This Word module should be used for all taxonomic proposals.

Please complete **Part 1** and:

either **Part 3** for proposals to create new taxa or change existing taxa

or **Part 2** for proposals of a general nature.

Submit the completed Word module, together with the accompanying Excel module named in Part 3, to the appropriate ICTV Subcommittee Chair.

For guidance, see the notes written in blue, below, and the help notes in file Taxonomic\_Proposals\_Help\_2018.

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

|  |  |  |  |
| --- | --- | --- | --- |
| **Code assigned:** | ***2018.028P*** | | (to be completed by ICTV officers) |
| **Short title:** Three new species in the genus *Mastrevirus*,one new species in the genus *Becurtovirus*, two new species in the genus *Grablovirus* | | | |
|  | | | |
| **Author(s):** | | | |
| Arvind Varsani, Philippe Roumagnac, Jean-Michel Lett, Darren P. Martin on behalf of the *Geminiviridae* and *Tolecusatellitidae* SG | | | |
| **Corresponding author with e-mail address:** | | | |
| Arvind Varsani, Arvind.varsani@asu.edu | | | |
| **List the ICTV study group(s) that have seen this proposal:** | | | |
| A list of study groups and contacts is provided at <http://www.ictvonline.org/subcommittees.asp> . If in doubt, contact the appropriate subcommittee chair (there are six virus subcommittees: animal DNA and retroviruses, animal ssRNA-, animal ssRNA+, fungal and protist, plant, bacterial and archaeal) | | *Geminiviridae and Tolecusatellitidae SG* | |
| **ICTV Study Group comments (if any) and response of the proposer:** | | | |
|  | | | |
|  | | | |
| Date first submitted to ICTV: | | | June 4th, 2018 |
| Date of this revision (if different to above): | | |  |

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

**Part 2:** **NON-STANDARD**

Template for any proposal regarding ICTV procedures, rules or policy, not involving the creation of new taxonomy.

| **Text of proposal:** |
| --- |
|  |

**Part 3:** **PROPOSED TAXONOMY**

|  |
| --- |
| **Name of accompanying Excel module:** 2018.028P.N.v1.Geminiviridae\_6sp.xlsx |

**Supporting material:**

**Three new species in the genus *Mastrevirus***

There are currently 37 species in the genus *Mastrevirus* in the family *Geminiviridae*. Of these, members of six infect dicots and the rest (n=31) infect monocots. Most of the viruses in this latter group have been identified infecting various grasses in Africa and Australia (Muhire *et al*., 2013).

A framework for classification of mastreviruses was established by Muhire *et al*. (2013) where a 78% genome-wide pairwise identity (PI) threshold coupled with phylogenetic support were proposed, and accepted, as species demarcation criteria. Based on this framework, three new species need to be established to allow the classification of new mastrevirus isolates that have been recently characterized from Australia and Brazil.

**New species to be created and isolates that should be assigned to these species**

**1. Maize striate mosaic virus**

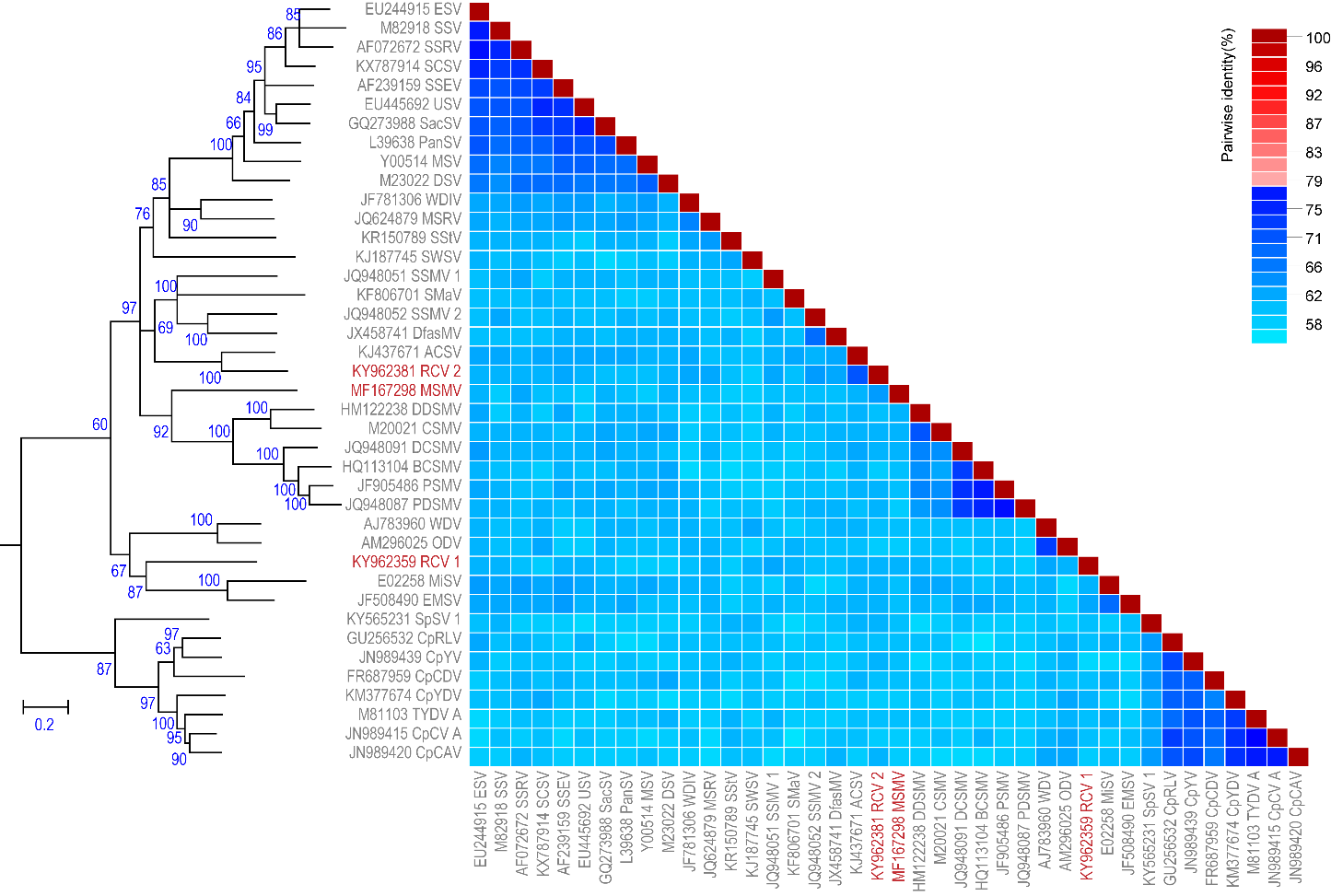
Eleven isolates of maize striate mosaic virus (table 1) have been identified from *Zea mays* (n=10) and the leafhopper *Dalbulus maidi*s (n=1) (Fontenele *et al*., 2018). The 11 isolates share >99% genome-wide pairwise identity with each other and <63% with all other known mastreviruses within currently established species (Figure 1).

**2. Rice latent virus 1**

Twenty two isolates of rice latent virus 1 have been identified in *Oryza* sp. ‘Taxon A’ (n=16) and *Oryza* sp. ‘Taxon B’ (n=6) from Australia (Kraberger *et al*., 2017). Rice latent virus 1 isolates share >98% genome-wide pairwise identity with each other and <62% with all other known mastreviruses within currently established species.

**3. Rice latent virus 2**

One isolate of rice latent virus 2 has been identified in *Oryza* sp. ‘Taxon B’ from Australia (Kraberger *et al*., 2017). This isolate shares <70% genome-wide pairwise with all other known mastreviruses within currently established species.



**Figure 1.** Maximum likelihood phylogenetic tree (rooted with becurtovirus sequences) of representative genomes from each mastrevirus species inferred using PHYML (Guindon *et al*., 2010) with GTR+I+G4 chosen as the best fit model and a two-colour pairwise identity matrix inferred using SDT v1.2 (Muhire *et al*., 2014). Sequences of representative isolates for each new species are in red font.

**Table 1.** Details of new isolates and species being proposed in the genus *Mastrevirus*

|  |  |  |  |  |  |
| --- | --- | --- | --- | --- | --- |
| **Species name** | **GenBank accession** | **Virus acronym** | **Isolate ID** | **Country of isolate** | **Host** |
| Maize striate mosaic virus | MF167297 | MSMV | BR\_974\_Pla\_2016 | Brazil | *Zea mays* |
|  | MF167298 | | BR\_975\_Pla\_2016 | Brazil | *Zea mays* |
|  | MF167299 | | BR\_976\_Pla\_2016 | Brazil | *Zea mays* |
|  | MF167300 | | BR\_981\_Pla\_2016 | Brazil | *Zea mays* |
|  | MF167301 | | BR\_982\_Pla\_2016 | Brazil | *Zea mays* |
|  | MF167302 | | BR\_984\_Pla\_2016 | Brazil | *Zea mays* |
|  | MF167303 | | BR\_985\_Pla\_2016 | Brazil | *Zea mays* |
|  | MF167304 | | BR\_987\_Pla\_2016 | Brazil | *Zea mays* |
|  | MF167305 | | BR\_988\_Pla\_2016 | Brazil | *Zea mays* |
|  | MF167306 | | BR\_989\_Pla\_2016 | Brazil | *Zea mays* |
|  | MF167307 | | BR\_J455\_Pla\_2016 | Brazil | *Dalbulus maidis\** |
| Rice latent virus 1 | KY962377 | RLV 1 | NA67 | Australia | *Oryza* sp. ‘Taxon A’ |
|  | KY962378 |  | NA68 | Australia | *Oryza* sp. ‘Taxon A’ |
|  | KY962379 |  | NA69 | Australia | *Oryza* sp. ‘Taxon A’ |
|  | KY962380 |  | NA70 | Australia | *Oryza* sp. ‘Taxon A’ |
|  | KY962359 |  | NA15 | Australia | *Oryza* sp. ‘Taxon B’ |
|  | KY962360 |  | NA16 | Australia | *Oryza* sp. ‘Taxon B’ |
|  | KY962361 |  | NA18 | Australia | *Oryza* sp. ‘Taxon B’ |
|  | KY962362 |  | NA22 | Australia | *Oryza* sp. ‘Taxon B’ |
|  | KY962364 |  | NA30 | Australia | *Oryza* sp. ‘Taxon B’ |
|  | KY962363 |  | NA26 | Australia | *Oryza* sp. ‘Taxon B’ |
|  | KY962365 |  | NA49 | Australia | *Oryza* sp. ‘Taxon A’ |
|  | KY962366 |  | NA52 | Australia | *Oryza* sp. ‘Taxon A’ |
|  | KY962367 |  | NA53 | Australia | *Oryza* sp. ‘Taxon A’ |
|  | KY962368 |  | NA55 | Australia | *Oryza* sp. ‘Taxon A’ |
|  | KY962369 |  | NA56 | Australia | *Oryza* sp. ‘Taxon A’ |
|  | KY962370 |  | NA57 | Australia | *Oryza* sp. ‘Taxon A’ |
|  | KY962371 |  | NA59 | Australia | *Oryza* sp. ‘Taxon A’ |
|  | KY962372 |  | NA60 | Australia | *Oryza* sp. ‘Taxon A’ |
|  | KY962373 |  | NA62 | Australia | *Oryza* sp. ‘Taxon A’ |
|  | KY962374 |  | NA63 | Australia | *Oryza* sp. ‘Taxon A’ |
|  | KY962375 |  | NA64 | Australia | *Oryza* sp. ‘Taxon A’ |
|  | KY962376 |  | NA65 | Australia | *Oryza* sp. ‘Taxon A’ |
| Rice latent virus 2 | KY962381 | RLV 2 | NA24 | Australia | *Oryza* sp. ‘Taxon B’ |

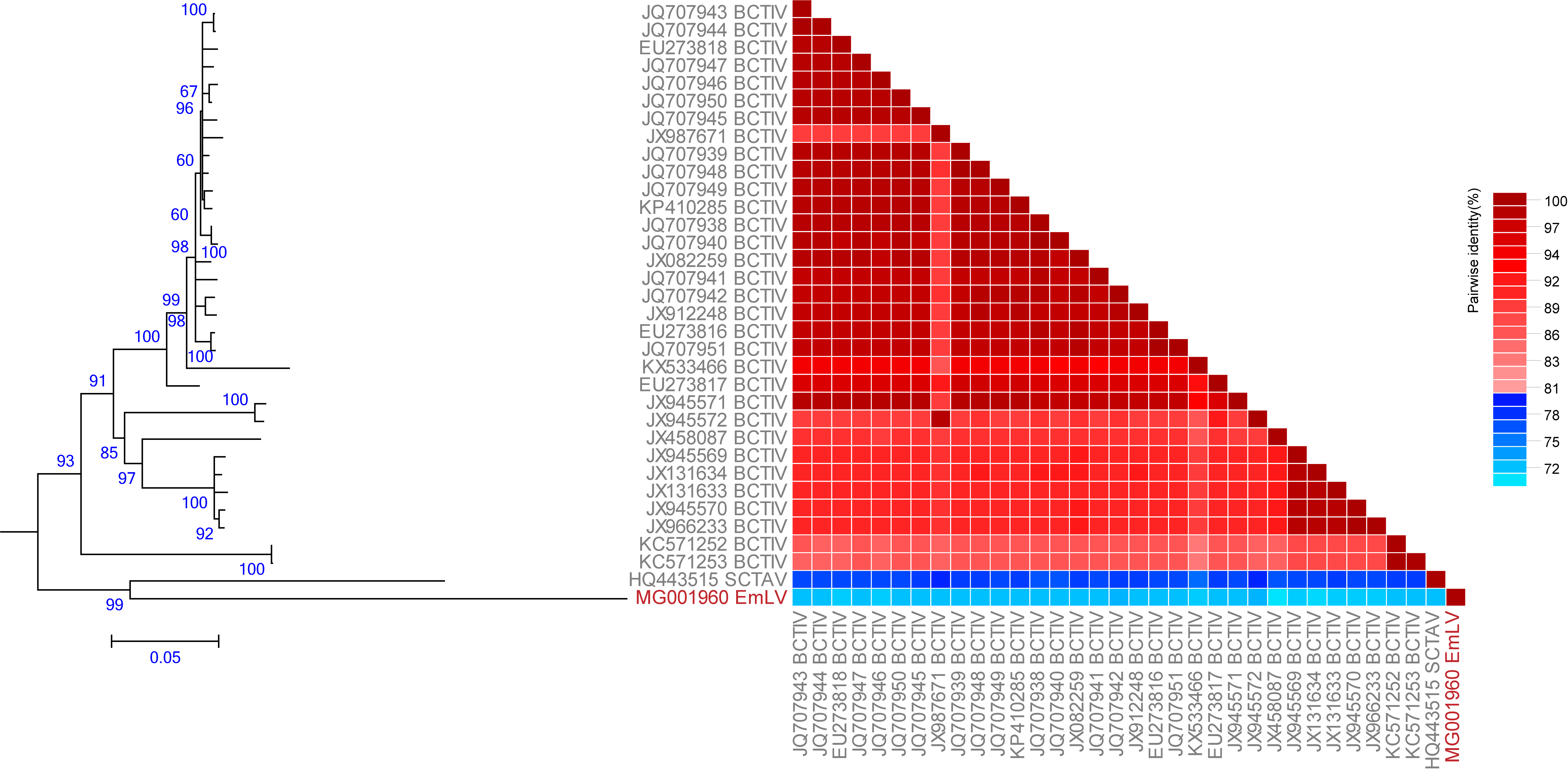
\*Leafhopper (Hemiptera:Cicadellidae)

**One new species in the genus *Becurtovirus***

There are currently two species in the genus *Becurtovirus* (Varsani *et al*., 2014) (Figure 2). Varsani *et al*., 2014 proposed a species demarcation threshold of 80% genome-wide identity for becurtoviruses.

**1. Exomis microphylla latent virus**

Recently a new becurtovirus was identified in *Exomis microphylla* from South Africa (Claverie *et al*., 2018) (Figure 2, Table 2). The genome of Exomis microphylla latent virusshares <72% genome-wide identity with other known becurtoviruses within currently established species.



**Figure 2.** Maximum likelihood phylogenetic tree (rooted with turncurtovirus sequences) of genomes of viruses in the genus *Becurtovirus* inferred using PHYML (Guindon *et al*., 2010) with GTR+I+G4 chosen as the best fit model and a ‘two colour’ pairwise identity matrix inferred using SDT v1.2 (Muhire *et al*., 2014). Sequences of the isolate for the new species is in red font.

**Table 2.** Details of new isolate and species being proposed in the genus *Becurtovirus*

|  |  |  |  |  |  |
| --- | --- | --- | --- | --- | --- |
| **Species name** | **GenBank accession** | **Virus acronym** | **Isolate ID** | **Country of isolate** | **Host** |
| Exomis microphylla latent virus | MG001960 | EmLV | 2-90-C1 | South Africa | *Exomis microphylla* |

**Two new species in the genus *Grablovirus***

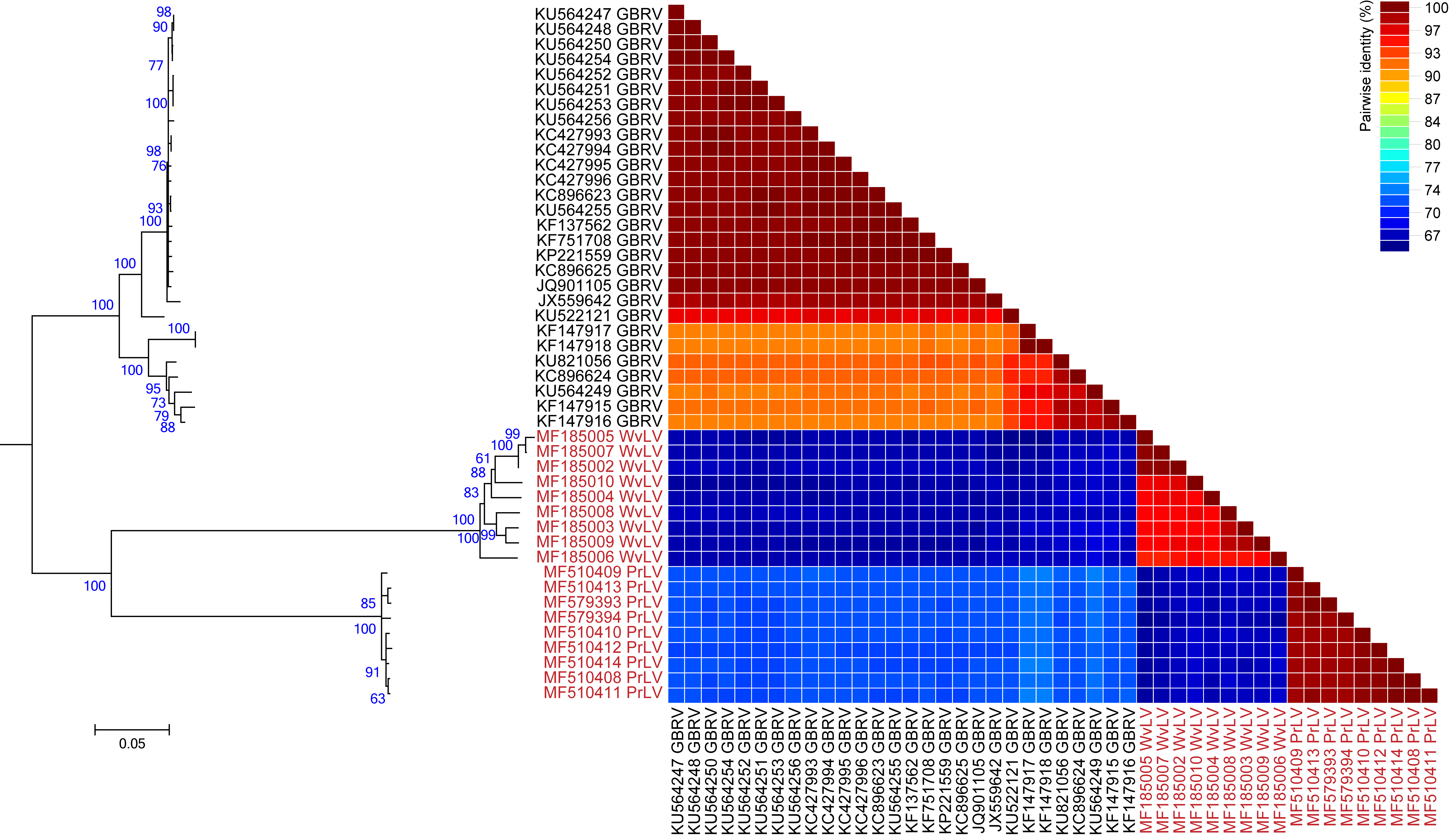
There is currently one species in the genus *Grabloviru*s (Varsani *et al*., 2014) (Figure 3) and thus no species demarcation has been seen. Grapevine red blotch virus isolate sequences (n=28) share >91% genome-wide pairwise identities.

**1. Wild Vitis latent virus**

1. Wild *Vitis* viruses (n=9) were recently identified in non-cultivated (wild) grapevine (Perry *et al*., 2017). They share >95% identity. They are most closely related to grapevine red blotch virus (67-68% genome-wide identity; Figure 3) and have a similar genome organisation. Thus, we propose that the nine wild *Vitis* viruses isolates be assigned to a new species – *Wild Vitis latent virus*.

**2. Prunus latent virus**

Prunus geminivirus A isolates (n=9) were identified in various *Prunus* species (Al Rwahnib et al., in press). They share >99% identity. They share ~74% genome-wide identity with grapevine red blotch viruses. We propose that the nine *Prunus* geminiviruses be assigned to a new species – *Prunus latent virus*.



**Figure 3.** Maximum likelihood phylogenetic tree (rooted with grapevine geminivirus A sequences) of genomes of grabloviruses inferred using PHYML (Guindon *et al*., 2010) with GTR+G4 chosen as the best fit model pairwise identity matrix inferred using SDT v1.2 (Muhire *et al*., 2014). Sequences of isolates for the new species are in red font.

**Table 3.** Details of new isolates and the species being proposed in the genus *Grablovirus*

|  |  |  |  |  |  |
| --- | --- | --- | --- | --- | --- |
| **Species name** | **GenBank accession** | **Virus acronym** | **Isolate ID** | **Country of isolate** | **Host** |
| Wild vitis latent virus | MF185002 | WvLV | WVV1-NY1298 | USA | *Vitis* sp. |
|  | MF185003 |  | WVV1-NY1308 | USA | *Vitis* sp. |
|  | MF185004 |  | WVV1-NY1325 | USA | *Vitis* sp. |
|  | MF185005 |  | WVV1-NY1358 | USA | *Vitis* sp. |
|  | MF185006 |  | WVV1-NY1424 | USA | *Vitis* sp. |
|  | MF185007 |  | WVV1-NY1466 | USA | *Vitis* sp. |
|  | MF185008 |  | WVV1-NY1467 | USA | *Vitis* sp. |
|  | MF185009 |  | WVV1-NY1468 | USA | *Vitis* sp. |
|  | MF185010 |  | WVV1-NY1616 | USA | *Vitis* sp. |
| Prunus latent virus | MF510408 | PrLV | PL4 | USA | *Prunus salicina* cv. Formosa |
|  | MF510409 |  | PL6 |  | *Prunus domestica* cv. Reine Claude De Bravay |
|  | MF510410 |  | PL8 |  | *Prunus domestica* cv. Pervenec 36Neg2*3* |
|  | MF510411 |  | PL9 |  | *Prunus domestica* cv. Purple Gage |
|  | MF510412 |  | PL10 |  | *Prunus salicina* cv. Wickson |
|  | MF510413 |  | PL11 | China | *Prunus salicina* cv. NA 67714 |
|  | MF510414 |  | PL13 | USA | *Prunus salicina* cv. Abundance |
|  | MF579393 |  | GF305 | USA | *Prunus persica* cv. GF 305 |
|  | MF579394 |  | HTS | USA | *Prunus* sp*.* |

| **References:** |
| --- |
| Al Rwahnib, M., Alabi, I, J., Westrick, N.M., Golino, D., (in press) Prunus geminivirus A: a novel grablovirus infecting *Prunus* spp. https://doi.org/10.1094/PDIS-09-17-1486-RE  Claverie, S., Bernardo, P., Kraberger, S., Hartnady, P., Lefeuvre, P., Lett, J-M., Galzi, S., Filloux, D., Harkins, G.W., Varsani, A., Martin, D.P., Roumagnac, P. (2018) From spatial metagenomics to molecular characterization of plant viruses: a geminivirus case study. Advances in Virus Research DOI: oi.org/10.1016/bs.aivir.2018.02.003  Fontenele, R.S., Alves-Freitas, D.M.T., Silva, P.I.T., Foresti, J., Silva, P.R., Godinho, M.T., Varsani, A., Ribeiro, S.G. (2018) Discovery of the first maize-infecting mastrevirus in the Americas using a vector-enabled metagenomics approach. Archives of Virology 163:263-267  Guindon, S., Dufayard, J. F., Lefort, V., Anisimova, M., Hordijk, W. & Gascuel, O. (2010). New algorithms and methods to estimate maximum-likelihood phylogenies: assessing the performance of PhyML 3.0. Systematic biology 59, 307-321.  Kraberger, S., Geering, A.D.W., Walters, M., Martin, D.P., Varsani, A. (2017) Novel mastreviruses identified in Australian wild rice. Virus Research. 238: 193-197  Muhire, B., Martin, D.P., Brown, J.K., Navas-Castillo, J., Moriones, E., Zerbini, F.M., Rivera-Bustamante, R., Malathi, V.G., Briddon, R.W., Varsani, A., 2013. A genome-wide pairwise-identity-based proposal for the classification of viruses in the genus *Mastrevirus* (family *Geminiviridae*). Arch Virol 158(6), 1411-1424.  Muhire, B.M., Varsani, A., Martin, D.P., 2014. SDT: a virus classification tool based on pairwise sequence alignment and identity calculation. PLoS One 9(9), e108277.  Perry, K.l., McLane, H., Thompson, J.R., Fuchs, M. (2017) A novel grablovirus from non-cultivated grapevine (Vitis sp.) in North America. Arch Virol 163:259-262  Varsani, A., Navas-Castillo, J., Moriones, E., Hernández-Zepeda, C., Idris, A., Brown, J.K., Zerbini, F.M., Martin, D.P. (2014) Establishment of three new genera in the family *Geminiviridae*: *Becurtovirus, Eragrovirus* and *Turncurtovirus*. Arch Virol 159:2193-2203 |