

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

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| **Code assigned:** | **2020.006P** |  |
| **Short title:** Create 22 species and abolish one species in the genus *Begomovirus* (*Geplafuvirales*: *Geminiviridae*) | | |
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**List the ICTV Study Group(s) that have seen this proposal**

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| *Geminiviridae* and *Tolecusatellitidae* Study Group |

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

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

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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 | July 30, 2020 |
| 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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| 2020.006P.R.Begomovirus\_22nsp.xlsx |

**Abstract**

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| In this TP we propose to create 22 species and to abolish one species in the genus *Begomovirus*, family *Geminiviridae*. This proposal has been prepared following the taxonomic criteria established for this genus. |

**Text of proposal**

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| |  | | --- | | Begomoviruses (genus *Begomovirus*, family *Geminiviridae*) are single-stranded DNA plant viruses transmitted by whiteflies of the *Bemisia tabaci* complex. They are considered emergent viruses and infect a wide range of crops and wild plants in tropical and subtropical regions (Navas-Castillo et al., 2011). Begomoviruses have one or two small (2.6 kb) circular ssDNA genome components  Brown *et al*. (2015) established the current species demarcation criteria for the genus *Begomovirus* that is based on pairwise sequence comparison as the main criterion. However, considering the frequent occurrence of recombination among begomovirus genomes, phylogenetic support is highly desirable to support new species. Using these criteria, 22 new species are being proposed in the genus (see Table 1 and accompanying Excel module). Members of these 22 species have <91% nucleotide sequence identity for the complete genome (or the complete DNA-A in the case of bipartite viruses) with members of existing species, which is the cut off value established. The proposed begomovirus species contain 1 to 5 isolates completely sequenced. The new begomoviruses have been isolated from cultivated (n=14, including food and ornamental crops), non-cultivated (n=7) plants, and one of them was isolated from both type of plants (the cultivated cucumber and an unidentified weed).  Phylogenetic analysis supports the proposal of all 22 species (Figures 1 and 2). Also, phylogeny shows that proposed begomovirus species belong to the New World (n=13) and Old World (n=9) clusters.  Following the species demarcation criteria in the genus *Begomovirus* (Brown *et al*., 2015), one species is being proposed to be abolished, *Radish leaf curl virus* (Table 2). Recently, a virus isolate of this begomovirus has been deposited in GenBank (KF218188). This isolate has also 91% nt identity with an isolate of *Pedilanthus leaf curl virus* (AM948961), a species previously established. Thus, both species should be merged, maintaining the name *Pedilanthus leaf curl virus*. | |

**Table 1.** Details of the 22 proposed begomovirus species.

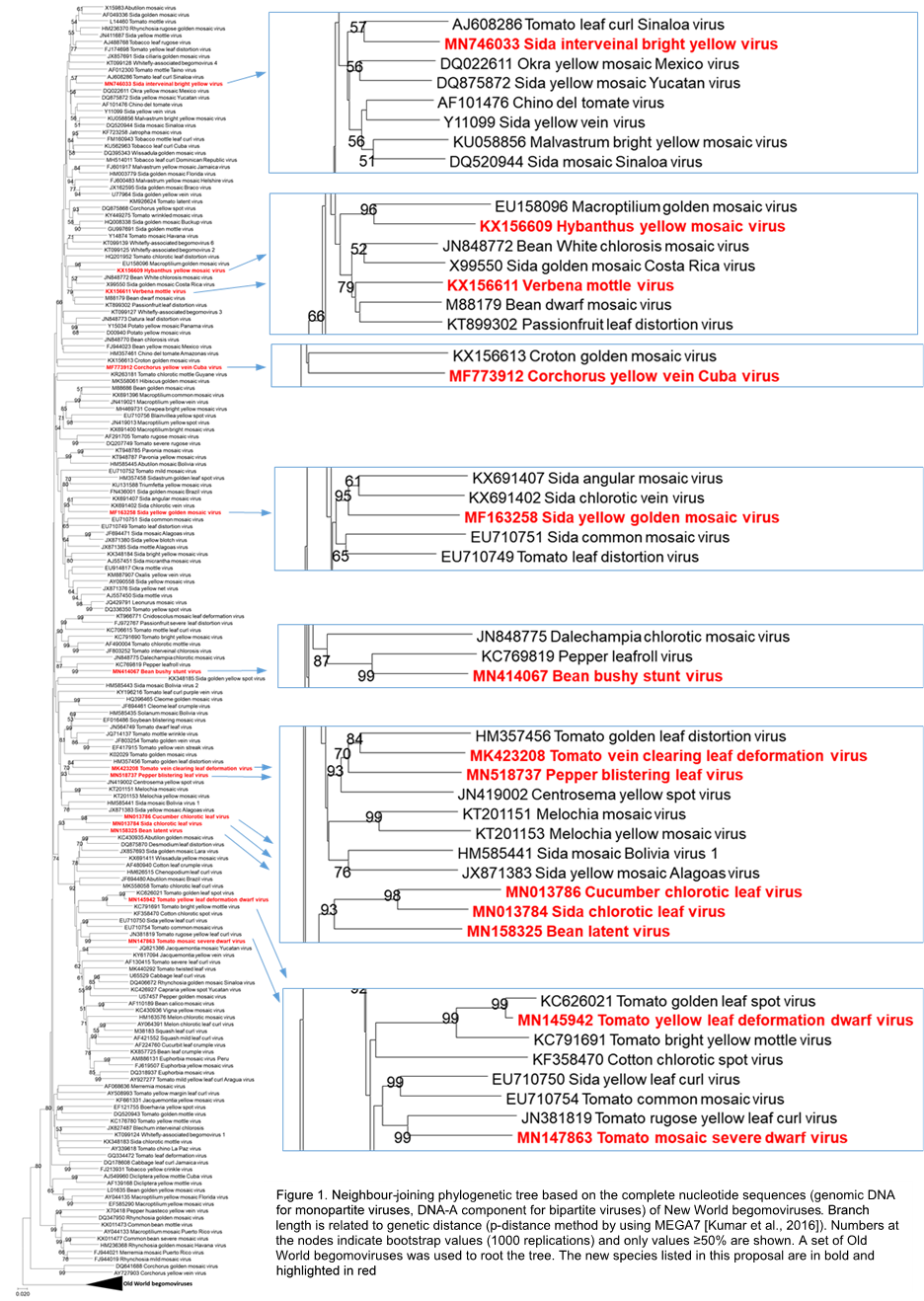
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| --- | --- | --- | --- | --- | --- |
| **Species name** | **Virus acronym** | **GenBank Acc. No.\*** | **Isolate** | **Highest nt sequence identity with (%)** | **Reference** |
| *Bean bushy stunt virus* | BBSV | MN414067 | AR- General Mosconi-17 | PepLRV (85) | Unpublished |
| *Bean latent virus* | BLV | MN158325 | MX-Nayarit CN30-14 | ToMoWV (81) | Martínez-Marrero et al (2020) |
| *Corchorus yellow vein Cuba virus* | CoYVCUV | MF773912 | CU-Co705-1-13 | TbYCV (82), JMV (82) | Fiallo-Olivé and Navas-Castillo (2020) |
|  |  | MF773913 | CU-Co705-2-13 |  |
|  |  | MF773914 | CU-Co705-3-13 |  |
|  |  | MF773915 | CU-Co705-4-13 |  |
|  |  | MF773916 | CU-Co706-1-13 |  |
|  |  |  |  |  |
| *Cucumber chlorotic leaf virus* | CuChLV | MN013786 | MX-Colima-18 | SiChLV (86) | Sanchez-Chavez et al (2020) |
| MN203175 | MX-weed UHBV-14 | SiChLV (86) | Alcalá-Briseño et al (2020) |
| *Hibiscus yellow vein leaf curl virus* | HYVLCV | MF140451 | TW-HibA\_1-13 | CLCuMuV (89.4) | Huang et al. (2020) |
| MF140452 | TW-Hib2\_2-14 | CLCuMuV (89.4) |  |
| MF140453 | TW-Hib5\_5-14 | CLCuMuV (89.4) |  |
| MK482364 | TW-Chou-18 | CLCuMuV (89.4) |  |
| *Hybanthus yellow mosaic virus* | HybYMV | KX156609 | CO-Valle-14 | MacGMV (84) | Unpublished |
| *Ocimum yellow vein virus* | OcYVV | MN313667 | UG-UG14-2015 | ClGMJsV (72) | Mollel et al (2020) |
|  |  | MN313665 | UG-UG16-2015 | ClGMJsV (73) |  |
|  |  | MN313663 | UG-UG32-2015 | ClGMJsV (72) |  |
| *Ocimum mosaic virus* | OcMV | MN313669 | UG-UG24-2015 | ClGMJsV (72) | Mollel et al (2020) |
| *Ocimum golden mosaic virus* | OcGMV | MN313661 | UG-UG31-2015 | ToLCUV (83) | Mollel et al (2020) |
|  |  | MN313659 | UG-UG33-2015 | ToLCUV (83) |  |
| *Papaya severe leaf curl virus 1* | PaSLCV1 | MH988457 | IN-PSB\_8-14 | PepLCBV (90) | Unpublished |
| *Papaya severe leaf curl virus 2* | PaSLCV2 | MH988458 | IN-PSB\_14-14 | PaLCuV (88) | Unpublished |
| *Papaya yellow leaf curl virus* | PaYLCV | MH807204 | IN-PSB\_51-16 | PeLCV (83) | Nehra et al (2019) |
|  |  | KX353622 | IN-DP2-15 | PeLCV (90) |  |
| *Pepper blistering leaf virus* | PepBLV | MN518737 | AR-Salta-Oran-Pepper663-2014 | SoMBoV (83) | Bornancini et al. (2020) |
|  |  | MN518738 |  | SoMBoV (83) |  |
|  |  | MN518735 |  | SoMBoV (83) |  |
| *Polygala garcinii virus* | PgV | MG001959 | ZA-1-1-12 | TYLCCNV (68) | Claverie et al (2018) |
| *Sida chlorotic leaf virus* | SiChLV | MN013784 | MX-Colima-18 | CuChLV (86) | Unpublished |
| *Sida interveinal bright yellow virus* | SiIBYV | MN746033 | MX- Conca 1-18 | SiYVV (89) | Unpublished |
| *Sida yellow golden mosaic virus* | SiYGMV | MF163258 | BR-SPI15-15 | SiAMV (84) | Macedo et al. (2019) |
| *Tomato leaf curl Kunene virus* | ToLCKunV | MT045996 | NA-Namibia-2019 | ToLCZWV (83) | Lett et al (2020) |
| *Tomato mosaic severe dwarf virus* | ToMSDV | MN147863 | BR-DF-640\_AA\_LVV-16 | TRYLCV (85) | Unpublished |
| *Tomato vein clearing leaf deformation virus* | ToVCLDeV | MK423208 | AR-Cordoba-Monte Cristo-Tom51-05 | PepBLV (83) | Vaghi Medina et al (2020) |
| *Tomato yellow leaf deformation dwarf virus* | ToYLDeDV | MN145942 | BR-TO\_83-08 | ToBYMoV (90) | Unpublished |
| *Verbena mottle virus* | VMoV | KX156611 | CO-Valle-14 | BWCMV (87) | Unpublished |

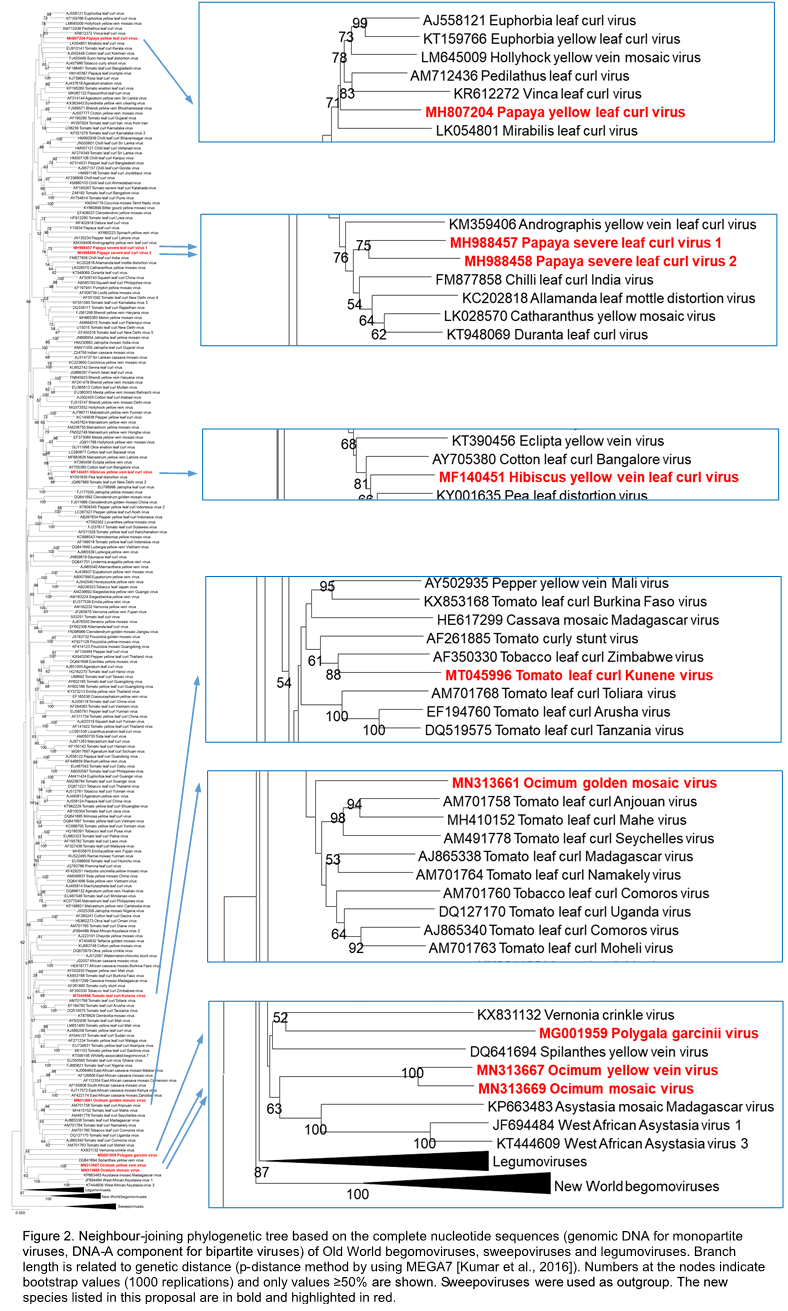
\*GenBank Acc. Nos. correspond to complete genomes (monopartite begomoviruses) or DNA-A (bipartite begomoviruses).

**Table 2.** Details of the begomovirus species to be abolished.

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| --- | --- | --- | --- | --- |
| **Abolished species** | **GenBank Acc. No.** | **Merges with** | **GenBank Acc. No.** | **% nt identity** |
| *Radish leaf curl virus* | KF218188 | *Pedilanthus leaf curl virus* | AM948961 | 91 |

**Supporting evidence**

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