

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

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| **Code assigned:** | **2021.009P** |  |
| **Short title:** Create one new species in the genus *Sobemovirus* (*Sobelivirales*: *Solemoviridae*) | | |
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**Author(s) and email address(es)**

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

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| *Solemoviridae* SG |

**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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| **Is any taxon name used here derived from that of a living person (Y/N)** | N |

**Submission dates**

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| Date first submitted to SC Chair | 21-05-2021 |
| Date of this revision (if different to above) | 14-09-2021 |

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

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| The proposed species name *Sobemovirus SMAMV* has been changed to *Sobemovirus smamv*, in agreement with the suggested guidelines |

**Part 3:** **TAXONOMIC PROPOSAL**

**Name of accompanying Excel module**

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| 2021.009P.R.Sobemovirus\_1ns |

**Abstract**

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| Snake melon asteroid mosaic virus (SMAMV) was isolated from snake melon *(Cucumis melo* var. *flexuosus)* in Sudan. This new virus can be mechanically transmitted to melon and watermelon, and is also transmitted by seed at a low rate, by the red melon beetle (*Aulacophora foveicollis*), but not by the melon aphid (*Aphis gossypii*). The virions are isometric, 30 nm in diameter, containing a polycistronic positive sense single–stranded RNA genome 4225 nt long with five tentative ORFs. The genome organization of SMAMV is characteristic of sobemoviruses and the phylogenetic analysis supports this taxonomical classification. Identity of SMAMV with other sobemoviruses, both in the full-length nucleotide sequence and in deduced amino-acid sequences of the different proteins, did not exceed 50%. SMAMV host range is different from other sobemoviruses, and its full-length sequence shares less than 50% identity with other viruses. It can thus be considered as a distinct sobemovirus species, *Sobemovirus smamv*. |

**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 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 cleaved to different functional subunits (membrane anchor, serine protease, VPg, and C-terminal domains) autocatalytically. 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).    Fig. 1. Genome organization of southern bean mosaic virus, a member of the genus *Sobemovirus*. Red bullet indicates the genome linked viral protein (VPg); dashed line indicates the –1 programmed ribosomal frameshifting signal.  **Snake melon asteroid mosaic virus (SMAMV)** was isolated from snake melon (*Cucumis melo* var. *flexuosus*) in Sudan (Lecoq et al. 2011). This new virus can be mechanically transmitted to melon and watermelon, and is also transmitted by seed at a low rate and by the red melon beetle (*Aulacophora foveicollis*) It has isometric particles, *ca*. 30 nm in diameter. The complete virus genome of 4225 nt (GenBank accession No. MT989351) was sequenced by high-throughput sequencing with validation of the 5’ and 3’ ends. Five open reading frames (ORF1, ORFx, ORF2a, ORF2b and ORF3) were identified in the genome (Desbiez et al. 2021):   * ORF1 (nt 121-636; 172 aa) encodes the putative P1 protein of 19.8 kDa; it has a low degree of similarity to sequences of other members of this genus and is unrelated to any other known protein). The conserved CxxC-(6-50)-CxxC putative zinc-finger motif of sobemovirus P1 was identified as CETC-(46)-CNHC in SMAMV. * ORFx (nt 642 -923, 94 aa) is most likely initiated at a CTG codon at position 642, resulting in a putative Px protein of 10.5 kDa; * ORF2a (nt 724-2346, 541 aa) encodes a putative P2a polyprotein of 59.3 kDa, containing the putative transmembrane domain, serine protease and viral protein genome-linked (VPg). The typical serine protease motif was identified as TAPRWSG, and the conserved amino acid motif WAD was modified to WSA in VPg sequence; * The large ORF2ab (966 aa, 108.6 kDa), as in other sobemoviruses, appears most likely expressed through a (-1) frameshift at a slippery sequence UUUAAAC followed by a stem-loop structure located seven nucleotides downstream. * ORF3 (nt 3388-4140; 251 aa) overlaps the 3’ end of ORF2b and it encodes the capsid protein (CP) of 27.8 kDa.   Snake melon asteroid mosaic virus shares all these features with sobemoviruses. The phylogenetic relationships within the genus are depicted in Fig. 2. In the complete nt sequence or in aa sequences, SMAMV did not appear particularly related to any other sobemovirus: its full-length sequence shares less than 50% identity with other virus genomes. SMAMV host range is different from other sobemoviruses**.**  Sobemovirus species are distinguished by the host range of member viruses combined with analysis of their genome sequences. The genome sequence overall identity less than 75% is in agreement with the species demarcation criteria within the genus *Sobemovirus* (Truve and Fargette 2012). Thus we propose the creation of the new species *Sobemovirus smamv* to accommodate SMAMV as the exemplar isolate.    Figure 2: maximum likelihood tree obtained for the deduced amino-acid sequences of the putative RNA-dependent RNA polymerase (encoded by ORF 2b) of sobemoviruses and SMAMV. The scale bar represents a genetic distance of 0.2. Bootstrap values (500 bootstraps) above 60% are indicated for each node | |

**Supporting evidence**

See the maximum likelihood phylogenetic trees of RdRp amino acid sequences presented in the Fig.2.

**References**

Desbiez C, Verdin E, Lecoq H (2021) Complete sequence of an isolate of snake melon asteroid mosaic virus confirms that it is a member of a distinct sobemovirus species. Arch Virol, in press. doi : 10.1007/s00705-021-05109-8. PMID: **34028605**Lecoq H, Dafalla G, Delecolle B, Wipf-Scheibel C, Desbiez C (2011) Snake melon asteroid mosaic virus, a tentative new member of the genus Sobemovirus infecting cucurbits. Plant Dis 95: 153-157. DOI: [10.1094/PDIS-06-10-0447](https://doi.org/10.1094/pdis-06-10-0447). PMID: **30743409**

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. 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, 2012; 1185–1189. ISBN-13: 978-0123846846; ISBN-10: 0123846846.