

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

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| **Code assigned:** | **2020.027P** |  |
| **Short title:** Create one new species (*Paper mulberry leaf curl virus 1*) in the genus *Mulcrilevirus* and one new species (*Paper mulberry leaf curl virus 2*) in the genus *Citlodavirus* (*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 | June 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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| 2020.027P.R.Geminiviridae\_2nsp.xlxs |

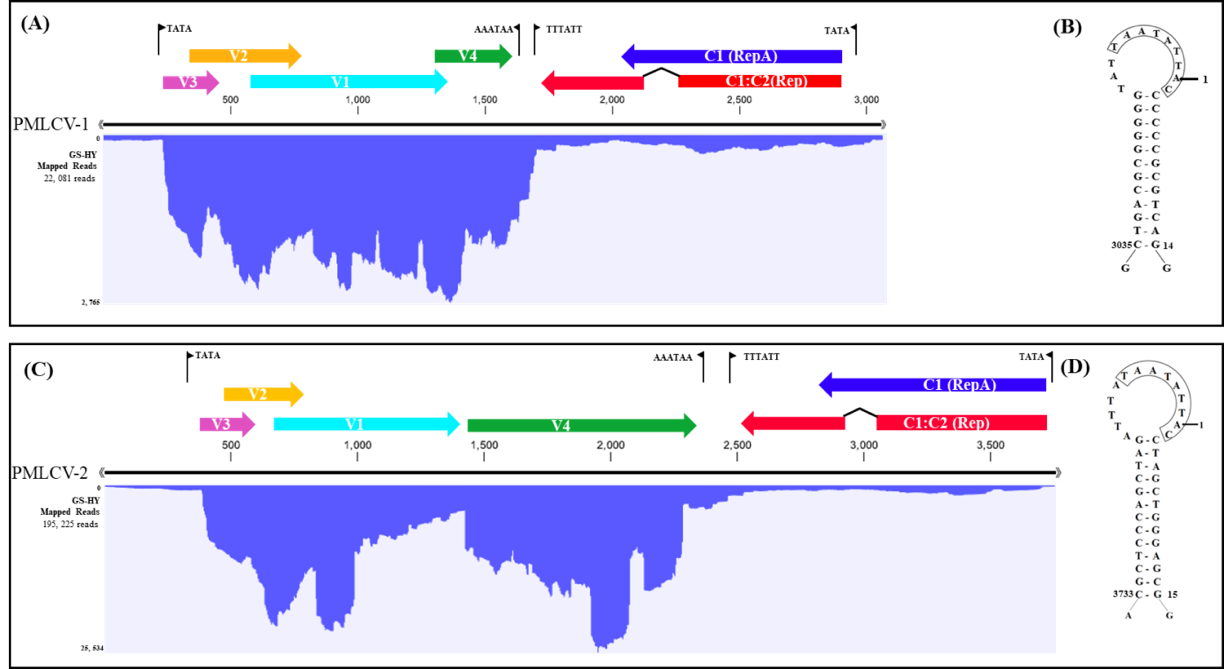
**Abstract**.

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| Paper mulberry leaf curl virus 1 and paper mulberry leaf curl virus 2 (PMLCV-1, and PMLCV-2) have been characterized from diseased paper mulberry (*Broussonetia papyrifera*) plants displaying leaf curl, puckering, and V-shaped margins (Qiu et al., 2020). These two viruses, with a circular DNA genome, are clearly related to geminiviruses in genome organization, replication origin (5'-TAATATTAC-3'), and encoded proteins. Phylogenetic analyses support a close relationship between PMLCV-1, PMLCV-2 and representative members of the family *Geminiviridae*. Since PMLCV-1 and PMLCV-2 share the highest sequence identities with viruses of the proposed new genera *Mulcrilevirus* and *Citlodavirus*, respectively, we propose to classify PMLCV-1 and PMLCV-2 as new species of these genera. |

**Text of proposal**

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| |  | | --- | | Paper mulberry leaf curl virus 1 and paper mulberry leaf curl virus 2 (PMLCV-1, and PMLCV-2) were characterized from *B. papyrifera* (Qiu *et al*., 2020). PMLCV-1 and PMLCV-2 have similar genomic and protein features to those of members of proposed new genera *Mulcrilevirus* (mulberry crinkle leaf virus) and *Citlodavirus* (citrus chlorotic dwarf associated virus, camellia chlorotic dwarf associated virus and passion fruit chlorotic mottle virus), respectively (family *Geminiviridae*). Several aspects are in support of our proposal classifying PMLCV-1 and PMLCV-2 into these new genera:   1. Genome structure: both PMLCV-1 and PMLCV-2 have a monopartite genome with four ORFs in the virion-sense strand (V1-V4) and two ORFs in the complementary-sense strand (C1, C1:C2) (Figure 1), similar to mulberry crinkle leaf virus (MCLV), citrus chlorotic dwarf associated virus (CCDaV), camellia chlorotic dwarf associated virus (CaCDaV) and passion fruit chlorotic mottle virus (PCMoV) (Loconsole et al., 2012; Ma et al., 2015; Zhang et al., 2018; Fontenele et al., 2018); 2. Sequence homology: PMLCV-1 (3,056 nt) and PMLCV-2 (3,763 nt) share less than 61.7% and 65.7% nt sequence identities with the other known geminiviruses, respectively (Figure 2); 3. Phylogenetic relationship: PMLCV-1 clusters with MCLV, and PMLCV-2 clusters with CCDaV, CaCDaV and PCMoV in the phylogeny of full-length genomes (Figure 3), of the replication-associated protein (Rep) (Figure 4) and of the coat protein (CP) (Figure 5)*.* | |

**Supporting evidence**

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**Figure 1**.Linear representations of the circular genomes of (A) paper mulberry leaf curl virus 1 (PMLCV-1) and (C) paper mulberry leaf curl virus 2 (PMLCV-2) with the virus-related RNA reads from the GS-HY library mapped on the viral genomes. Genome hallmarks, including TATA boxes and polyadenylation signals, are indicated. Coding sequences of the genes are denoted in the virion (V) or complementary (C)-sense strands, and the intron in C1:C2 is also indicated. Rep, replication-associated protein. (B, D) Nonanucleotide sequence within the stem-loop in the large intergenic regions (LIR) of the PMLCV-1 and PMLCV-2, respectively. Number 1 indicates the first position in the viral genome which, according to convention, is coincident with the origin of replication.

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**Figure 2**. Genome-wide pairwise identities of representative isolates from geminivirus genera, determined using SDT v1.2 with the MUSCLE alignment option.

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**Figure 3**. Phylogenetic analysis of paper mulberry leaf curl virus 1 (PMLCV-1), paper mulberry leaf curl virus 2 (PMLCV-2), plus representative members of the different genera in the family *Geminiviridae*, based on full genome nucleotide sequences using the neighbour-joining method. GenBank accession numbers are placed before each virus name. Numbers associated with branches indicate bootstrap support for these branches. Branches with less than 60% bootstrap support have been collapsed.

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**Figure 4**. Phylogenetic relationships between paper mulberry leaf curl virus 1 (PMLCV-1), paper mulberry leaf curl virus 2 (PMLCV-2), and other members in the family *Geminiviridae*. Phylogenetic trees were constructed based on the Rep deduced amino acid sequences using the maximum-likelihood method. The tree is rooted with Rep sequences of representative genomoviruses. Branch length is proportional to number of amino acid changes. Bootstrap percentages (higher than 60%), determined from 1,000 bootstrap replicates, are shown at the branches.

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**Figure 5**. Phylogenetic relationships between paper mulberry leaf curl virus 1 (PMLCV-1), paper mulberry leaf curl virus 2 (PMLCV-2), and other members in the family *Geminiviridae*. Phylogenetic trees were constructed based on the CP deduced amino acid sequences using the maximum-likelihood method. The tree is rooted with CP sequences of representative genomoviruses. Branch length is proportional to number of amino acid changes. Bootstrap percentages (higher than 60%), determined from 1,000 bootstrap replicates, are shown at the branches.

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