

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

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| **Code assigned:** | **2020.034P** |  |
| **Short title:** Create two new species in genus *Umbravirus* (*Tolivirales*: *Tombusviridae*) | | |
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**Author(s) and email address(es)**

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| --- | --- |
| Scheets K    on behalf of the *Tombusviridae* Study Group | kay.scheets@okstate.edu |

**Author(s) institutional address(es) (optional)**

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| Oklahoma State University |

**Corresponding author**

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| Kay Scheets (kay.scheets@okstate.edu) |

**List the ICTV Study Group(s) that have seen this proposal**

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| *Tombusviridae* Stugy Group |

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

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| Two members responded, and agree with proposal. |

**Submission dates**

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| --- | --- |
| Date first submitted to SC Chair | Aug 18, 2020 |
| 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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| 2020.034P.R.Umbravirus\_2nsp.xlsx |

**Abstract**

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| Ixeridium yellow mottle virus 2 and patrinia mild mottle virus are two new viruses discovered in South Korea, and they have the characteristics of distinct new species in genus *Umbravirus*. |

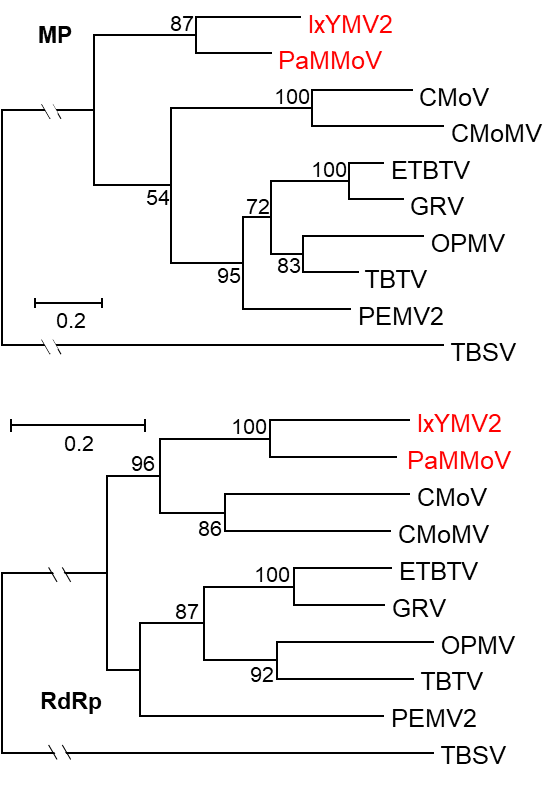
**Text of proposal**

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| |  | | --- | | Two umbraviruses were found in two different counties of North Gyeongsang Province, S. Korea. They were both isolated from unrelated hosts from the eudicot clade *Asterids*. From the order level down (*Asterales* for ixeridium yellow mottle virus 2 (IxYMaV2) [5] and *Dipsacales* for patrinia mild mottle virus (PatMMoV) [3] the host species are far apart, so these viruses are unlikely to have overlapping host ranges. Both viruses encode RNA dependent RNA polymerases (RdRps) that are expressed via stop codon readthrough of the upstream replicase associated protein (RAP).  Criteria for inclusion as a new umbravirus species requires at least two of the following three criteria be met [4]:  natural host range (including insect vector and helper virus as well as plant species)  less than 75% aa sequence identity of the viral replicase  less than 75% aa sequence identity of cell-to-cell movement protein (MP)  BLAST searches with the RdRps and MPs show that both viruses are most similar to each other and to current umbravirus proteins, and MUSCLE analyses [1] also indicates their similarity to each other and current umbraviruses (Table 1). Separate phylogenetic trees for the proteins of current and proposed umbraviruses versus the analogous proteins of tomato bushy stunt virus (TBSV) show their relationships to the analogous proteins of the family type species. Note that a sequence for IxYMaV1 (Bonghua isolate) [KT946712.1] [5] was submitted from the same laboratory, and it is listed in GenBank as a polerovirus, which indicates it is the helper virus for IxYMaV2. There is no sequence with the name of the likely helper virus for PatMMoV available on the web, and emails to the submitter's laboratory go unanswered. | |

**Supporting evidence**

**Table 1**. Percent identities of umbravirus RdRps and ORF4 proteins.

|  |  |  |  |  |  |  |  |  |  |  |
| --- | --- | --- | --- | --- | --- | --- | --- | --- | --- | --- |
|  |  | **Cell to cell movement proteins** | | | | | | | | |
|  |  | **IxYMV2** | **PaMMoV** | CMoV | CMoMV | ETBTV | GRV | OPMV | TBTV | PEMV2 |
| **RdRps** | **IxYMV2** | **100** | **61.8** | 31.9 | 34.6 | 38.2 | 37.8 | 37.0 | 39.0 | 36.8 |
| **PaMMoV** | **63.8** | **100** | 37.8 | 34.8 | 40.5 | 39.3 | 42.1 | 42.4 | 39.0 |
| CMoV | 49.2 | 51.5 | **100** | 55.7 | 40.1 | 39.0 | 39.5 | 44.0 | 38.8 |
| CMoMV | 52.8 | 53.0 | 58.5 | **100** | 35.7 | 35.3 | 35.4 | 41.1 | 39.1 |
| ETBTV | 49.0 | 49.3 | 50.9 | 50.3 | **100** | 77.9 | 57.4 | 62.6 | 55.2 |
| GRV | 49.8 | 50.0 | 49.4 | 50.3 | 71.8 | **100** | 55.9 | 60.1 | 54.8 |
| OPMV | 46.7 | 46.7 | 48.1 | 45.1 | 55.1 | 57.0 | **100** | 63.9 | 51.2 |
| TBTV | 48.3 | 48.0 | 50.1 | 49.0 | 57.4 | 58.2 | 62.6 | **100** | 59.2 |
| PEMV2 | 48.5 | 50.2 | 48.4 | 47.0 | 50.2 | 50.3 | 50.5 | 50.8 | **100** |

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**Fig. 1** Phylogenetic (distance) analyses of the umbravirus cell-to-cell movement proteins (MPs) vs TBSV MP, and RdRps vs TBSV RdRp. Protein alignments were performed using MUSCLE [1] while trees were generated in Mega 7 [2] with the Maximum Likelihood algorithm using 200 bootstrap replicates. All positions with less than 50% site coverage were eliminated. There were 256 positions for MPs and 859 positions for RdRps. Trees are shown with their scale bars; for both trees the brackets connecting TBSV protein to umbravirus proteins were shortened proportionately to save space**.**

**References**

1. Edgar RC (2004) MUSCLE: a multiple sequence alignment method with reduced time and space complexity. BMC Bioinf 5:113. PMC 517706. DOI:10.1186/1471-2105-5-113

2. Kumar S, Stecher G, Tamura K (2016) MEGA7: Molecular Evolutionary Genetics Analysis Version 7.0 for bigger datasets. Mol Biol Evol 33:1870-1874. PMID: 27004904 DOI:10.1093/molbev/msw054.

3. Lim S, Lee S-H, Moon JS (2019) Complete genome sequence of a tentative new umbravirus isolated from *Patrinia scabiosaefolia*. Arch Virol 164:2375-2378. PMID: 31183555 DOI:10.1007/s00705-019-04312-y.

4. Rochon DA, Scheets K, White A, Martelli G, Rubino L (2014) ICTV Taxonomic Proposal 2013.010a,bP.A.v2.Umbravirus\_move. Move genus *Umbravirus* into family *Tombusviridae*. http://www.ictvonline.org/proposals-14/2013.010a,bP.A.v2.Umbravirus\_move.pdf.

5. Yoo RH, Lee S-W, Lim S, Zhao F, Igori D, Baek D, Hong J-S, Lee S-H, Moon JS (2017) Complete genome analysis of a novel umbravirus-polerovirus combination isolated from *Ixeridium dentatum*. Arch Virol 162:3893-3897. PMID: 28905257 DOI:10.1007/s00705-017-3512-0