mitoviridae*. We discussed using Greek letters as prefixes (*Alphamitovirus*, *Betamitovirus*, *Gammamitovirus*, and *Deltamitovirus*), but because those have been used so broadly in different families, we have decided to propose the use of ordinal numbers in Esperanto instead. The proposed names for the 4 new genera in family *Mitoviridae* are therefore *Unuamitovirus*, *Duamitovirus*, *Triamitovirus*, and *Kvaramitovirus*. The names of any other new genera in family *Mitoviridae* that may be proposed in the future could—but **need not—**adhere to this format. Regarding the color-coded clades in Figures 1–3, we propose to assign the genus names *Unuamitovirus*, *Duamitovirus*, *Triamitovirus*, and *Kvaramitovirus* to the orange, blue, green, and magenta clades, respectively. We have decided to recognize the orange clade as genus *Unuamitovirus* because it encompasses most of the viruses that defined Clade I in Hillman and Cai [5], including members of recognized species *Ophiostoma mitovirus 4*, *Ophiostoma mitovirus 5*, and *Ophiostoma mitovirus 6* (newly proposed names *Unuamitovirus opno4*, *Unuamitovirus opno5*, and *Unuamitovirus opno6*, respectively, as explained in the next section). We have decided to recognize the blue clade as genus *Duamitovirus* because it encompasses the viruses that defined Clade II in Hillman and Cai [5], including members of previously recognized species *Cryphonectria mitovirus 1 and Ophiostoma mitovirus 3a* (newly proposed names *Duamitovirus crpa1* and *Duamitovirus opno3a*, respectively, as explained in the next section). We have then lastly decided to recognize the other two clades as genera in decreasing order of the number of proposed species that they contain in this proposal: *Triamitovirus* (green clade, 9 proposed species) and *Kvaramitovirus* (magenta clade, 1 proposed species).  **New names: species.** SG members have agreed to propose a new binomial format for naming species in family *Mitoviridae*. This binomial format includes the genus name for each species followed by a unique epithet. The epithet is proposed to be free-form, and for the names that we are proposing here, to consist of a 4-letter contraction of the host species name followed by a number or other identifier generally derived from the common name of the representative virus as devised by previous authors. For example, for recognized species *Cryphonectria mitovirus 1*, which derives from host species *Cryphonectria parasitica* and is proposed to be assigned to new genus *Duamitovirus*, we propose the new name *Duamitovirus crpa1* as noted in the previous section. For another example, for a new species to be represented by the virus with common name Ophiostoma mitovirus 7, which derives from host species *Ophiostoma novo-ulmi* and is assigned to new *Kvaramitovirus*, we propose the new name *Kvaramitovirus opno7.* The epithets for new species proposed in the future could—but **need not—**adhere to the same format. Names for new species proposed in the future need only adhere to the overall binomial format and for epithets to adhere to ICTV rules. | |

**Supporting evidence**

This proposal includes supporting evidence in the form of Figures 1-3 and Tables 1–3, which are found after the References.

**References**

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8. Starr EP, Nuccio EE, Pett-Ridge J, Banfield JF, Firestone MK (2019) Metatranscriptomic reconstruction reveals RNA viruses with the potential to shape carbon cycling in soil. Proc Natl Acad Sci U S A 116:25900–25908. https://doi.org/10.1073/pnas.1908291116. PMID: 31772013; PMCID: PMC6926006.

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**Table 1.** Hundred newly proposed species in family *Mitoviridae* and information about their representative viruses

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| **Proposed species** | **Organism name in GenBank** | **Label in proposal figures** | **Assigned host** | **Publication DOI** | **GenBank no. (nt)** | **GenBank no. (aa)** | **Length (nt)** | **Length (aa)** |
| ***Unuamitovirus agbi1*** | **Agaricus bisporus mitovirus 1** | **AgbiMV1** | ***Agaricus bisporus*** | **10.1038/s41598-017-01592-9** | **KY357500** | **AQM32767** | **3439** | **956** |
| ***Unuamitovirus alar1*** | **Alternaria arborescens mitovirus 1** | **AlarMV1** | ***Alternaria arborescens*** | **10.1007/s00705-016-2953-1** | **LC145036** | **BAV53122** | **2506** | **717** |
| ***Unuamitovirus albr1*** | **Alternaria brassicicola mitovirus** | **AlbrMV1** | ***Alternaria brassicicola*** | **10.1007/s00705-017-3371-8** | **KP705075** | **AKN79252** | **2506** | **719** |
| ***Unuamitovirus boci2*** | **Botrytis cinerea mitovirus 2** | **BociMV2** | ***Botrytis cinerea*** | **10.1111/mpp.12466** | **LN827941** | **CEZ26297** | **2497** | **710** |
| ***Unuamitovirus boci4*** | **Botrytis cinerea mitovirus 4** | **BociMV4** | ***Botrytis cinerea*** | **10.1111/mpp.12466** | **LN827947** | **CEZ26303** | **2768** | **731** |
| ***Unuamitovirus crri1*** | **Cronartium ribicola mitovirus 1** | **CrriMV1** | ***Cronartium ribicola*** | **10.1371/journal.pone.0154267** | **KT921179** | **AMQ67414** | **2715** | **800** |
| ***Unuamitovirus crri2*** | **Cronartium ribicola mitovirus 2** | **CrriMV2** | ***Cronartium ribicola*** | **10.1371/journal.pone.0154267** | **KT921180** | **AMQ67415** | **2471** | **689** |
| ***Unuamitovirus crri3*** | **Cronartium ribicola mitovirus 3** | **CrriMV3** | ***Cronartium ribicola*** | **10.1371/journal.pone.0154267** | **KT921181** | **AMQ67416** | **2522** | **713** |
| ***Unuamitovirus crri4*** | **Cronartium ribicola mitovirus 4** | **CrriMV4** | ***Cronartium ribicola*** | **10.1371/journal.pone.0154267** | **KT921182** | **AMQ67417** | **2479** | **721** |
| ***Unuamitovirus crri5*** | **Cronartium ribicola mitovirus 5** | **CrriMV5** | ***Cronartium ribicola*** | **10.1371/journal.pone.0154267** | **KT921183** | **AMQ67418** | **2631** | **772** |
| ***Unuamitovirus diru1*** | **Diaporthe rudis mitovirus 1** | **DiruMV1** | ***Diaporthe rudis*** | **10.1007/s00705-020-04755-8** | **MT216310** | **QNS28825** | **2455** | **701** |
| ***Unuamitovirus enmu1*** | **Entomophthora muscae mitovirus 1** | **EnmuMV1** | ***Entomophthora muscae*** | **10.3390/v11040351** | **MK682513** | **QCF24445** | **2804** | **757** |
| ***Unuamitovirus enmu2*** | **Entomophthora muscae mitovirus 2** | **EnmuMV2** | ***Entomophthora muscae*** | **10.3390/v11040351** | **MK682514** | **QCF24446** | **2421** | **689** |
| ***Unuamitovirus enmu3*** | **Entomophthora muscae mitovirus 3** | **EnmuMV3** | ***Entomophthora muscae*** | **10.3390/v11040351** | **MK682515** | **QCF24447** | **2550** | **709** |
| ***Unuamitovirus enmu4*** | **Entomophthora muscae mitovirus 4** | **EnmuMV4** | ***Entomophthora muscae*** | **10.3390/v11040351** | **MK682516** | **QCF24448** | **2561** | **681** |
| ***Unuamitovirus enmu5*** | **Entomophthora muscae mitovirus 5** | **EnmuMV5** | ***Entomophthora muscae*** | **10.3390/v11040351** | **MK682517** | **QCF24449** | **2487** | **680** |
| ***Unuamitovirus enmu6*** | **Entomophthora muscae mitovirus 6** | **EnmuMV6** | ***Entomophthora muscae*** | **10.3390/v11040351** | **MK682518** | **QCF24450** | **2362** | **708** |
| ***Unuamitovirus enmu7*** | **Entomophthora muscae mitovirus 7** | **EnmuMV7** | ***Entomophthora muscae*** | **10.3390/v11040351** | **MK682519** | **QCF24451** | **2300** | **701** |
| ***Unuamitovirus enmu8*** | **Entomophthora muscae mitovirus 8** | **EnmuMV8** | ***Entomophthora muscae*** | **10.3390/v11040351** | **BK010736** | **DAC76947** | **2479** | **636** |
| ***Unuamitovirus fuan1*** | **Fusarium andiyazi mitovirus 1** | **FuanMV1** | ***Fusarium andiyazi*** | **10.3390/v12101161** | **MT506025** | **QPK91779** | **2441** | **724** |
| ***Unuamitovirus fuci1*** | **Fusarium circinatum mitovirus 1** | **FuciMV1** | ***Fusarium circinatum*** | **10.1007/s00705-014-2012-8** | **KF803546** | **AHI43533** | **2419** | **731** |
| ***Unuamitovirus fuci2*** | **Fusarium circinatum mitovirus 2-1** | **FuciMV2-1** | ***Fusarium circinatum*** | **10.1007/s00705-014-2012-8** | **KF803547** | **AHI43534** | **2193** | **724** |
| ***Unuamitovirus fuco1*** | **Fusarium coeruleum mitovirus 1** | **FucoMV1** | ***Fusarium coeruleum*** | **10.1007/s11262-015-1182-0** | **LC006129** | **BAQ36630** | **2423** | **757** |
| ***Unuamitovirus fugl1*** | **Fusarium globosum mitovirus 1** | **FuglMV1** | ***Fusarium globosum*** | **10.1007/s11262-015-1182-0** | **LC006128** | **BAQ36629** | **2414** | **717** |
| ***Unuamitovirus fuox1*** | **Fusarium oxysporum f. sp. dianthi mitovirus 1** | **FuoxMV1** | ***Fusarium oxysporum*** | **10.3390/v12030279** | **MN586595** | **QIC51112** | **2313** | **675** |
| ***Unuamitovirus fupo1*** | **Fusarium poae mitovirus 1** | **FupoMV1** | ***Fusarium poae*** | **10.1007/s11262-016-1379-x** | **LC150564** | **BAV56289** | **2397** | **726** |
| ***Unuamitovirus fupo2*** | **Fusarium poae mitovirus 2** | **FupoMV2** | ***Fusarium poae*** | **10.1007/s11262-016-1379-x** | **LC150565** | **BAV56290** | **2414** | **764** |
| ***Unuamitovirus fuve1*** | **Fusarium verticillioides mitovirus 1** | **FuveMV1** | ***Fusarium verticillioides*** | **10.3390/v12101161** | **MT506024** | **QPK91778** | **2471** | **727** |
| ***Unuamitovirus grab1*** | **Gremmeniella mitovirus S1** | **GrabMV1** | ***Gremmeniella abietina*** | **doi: 10.1007/s00705-003-0195-5** | **AF534641** | **AAN05635** | **2572** | **741** |
| ***Unuamitovirus grab2*** | **Gremmeniella abietina non-host-specific mitochondrial RNA virus S1** | **GrabMV2** | ***Gremmeniella abietina*** | **10.1016/j.funbio.2012.05.004** | **JN654496** | **AEY76153** | **2544** | **691** |
| ***Unuamitovirus hemo1*** | **Helicobasidium mompa mitovirus 1-18** | **HemoMV1** | ***Helicobasidium mompa*** | **10.1016/j.virusres.2004.06.010** | **AB110977** | **BAD72871** | **2411** | **700** |
| ***Unuamitovirus hean2*** | **Heterobasidion mitovirus 2** | **HeanMV2** | ***Heterobasidion annosum*** | **10.1016/j.virusres.2019.197681** | **MN058206** | **QED55404** | **2923** | **756** |
| ***Unuamitovirus hyal1*** | **Hymenoscyphus fraxineus [albidus] mitovirus 1** | **HyalMV1** | ***Hymenoscyphus albidus*** | **10.3390/v10110628** | **MK079847** | **AZG04290** | **2151** | **717** |
| ***Unuamitovirus hyfr1*** | **Hymenoscyphus fraxineus mitovirus 1** | **HyfrMV1** | ***Hymenoscyphus fraxineus*** | **10.1016/j.meegid.2014.09.001** | **KJ667051** | **AIU44705** | **2387** | **717** |
| ***Unuamitovirus lebi1*** | **Leptosphaeria biglobosa mitovirus 1** | **LebiMV1** | ***Leptosphaeria biglobosa*** | **10.1007/s00705-018-04143-3** | **MG659316** | **AVZ65960** | **2568** | **756** |
| ***Unuamitovirus nior2*** | **Nigrospora oryzae mitovirus 2** | **NiorMV2** | ***Nigrospora oryzae*** | **10.3390/v11010083** | **MH823902** | **AZP53929** | **2507** | **704** |
| ***Unuamitovirus pust1*** | **Puccinia striiformis mitovirus 1** | **PustMV1** | ***Puccinia striiformis*** | **10.1007/s00705-018-04134-4** | **MK033478** | **AZY91986** | **2496** | **743** |
| ***Unuamitovirus scni1*** | **Sclerotinia nivalis mitovirus 1** | **ScniMV1** | ***Sclerotinia nivalis*** | **10.1016/j.virusres.2016.06.009** | **KT365895** | **ANJ77669** | **2720** | **731** |
| ***Unuamitovirus scsc1*** | **Sclerotinia sclerotiorum mitovirus 1** | **ScscMV1** | ***Sclerotinia sclerotiorum*** | **10.1016/j.virol.2012.03.015** | **JQ013377** | **AEX91878** | **2513** | **691** |
| ***Unuamitovirus scsc2*** | **Sclerotinia sclerotiorum mitovirus 2** | **ScscMV2** | ***Sclerotinia sclerotiorum*** | **10.1016/j.virol.2012.03.015** | **JQ013378** | **AEX91879** | **2445** | **676** |
| ***Unuamitovirus scsc4*** | **Sclerotinia sclerotiorum mitovirus 4** | **ScscMV4** | ***Sclerotinia sclerotiorum*** | **10.1016/j.virol.2013.03.002** | **JX401538** | **AGC24233** | **2744** | **731** |
| ***Unuamitovirus scsc7*** | **Sclerotinia sclerotiorum mitovirus 7** | **ScscMV7** | ***Sclerotinia sclerotiorum*** | **10.1007/s00705-014-2171-7** | **KJ462514** | **AHX84135** | **2815** | **689** |
| ***Unuamitovirus thba1*** | **Thielaviopsis basicola mitovirus** | **ThbaMV1** | ***Thielaviopsis basicola*** | **10.1094/PHYTO-96-0468** | **AY563138** | **AAT09164** | **2896** | **705** |
| ***Duamitovirus alal1*** | **Alternaria alternata mitovirus 1** | **AlalMV1** | ***Alternaria alternata*** | **10.1111/1462-2920.14651** | **MK584829** | **QDB74990** | **3607** | **850** |
| ***Duamitovirus azfi1*** | **Azolla filiculoides mitovirus 1** | **AzfiMV1** | ***Azolla filiculoides*** | **10.1016/j.virol.2018.02.005** | **BK010423** | **DAB41741** | **2871** | **795** |
| ***Duamitovirus bevu1*** | **Beta vulgaris mitovirus 1** | **BevuMV1** | ***Beta vulgaris*** | **10.1016/j.virol.2018.02.005** | **MG721540** | **AVH76945** | **2750** | **793** |
| ***Duamitovirus bodo1*** | **Botryosphaeria dothidea mitovirus 1** | **BodoMV1** | ***Botryosphaeria dothidea*** | **10.1007/s00705-020-04886-y** | **MT676452** | **QMU24933** | **2667** | **727** |
| ***Duamitovirus boci1*** | **Botrytis cinerea mitovirus 1** | **BociMV1** | ***Botrytis cinerea*** | **10.1016/j.virol.2010.07.010** | **EF580100** | **ABQ65153** | **2804** | **738** |
| ***Duamitovirus boci3*** | **Botrytis cinerea mitovirus 3** | **BociMV3** | ***Botrytis cinerea*** | **10.1111/mpp.12466** | **LN827942** | **CEZ26298** | **2922** | **786** |
| ***Duamitovirus busp1*** | **Buergenerula spartinae mitovirus 1** | **BuspMV1** | ***Buergenerula spartinae*** | **10.1007/s12250-014-3470-6** | **KJ485703** | **AHY03257** | **2735** | **809** |
| ***Duamitovirus casa1*** | **Cannabis sativa mitovirus 1** | **CasaMV1** | ***Cannabis sativa*** | **10.1016/j.virol.2018.02.005** | **BK010428** | **DAB41746** | **2857** | **762** |
| ***Duamitovirus cesp1*** | **Ceratobasidium mitovirus 1** | **CespMV1** | ***Ceratobasidium sp.*** | **10.1093/ve/veaa076** | **MN736968** | **QNN89183** | **4501** | **860** |
| ***Duamitovirus chqu1*** | **Chenopodium quinoa mitovirus 1** | **ChquMV1** | ***Chenopodium quinoa*** | **10.1128/JVI.01998-18** | **MF375475** | **AWL21855** | **2730** | **766** |
| ***Duamitovirus clod1*** | **Clitocybe odora virus** | **ClodMV1** | ***Clitocybe odora*** | **10.1007/s00705-012-1373-0** | **HE717021** | **CCG47524** | **3765** | **1137** |
| ***Duamitovirus dapi1*** | **Dahlia pinnata mitovirus 1** | **DapiMV1** | ***Dahlia pinnata*** | **10.1016/j.virol.2018.02.005** | **BK010429** | **DAB41747** | **2806** | **782** |
| ***Duamitovirus epni1*** | **Epicoccum nigrum mitovirus 1** | **EpniMV1** | ***Epicoccum nigrum*** | **10.1111/1462-2920.14651** | **MK584828** | **QDB74989** | **3520** | **840** |
| ***Duamitovirus fubo1*** | **Fusarium boothii mitovirus 1** | **FuboMV1** | ***Fusarium boothii*** | **10.3390/v10110584** | **LC425112** | **BBG56022** | **2802** | **823** |
| ***Duamitovirus fupo3*** | **Fusarium poae mitovirus 3** | **FupoMV3** | ***Fusarium poae*** | **10.1007/s11262-016-1379-x** | **LC150566** | **BAV56291** | **2718** | **789** |
| ***Duamitovirus fupo4*** | **Fusarium poae mitovirus 4** | **FupoMV4** | ***Fusarium poae*** | **10.1007/s11262-016-1379-x** | **LC150567** | **BAV56292** | **2387** | **689** |
| ***Duamitovirus gima1*** | **Gigaspora margarita mitovirus 1** | **GimaMV1** | ***Gigaspora margarita*** | **10.1111/1462-2920.14060** | **MG256173** | **AVA17449** | **3243** | **714** |
| ***Duamitovirus gima2*** | **Gigaspora margarita mitovirus 2** | **GimaMV2** | ***Gigaspora margarita*** | **10.1111/1462-2920.14060** | **MG256174** | **AVA17450** | **3394** | **986** |
| ***Duamitovirus gima3*** | **Gigaspora margarita mitovirus 3** | **GimaMV3** | ***Gigaspora margarita*** | **10.1111/1462-2920.14060** | **MG256175** | **AVA17451** | **3387** | **1010** |
| ***Duamitovirus gima4*** | **Gigaspora margarita mitovirus 4** | **GimaMV4** | ***Gigaspora margarita*** | **10.1111/1462-2920.14060** | **MG256176** | **AVA17452** | **3389** | **1008** |
| ***Duamitovirus hean1*** | **Heterobasidion mitovirus 1** | **HeanMV1** | ***Heterobasidion annosum*** | **10.1099/jgv.0.000003** | **KJ873059** | **AIF33766** | **4379** | **836** |
| ***Duamitovirus hean3*** | **Heterobasidion mitovirus 3** | **HeanMV3** | ***Heterobasidion annosum*** | **10.1016/j.virusres.2019.197681** | **MN058208** | **QED55406** | **4955** | **816** |
| ***Duamitovirus hepa3*** | **Heterobasidion [parviporum] mitovirus 3** | **HepaMV3** | ***Heterobasidion parviporum*** | **10.1016/j.virusres.2019.197681** | **MN058214** | **QED55412** | **3580** | **810** |
| ***Duamitovirus hulu1*** | **Humulus lupulus mitovirus 1** | **HuluMV1** | ***Humulus lupulus*** | **10.1016/j.virol.2018.02.005** | **BK010431** | **DAB41749** | **2795** | **763** |
| ***Duamitovirus nepa1*** | **Neofusicoccum parvum mitovirus 1** | **NepaMV1** | ***Neofusicoccum parvum*** | **10.1111/1462-2920.14651** | **MK584831** | **QDB74992** | **2659** | **697** |
| ***Duamitovirus nior1*** | **Nigrospora oryzae mitovirus 1** | **NiorMV1** | ***Nigrospora oryzae*** | **10.3390/v11010083** | **MH823901** | **AZP53928** | **2865** | **790** |
| ***Duamitovirus opno1a*** | **Ophiostoma mitovirus 1a** | **OpnoMV1a** | ***Ophiostoma novo-ulmi*** | **10.1007/s11262-005-0029-5** | **AM087548** | **CAJ32466** | **3147** | **782** |
| ***Duamitovirus opno1b*** | **Ophiostoma mitovirus 1b** | **OpnoMV1b** | ***Ophiostoma novo-ulmi*** | **10.1007/s11262-005-0029-5** | **AM087549** | **CAJ32467** | **2572** | **776** |
| ***Duamitovirus opno1c*** | **Ophiostoma mitovirus 1c** | **OpnoMV1c** | ***Ophiostoma novo-ulmi*** | **10.1186/1743-422X-10-252** | **KF026355** | **AGT55876** | **3107** | **788** |
| ***Duamitovirus opno3b*** | **Ophiostoma mitovirus 3b** | **OpnoMV3b** | ***Ophiostoma novo-ulmi*** | **10.1007/s11262-005-0029-5** | **AM087550** | **CAJ32468** | **2332** | **738** |
| ***Duamitovirus oxru1*** | **Oxybasis rubra mitovirus 1** | **OxruMV1** | ***Oxybasis rubra*** | **10.1016/j.virol.2018.02.005** | **BK010427** | **DAB41745** | **2734** | **763** |
| ***Duamitovirus peex1*** | **Petunia exserta mitovirus 1** | **PeexMV1** | ***Petunia exserta*** | **10.1016/j.virol.2018.02.005** | **BK010426** | **DAB41744** | **2701** | **750** |
| ***Duamitovirus rhce1*** | **Rhizoctonia cerealis mitovirus** | **RhceMV1** | ***Rhizoctonia cerealis*** | **10.1007/s00705-015-2431-1** | **KM517201** | **AIT71973** | **3149** | **812** |
| ***Duamitovirus rhso21*** | **Rhizoctonia solani mitovirus 21** | **RhsoMV21** | ***Rhizoctonia solani*** | **10.3389/fcimb.2019.00244** | **MK372892** | **QDW65413** | **4100** | **1041** |
| ***Duamitovirus rhso25*** | **Rhizoctonia solani mitovirus 25** | **RhsoMV25** | ***Rhizoctonia solani*** | **10.3389/fcimb.2019.00244** | **MK372894** | **QDW65415** | **3767** | **861** |
| ***Duamitovirus rhso26*** | **Rhizoctonia solani mitovirus 26** | **RhsoMV26** | ***Rhizoctonia solani*** | **10.3389/fcimb.2019.00244** | **MK372895** | **QDW65416** | **2580** | **791** |
| ***Duamitovirus rhso27*** | **Rhizoctonia solani mitovirus 27** | **RhsoMV27** | ***Rhizoctonia solani*** | **10.3389/fcimb.2019.00244** | **MK372896** | **QDW65417** | **3176** | **854** |
| ***Duamitovirus rhso31*** | **Rhizoctonia solani mitovirus 31** | **RhsoMV31** | ***Rhizoctonia solani*** | **10.3389/fcimb.2019.00244** | **MK372900** | **QDW65421** | **3820** | **904** |
| ***Duamitovirus rhso32*** | **Rhizoctonia solani mitovirus 32** | **RhsoMV32** | ***Rhizoctonia solani*** | **10.3389/fcimb.2019.00244** | **MK372901** | **QDW65422** | **3409** | **885** |
| ***Duamitovirus rhso34*** | **Rhizoctonia solani mitovirus 34** | **RhsoMV34** | ***Rhizoctonia solani*** | **10.3389/fcimb.2019.00244** | **MK372903** | **QDW65424** | **3389** | **869** |
| ***Duamitovirus rhir1*** | **Rhizophagus irregularis mitovirus 1** | **RhirMV1** | ***Rhizophagus irregularis*** | **10.3390/v10120707** | **MH732933** | **AXY40444** | **3601** | **811** |
| ***Duamitovirus scho1*** | **Sclerotinia homoeocarpa mitovirus** | **SchoMV1** | ***Sclerotinia homoeocarpa*** | **10.1094/PHYTO.2003.93.11.1407** | **AY172454** | **AAO21337** | **2632** | **720** |
| ***Duamitovirus scni2*** | **Sclerotinia nivalis mitovirus 2** | **ScniMV2** | ***Sclerotinia nivalis*** | **10.1016/j.virusres.2016.06.009** | **KT365896** | **ANJ77670** | **2583** | **712** |
| ***Duamitovirus scsc3*** | **Sclerotinia sclerotiorum mitovirus 3** | **ScscMV3** | ***Sclerotinia sclerotiorum*** | **10.1016/j.virol.2013.03.002** | **JX401537** | **AGC24232** | **2588** | **712** |
| ***Duamitovirus scsc6*** | **Sclerotinia sclerotiorum mitovirus 6** | **ScscMV6** | ***Sclerotinia sclerotiorum*** | **10.1007/s00705-014-2171-7** | **KJ462512** | **AHX84133** | **2584** | **715** |
| ***Duamitovirus soch1*** | **Solanum chacoense mitovirus 1** | **SochMV1** | ***Solanum chacoense*** | **10.1016/j.virol.2018.02.005** | **BK010425** | **DAB41743** | **2773** | **776** |
| ***Duamitovirus tuae1*** | **Tuber aestivum mitovirus** | **TuaeMV1** | ***Tuber aestivum*** | **10.1007/s00705-011-0998-8** | **HQ992989** | **AEG79311** | **3480** | **793** |
| ***Triamitovirus cespA*** | **Ceratobasidium mitovirus A** | **CespMV-A** | ***Ceratobasidium sp.*** | **10.1016/j.virusres.2017.11.026** | **KU291923** | **AOX47577** | **2850** | **817** |
| ***Triamitovirus gesu1*** | **Geopora sumneriana mitovirus 1** | **GesuMV1** | ***Geopora sumneriana*** | **10.1007/s00705-019-04367-x** | **MN043682** | **QDM55307** | **3146** | **827** |
| ***Triamitovirus rhor1*** | **Rhizoctonia oryzae-sativae mitovirus 1** | **RhorMV1** | ***Rhizoctonia oryzae-sativae*** | **10.1007/s00705-017-3229-0** | **KU057949** | **ANA08076** | **3038** | **820** |
| ***Triamitovirus rhso1*** | **Rhizoctonia mitovirus 1 RS002** | **RhsoMV1** | ***Rhizoctonia solani*** | **10.1016/j.funbio.2015.11.002** | **KC792591** | **AHL25281** | **2797** | **826** |
| ***Triamitovirus rhso23*** | **Rhizoctonia solani mitovirus 23** | **RhsoMV23** | ***Rhizoctonia solani*** | **10.3389/fcimb.2019.00244** | **MK375261** | **QDW65458** | **2792** | **818** |
| ***Triamitovirus rhso30*** | **Rhizoctonia solani mitovirus 30** | **RhsoMV30** | ***Rhizoctonia solani*** | **10.3389/fcimb.2019.00244** | **MK372899** | **QDW65420** | **2904** | **818** |
| ***Triamitovirus rhso39*** | **Rhizoctonia solani mitovirus 39** | **RhsoMV39** | ***Rhizoctonia solani*** | **10.1007/s00705-020-04664-w** | **MN448505** | **QIS79099** | **2805** | **840** |
| ***Triamitovirus rhcl1*** | **Rhizophagus sp. RF1 mitovirus** | **RhclMV1** | ***Rhizophagus clarus*** | **10.1007/s00705-014-1999-1** | **AB558120** | **BAJ23143** | **2895** | **820** |
| ***Triamitovirus tuex1*** | **Tuber excavatum mitovirus** | **TuexMV1** | ***Tuber excavatum*** | **10.1007/s00705-012-1228-8** | **JN222389** | **AEP83726** | **3305** | **797** |
| ***Kvaramitovirus opno7*** | **Ophiostoma mitovirus 7** | **OpnoMV7** | ***Ophiostoma novo-ulmi*** | **10.1186/1743-422X-10-252** | **KF031943** | **AGT55877** | **2804** | **720** |

Proposed species are listed in alphabetical order of GenBank organism name within each proposed genus and are color-coded as in Figures 1–3.

**Table 2.** Summary of pairwise sequence (amino acid) identity scores for representative viruses of the 5 previously recognized and 100 newly proposed mitovirus species

|  |  |  |  |  |  |  |
| --- | --- | --- | --- | --- | --- | --- |
| **Proposed genus** |  | ***Unuamitovirus*** | ***Duamitovirus*** | ***Triamitovirus*** | ***Kvaramitovirus*** |  |
|  | **Clade** | **Oramge** | **Blue** | **Green** | **Magenta** |  |
| ***Unuamitovirus*** | **Orange** | **17.7–97.1** | **12.8–26.3** | **15.8–24.7** | **15.4–21.8** | **range** |
| ***Duamitovirus*** | **Blue** |  | **14.1–96.2** | **14.2–25.3** | **13.7–21.9** |  |
| ***Triamitovirus*** | **Green** |  |  | **25.0–63.5** | **17.7–22.1** |  |
| ***Kvaramitovirus*** | **Magenta** |  |  |  | **100** |  |
| ***Unuamitovirus*** | **Orange** | **25.4** | **21.0** | **21.0** | **18.6** | **median** |
| ***Duamitovirus*** | **Blue** |  | **22.8** | **20.9** | **18.6** |  |
| ***Triamitovirus*** | **Green** |  |  | **30.2** | **19.6** |  |
| ***Kvaramitovirus*** | **Magenta** |  |  |  | **100** |  |
| ***Unuamitovirus*** | **Orange** | **27.8** | **20.8** | **20.9** | **18.6** | **average** |
| ***Duamitovirus*** | **Blue** |  | **23.8** | **20.6** | **18.4** |  |
| ***Triamitovirus*** | **Green** |  |  | **34.2** | **19.6** |  |
| ***Kvaramitovirus*** | **Magenta** |  |  |  | **100** |  |

The upper, middle, and lower blocks respectively show the range of scores, median score, and average score (each in %) for the viruses in each clade-to-clade comparison (105×105 pairwise comparisons of sequences overall).

**Table 3.** Putative mitoviruses added to the 205 and 297 collections, for testing the stability of the clades first identified with the 111 collection

|  |  |  |  |
| --- | --- | --- | --- |
| **94 viruses added in the 205 collection** | | **92 viruses added in the 297 collection** | |
| **GenBank no. (aa)** | **Organism name in GenBank** | **GenBank no. (aa)** | **Organism name in GenBank** |
| **AAR01970** | **Cryphonectria cubensis mitovirus 1a** | **QDH86472** | **Mitovirus sp.** |
| **­AAR01973** | **Cryphonectria cubensis mitovirus 2a** | **QDH86473** | **Mitovirus sp.** |
| **AGW51760** | **Mitovirus AEF-2013** | **QDH86523** | **Mitovirus sp.** |
| **AHF48622** | **Sclerotinia sclerotiorum mitovirus 6** | **QDH86532** | **Mitovirus sp.** |
| **AHF48623** | **Sclerotinia sclerotiorum mitovirus 7** | **QDH86591** | **Mitovirus sp.** |
| **AHF48624** | **Sclerotinia sclerotiorum mitovirus 8** | **QDH86687** | **Mitovirus sp.** |
| **AHF48625** | **Sclerotinia sclerotiorum mitovirus 9** | **QDH86714** | **Mitovirus sp.** |
| **AHF48627** | **Sclerotinia sclerotiorum mitovirus 11** | **QDH86793** | **Mitovirus sp.** |
| **AHF48631** | **Sclerotinia sclerotiorum mitovirus 15** | **QDH86956** | **Mitovirus sp.** |
| **ALD60243** | **Binucleate Rhizoctonia mitovirus K1** | **QDH86987** | **Mitovirus sp.** |
| **ALD89116** | **Rhizoctonia solani mitovirus 11** | **QDH86997** | **Mitovirus sp.** |
| **ALD89117** | **Rhizoctonia solani mitovirus 12** | **QDH87062** | **Mitovirus sp.** |
| **ALD89118** | **Rhizoctonia solani mitovirus 13** | **QDH87080** | **Mitovirus sp.** |
| **ALD89120** | **Rhizoctonia solani mitovirus 15** | **QDH87099** | **Mitovirus sp.** |
| **ALD89121** | **Rhizoctonia solani mitovirus 2** | **QDH87116** | **Mitovirus sp.** |
| **ALD89125** | **Rhizoctonia solani mitovirus 6** | **QDH87157** | **Mitovirus sp.** |
| **ALD89127** | **Rhizoctonia solani mitovirus 8** | **QDH87172** | **Mitovirus sp.** |
| **ALM62240** | **Soybean leaf-associated mitovirus 5** | **QDH87191** | **Mitovirus sp.** |
| **ALM62241** | **Soybean leaf-associated mitovirus 1** | **QDH87228** | **Mitovirus sp.** |
| **ALM62243** | **Soybean leaf-associated mitovirus 3** | **QDH87234** | **Mitovirus sp.** |
| **AMM45292** | **Macrophomina phaseolina mitovirus 3** | **QDH87249** | **Mitovirus sp.** |
| **APG77262** | **Wenling narna-like virus 9** | **QDH87276** | **Mitovirus sp.** |
| **ASL68498** | **Ocimum basilicum RNA virus 2** | **QDH87311** | **Mitovirus sp.** |
| **AWY10985** | **Sclerotinia sclerotiorum mitovirus 27** | **QDH87351** | **Mitovirus sp.** |
| **AWY10986** | **Sclerotinia sclerotiorum mitovirus 28** | **QDH87490** | **Mitovirus sp.** |
| **AWY10987** | **Sclerotinia sclerotiorum mitovirus 29** | **QDH87501** | **Mitovirus sp.** |
| **AWY10991** | **Sclerotinia sclerotiorum mitovirus 33** | **QDH87662** | **Mitovirus sp.** |
| **AXY40441** | **Rhizophagus diaphanum mitovirus 2** | **QDH87726** | **Mitovirus sp.** |
| **AXY40442** | **Rhizophagus diaphanum mitovirus 1** | **QDH87755** | **Mitovirus sp.** |
| **AZJ25096** | **Rhizophagus diaphanum mitovirus 3** | **QDH87757** | **Mitovirus sp.** |
| **AZJ25097** | **Rhizophagus diaphanum mitovirus 4** | **QDH87796** | **Mitovirus sp.** |
| **AZT88621** | **Colletotrichum falcatum mitovirus 1** | **QDH87829** | **Mitovirus sp.** |
| **AZT88622** | **Loramyces juncicola mitovirus 1** | **QDH87903** | **Mitovirus sp.** |
| **AZT88623** | **Ophiocordyceps sinensis mitovirus 1** | **QDH88099** | **Mitovirus sp.** |
| **AZT88624** | **Ophiocordyceps sinensis mitovirus 2** | **QDH88156** | **Mitovirus sp.** |
| **AZT88625** | **Setosphaeria turcica mitovirus 1** | **QDH88202** | **Mitovirus sp.** |
| **BAN85985** | **Rhizophagus sp. HR1 mitovirus-like ssRNA** | **QDH88208** | **Mitovirus sp.** |
| **BBN51032** | **Colletotrichum fructicola mitovirus 1** | **QDH88261** | **Mitovirus sp.** |
| **DAB41740** | **Ambrosia artemisiifolia mitovirus 1** | **QDH88284** | **Mitovirus sp.** |
| **DAB41748** | **Erigeron breviscapus mitovirus 1** | **QDH88347** | **Mitovirus sp.** |
| **DAD49837** | **Lutzomyia longipalpis mitovirus 1** | **QDH88411** | **Mitovirus sp.** |
| **QDW65425** | **Rhizoctonia solani mitovirus 37** | **QDH88455** | **Mitovirus sp.** |
| **QED42910** | **Diversispora mitovirus B** | **QDH88475** | **Mitovirus sp.** |
| **QED42925** | **Diversispora mitovirus A** | **QDH88495** | **Mitovirus sp.** |
| **QED42946** | **Scutellospora mitovirus B** | **QDH88566** | **Mitovirus sp.** |
| **QIP68024** | **Bremia lactucae associated mitovirus 1** | **QDH88589** | **Mitovirus sp.** |
| **QIP68030** | **Erysiphales associated mitovirus 1** | **QDH88642** | **Mitovirus sp.** |
| **QIP68031** | **Erysiphales associated mitovirus 1** | **QDH88711** | **Mitovirus sp.** |
| **QIP68032** | **Erysiphales associated mitovirus 1** | **QDH88747** | **Mitovirus sp.** |
| **QIP68033** | **Erysiphales associated mitovirus 1** | **QDH88811** | **Mitovirus sp.** |
| **QIP68034** | **Erysiphales associated mitovirus 1** | **QDH88919** | **Mitovirus sp.** |
| **QIR30225** | **Plasmopara viticola lesion associated mitovirus 1** | **QDH88941** | **Mitovirus sp.** |
| **QIR30227** | **Plasmopara viticola lesion associated mitovirus 3** | **QDH88953** | **Mitovirus sp.** |
| **QIR30228** | **Plasmopara viticola lesion associated mitovirus 4** | **QDH88969** | **Mitovirus sp.** |
| **QIR30229** | **Plasmopara viticola lesion associated mitovirus 5** | **QDH89039** | **Mitovirus sp.** |
| **QIR30232** | **Plasmopara viticola lesion associated mitovirus 9** | **QDH89084** | **Mitovirus sp.** |
| **QIR30233** | **Plasmopara viticola lesion associated mitovirus 10** | **QDH89466** | **Mitovirus sp.** |
| **QIR30236** | **Plasmopara viticola lesion associated mitovirus 13** | **QDH89561** | **Mitovirus sp.** |
| **QIR30237** | **Plasmopara viticola lesion associated mitovirus 14** | **QDH89590** | **Mitovirus sp.** |
| **QIR30238** | **Plasmopara viticola lesion associated mitovirus 15** | **QDH89602** | **Mitovirus sp.** |
| **QIR30240** | **Plasmopara viticola lesion associated mitovirus 17** | **QDH89659** | **Mitovirus sp.** |
| **QIR30242** | **Plasmopara viticola lesion associated mitovirus 19** | **QDH89715** | **Mitovirus sp.** |
| **QIR30243** | **Plasmopara viticola lesion associated mitovirus 20** | **QDH89765** | **Mitovirus sp.** |
| **QIR30244** | **Plasmopara viticola lesion associated mitovirus 21** | **QDH89786** | **Mitovirus sp.** |
| **QIR30245** | **Plasmopara viticola lesion associated mitovirus 22** | **QDH89797** | **Mitovirus sp.** |
| **QIR30247** | **Plasmopara viticola lesion associated mitovirus 24** | **QDH89815** | **Mitovirus sp.** |
| **QIR30248** | **Plasmopara viticola lesion associated mitovirus 25** | **QDH89881** | **Mitovirus sp.** |
| **QIR30251** | **Plasmopara viticola lesion associated mitovirus 28** | **QDH89883** | **Mitovirus sp.** |
| **QIR30252** | **Plasmopara viticola lesion associated mitovirus 29** | **QDH89951** | **Mitovirus sp.** |
| **QIR30253** | **Plasmopara viticola lesion associated mitovirus 30** | **QDH90007** | **Mitovirus sp.** |
| **QIR30255** | **Plasmopara viticola lesion associated mitovirus 32** | **QDH90014** | **Mitovirus sp.** |
| **QIR30257** | **Plasmopara viticola lesion associated mitovirus 34** | **QDH90048** | **Mitovirus sp.** |
| **QIR30261** | **Plasmopara viticola lesion associated mitovirus 38** | **QDH90061** | **Mitovirus sp.** |
| **QIR30263** | **Plasmopara viticola lesion associated mitovirus 40** | **QDH90101** | **Mitovirus sp.** |
| **QIR30264** | **Plasmopara viticola lesion associated mitovirus 41** | **QDH90133** | **Mitovirus sp.** |
| **QIR30265** | **Plasmopara viticola lesion associated mitovirus 42** | **QDH90170** | **Mitovirus sp.** |
| **QIR30266** | **Plasmopara viticola lesion associated mitovirus 43** | **QDH90500** | **Mitovirus sp.** |
| **QIR30269** | **Plasmopara viticola lesion associated mitovirus 46** | **QDH90572** | **Mitovirus sp.** |
| **QIR30270** | **Plasmopara viticola lesion associated mitovirus 47** | **QDH90751** | **Mitovirus sp.** |
| **QIR30271** | **Plasmopara viticola lesion associated mitovirus 48** | **QDH90807** | **Mitovirus sp.** |
| **QIR30272** | **Plasmopara viticola lesion associated mitovirus 49** | **QDH90861** | **Mitovirus sp.** |
| **QIR30273** | **Plasmopara viticola lesion associated mitovirus 50** | **QDH90904** | **Mitovirus sp.** |
| **QIR30275** | **Plasmopara viticola lesion associated mitovirus 52** | **QDH90905** | **Mitovirus sp.** |
| **QIR30276** | **Plasmopara viticola lesion associated mitovirus 53** | **QDH90967** | **Mitovirus sp.** |
| **QIR30277** | **Plasmopara viticola lesion associated mitovirus 54** | **QDH90980** | **Mitovirus sp.** |
| **QIR30278** | **Plasmopara viticola lesion associated mitovirus 55** | **QDH91042** | **Mitovirus sp.** |
| **QIR30279** | **Plasmopara viticola lesion associated mitovirus 56** | **QDH91058** | **Mitovirus sp.** |
| **QJX15643** | **Pea associated mitovirus 1** | **QDH91063** | **Mitovirus sp.** |
| **QJX15644** | **Pea associated mitovirus 2** | **QDH91176** | **Mitovirus sp.** |
| **QJX15645** | **Pea associated mitovirus 3** | **QDH91286** | **Mitovirus sp.** |
| **QKW91256** | **Botrytis cinerea mitovirus 9** | **QDH91288** | **Mitovirus sp.** |
| **QNM37823** | **Thrips tabaci associated mitovirus 2** | **QDH91290** | **Mitovirus sp.** |
| **QNM37829** | **Thrips tabaci associated mitovirus 3** |  |  |
| **QOX06058** | **Lentinula edodes mitovirus 1** |  |  |

Viruses in each collection are listed in order of their GenBank accession nos. (aa) and are color-coded here according to the clade with which they associate in Figures 2 and/or 3. This table has been added because the crowding of name labels makes some of them difficult or impossible to discern in those figures.