

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

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| **Code assigned:** | **2020.025P** |  |
| **Short title:** Create one new species in the genus *Sobemovirus* (*Sobelivirales*: *Solemoviridae*) | | |
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**List the ICTV Study Group(s) that have seen this proposal**

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| *Solemoviridae* Study Group |

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

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**Submission dates**

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| Date first submitted to SC Chair | July 31, 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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| 2020.025P.R.Solemoviridae\_1nsp.xlsx |

**Abstract**

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| Physalis rugose mosaic virus (PhyRMV) was isolated from *Physalis peruviana* in Brazil. In addition, this new virus can be mechanically transmitted to several other solanaceous species. The virions of PhyRMV are isometric, 30 nm in diameter, containing a polycistronic positive sense single–stranded RNA genome consists of five ORFs whose translation products show the highest identity to respective sobemovirus proteins if conserved (i.e. serine protease, RNA-directed RNA polymerase, capsid protein). As well, the genome organization is characteristic of sobemoviruses indicating that PhyRMV is a new member of the genus *Sobemovirus*. Species demarcation criteria in the genus *Sobemovirus* require overall genome sequence identity less than 75%. The highest sequence identity of PhyRMV genome is 54% with Solanum nodiflorum mottle virus and 53% with velvet tobacco mottle virus that infect solanaceous plants in Australia. Also, phylogenetic analysis supports the taxonomical classification of PhyRMV as a new member of the genus *Sobemovirus*. |

**Text of proposal**

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| |  | | --- | | Sobemoviruses have a polycistronic positive sense single–stranded RNA genome that consists of 4–5 ORFs and the non-enveloped icosahedral particles with a diameter of 26-33 nm. Sobemoviruses are transmitted mechanically or by different insect vectors. The genome is covalently bound by a viral genome-linked protein (VPg) at the 5’–end, and non-polyadenylated at the 3’–terminus. The 5’ proximal ORF1 encodes a non-conserved RNA silencing suppressor protein. The subsequent small non-conserved non-AUG ORFx has been ~~predicted~~ identified in several sobemovirus genomes and is predicted to encode a non-conserved protein X with unknown function. The next long ORF2a encodes a polyprotein that is autocatalytically cleaved to different functional subunits (membrane anchor, serine protease, VPg, and C-terminal domains). Expression of viral RNA-directed RNA polymerase (RdRP) as an alternative C-terminal domain of the polyprotein is regulated by –1 programmed ribosomal frameshifting signal. The 3’-proximal ORF encodes CP that is expressed from a subgenomic sgRNA [Sõmera et al, 2015] (Fig. 1).    **Figure 1.** A genome organization of southern bean mosaic virus, belonging to a type species of the genus *Sobemovirus.* Red bullet indicates the genome linked viral protein (VPg); dashed line indicates the –1 programmed ribosomal frameshifting signal.  **Physalis rugose mosaic virus (PhyRMV)**  This virus was isolated from *Physalis peruviana* in Brazil [Fariña et al, 2019]. In addition to *P. peruviana*, the new ~~virus can be~~ was transmitted to several other solanaceous species like *Capsicum annuum*, *Nicotiana tabacum* and *Solanum lycopersicum* by mechanical inoculation. It has isometric particles, ca. 30 nm in diameter. The near-complete virus genome of 4175 nt (GenBank acc. no MK681145) was sequenced by high-throughput sequencing. Five open reading frames (ORF1, ORFx, ORF2a, ORF2b and ORF3) were identified in the genome (Fariña et al, 2019):   * ORF1 (nt 76-528; 150 aa) encodes the putative P1 protein of 16.7 kDa; it has a low degree of similarity to sequences of other members of this genus and is unrelated to any other known protein; * A non-AUG started ORFx is most likely initiated at nt position 525, resulting a putative Px protein of 11.76 kDa; * ORF2a (nt 547-2316; 589 aa) encodes a putative P2a polyprotein of 64.4 kDa, containing the typical serine protease motif H(X34)D(X63)TXXGXXGS and the conserved amino acid motif WAD, followed by an ED-rich region characteristic of sobemo-like VPg-s; * ORF2b (nt 1749-3560; 603 aa) is translated via a-1 ribosomal frameshift from ORF2a, producing a fusion protein that contains the RNA-directed RNA polymerase (RdRP) of 68.2 kDa. The RdRP contains the conserved motif G(X3)T(X3)N(X19)GDD; * ORF3 (nt 3118-4101; 327 aa) overlaps the 3’ end of ORF2b and it encodes the capsid protein (CP) of 35.6 kDa.   The new virus Physalis rugose mosaic virus shares all these features with sobemoviruses. The phylogenetic relationships within the genus are depicted in Fig. 2. The highest overall genome sequence identity of PhyRMV is 54% with Solanum nodiflorum mottle virus and 53% with velvet tobacco mottle virus that infect solanaceous plants in Australia. The genome sequence overall identity less than 75% is in agreement with the species demarcation criteria within the genus *Sobemovirus* [Truve and Fargette, 2012].Therefore, we propose creation of a new species, named *Physalis rugose mosaic virus*, in the genus Sobemovirus to classify PhyRMV.      **Figure 2.** Maximum-likelihood trees showing phylogenetic relationships between the amino acid sequences of RdRP-s and CP-s of sobemoviruses and the viruses belonging to related genera from the families *Solemoviridae* (genus *Sobemovirus* is shown in turquoise; genus *Polemovirus* is shown in green) , *Barnaviridae* (genus *Barnavirus* is shown in yellow) and *Luteoviridae* (genus *Enamovirus* is shown in orange; genus *Polerovirus* is shown in red). Placement of Physalis rugose mosaic virus is indicated in red font and the type species of each genera are indicated in bold. The sequences of solemovirus RdRP-s and CPs were manually deduced and translated from the complete genome sequences of respective GenBank accessions which are indicated; the other sequences were retrieved from the GenBank as protein sequences. The ML trees were calculated with 100 bootstrap replicates using Le Gascuel (LG) model for RdRPs and the Whelan and Goldman (WAG) model for CPs . The percentage of trees in which the associated taxa clustered together is shown next to the branches if >60. Branch lengths are proportional to genetic divergence. Scale indicates the number of amino acid substitutions per site. | |

**Supporting evidence**

See the maximum likelihood phylogenetic trees of RdRP and CP amino acid sequences presented in Fig. 2.

**References**

Fariña AE, Gorayeb ES, Camelo-García VM, Bonin J, Nagata T, Silva JMF, Bogo A, Rezende JAM, da Silva FN, Kitajima EW (2019) Molecular and biological characterization of a putative new sobemovirus infecting *Physalis peruviana*. Arch Virol 164:2805-2810. PMID: 31451963 DOI: 10.1007/s00705-019-04374-y.

Sõmera M, Sarmiento C, Truve E (2015) Overview on sobemoviruses and a proposal for the creation of the family *Sobemoviridae*. Viruses 7:3076-115. PMID: 26083319 DOI: 10.3390/v7062761.

Truve E, Fargette D (2012) Genus *Sobemovirus*. In: King AMQ, Carstens E, Adams M, Lefkowitz E (eds) Virus Taxonomy. Elsevier, Ninth Report of the International Committee on Taxonomy of Viruses. pp. 1185-1189. ISBN-13: 978-0123846846; ISBN-10: 0123846846.