

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

|  |  |  |
| --- | --- | --- |
| **Code assigned:** | **2023.019P** |  |
| **Short title:** Rename all existing species assigned to genera in the family *Solemoviridae* (*Sobelivirales*) to comply with the binomial species format, and abolish or classify the unclassified member species | | |
|  | | |

**Author(s) and email address(es)**

|  |  |
| --- | --- |
| Sõmera M, Sarmiento C, Hebrard E, Fargette D | merike.somera@taltech.ee;  cecilia.sarmiento@taltech.ee;  eugenie.hebrard@ird.fr;  denis.fargette@ird.fr |

**Corresponding author**

|  |
| --- |
| Merike Sõmera merike.somera@taltech.ee |

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

|  |
| --- |
| *Solemoviridae* Study Group  *Tombusviridae* Study Group |

**ICTV Study Group comments and response of proposer**

|  |
| --- |
|  |

**ICTV Study Group votes on proposal**

|  |  |  |  |
| --- | --- | --- | --- |
| **Study Group** | **Number of members** | | |
| **Votes support** | **Votes against** | **No vote** |
| *Solemoviridae* SG | 4 |  | 0 |
| *Tombusviridae* SG | 3 |  | 3 |

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

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

|  |  |  |
| --- | --- | --- |
| **Taxon name** | **Person from whom the name is derived** | **Permission attached (Y/N)** |
|  |  |  |
|  |  |  |
|  |  |  |

**Submission dates**

|  |  |
| --- | --- |
| Date first submitted to SC Chair | June 22, 2023 |
| Date of this revision (if different to above) |  |

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

|  |
| --- |
| Following the EC request to reconsider the use of acronyms as species epithets, the Study Group confirmed the decision of using the acronyms as species epithets. |

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

**Name of accompanying Excel module**

|  |
| --- |
| 2023.019P.Uc.v1.Solemoviridae\_rename.xls |

**Abstract**

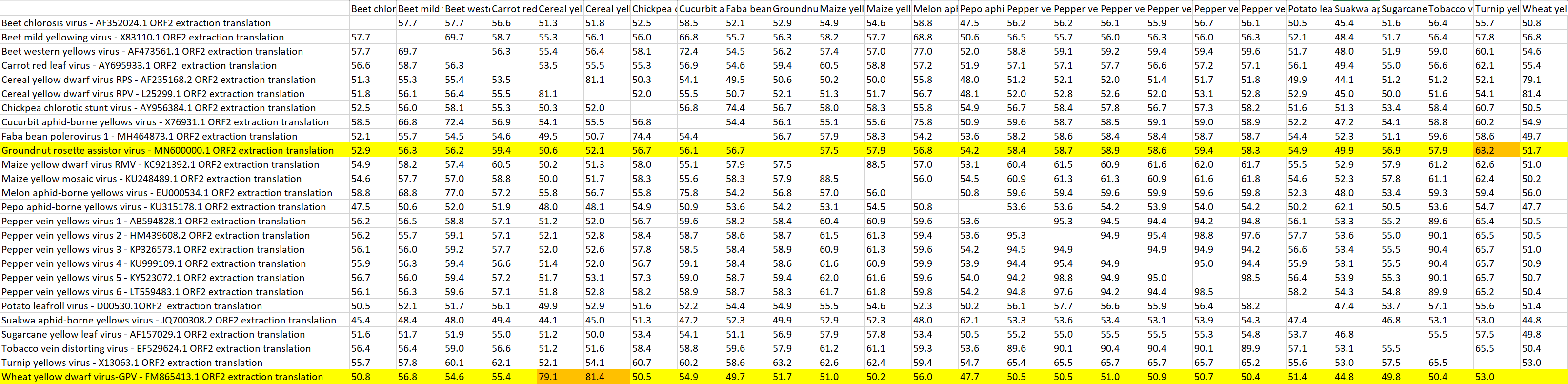
|  |
| --- |
| Following the ICTV request to change all established species names to a binomial format, this proposal considers new names for all approved species of the family *Solemoviridae*.  In addition, we propose a taxonomic classification of unclassified members of the family *Solemoviridae* which were transferred to the family *Solemoviridae* during abolishment of the family *Luteoviridae*. |

**Text of proposal**

|  |  |
| --- | --- |
| |  | | --- | | In March 2021, the ICTV ratified TaxoProp 2018.001G.R.binomial\_species, which requires all species names to follow a new codified rule:  "A species name shall consist of only two distinct word components separated by a space. The first word component shall begin with a capital letter and be identical in spelling to the name of the genus to which the species belongs. The second word component shall not contain any suffixes specific for taxa of higher ranks. The entire species name (both word components) shall be italicized."  This rule requires most established species names to be changed. Here, we propose to change the names of the species included in the family *Solemoviridae* following this rule by adopting binomial species names. The derivation/etymology of these new names are outlined in the corresponding Excel module.  In addition, we propose a genus level taxonomic classification of unclassified members of the family *Solemoviridae* (*Barley yellow dwarf virus GPV, Barley yellow dwarf virus SGV, Chickpea stunt disease associated virus, Groundnut rosette assistor virus, Indonesian soybean dwarf virus, Sweet potato leaf speckling virus, Tobacco necrotic dwarf virus*) which were transferred to the family *Solemoviridae* during abolishment of the family *Luteoviridae* and are not assigned to a genus yet*.*  Criteria used to demarcate species of the genera *Polerovirus* and *Enamovirus* include:   * Differences in breadth and specificity of host range; * Failure of cross-protection in either one-way or two-way relationships; * Differences in serological specificity with discriminatory polyclonal or monoclonal antibodies; * Differences in amino acid sequence identity of any gene product of greater than 10%.   We propose:  (1) to abolish the unclassified species *Indonesian soybean dwarf virus* (ISDV) which is known via the historical records only, and is missing any sequencing data in public databases. No material is stored at international collections (NARO, ATCC, DSMZ). ISDV was collected in Indonesia and Thailand in 1970s. It was described as a phloem-limited virus with small isometric particles in diameter of 26 nm, persistently transmitted by a widely-spread species of the aphid *Aphis glycines*, to soybean. ISDV did not show any relationship to soybean dwarf virus (*Luteovirus glycinis*) in serologic and cross protection tests (Iwaki et al 1980; Honda et al. 1986). According to this data, it is not possible to verify whether this virus could be classified as the member of *Polerovirus* or *Enamovirus* in the family *Solemoviridae*.  (2) to merge the unclassified species *Chickpea stunt disease associated virus* with *Polerovirus CLDV* (reported by Naidu et al. 1997)*.* A partial sequence of CP gene is available (Y11530 = NC\_043419) and it shows 98% of identities to the respective sequence of cotton leafroll dwarf virus (KP176644) with 100% of query coverage in BLASTN analysis performed at the NCBI website. According to the species demarcation criteria set for the genus *Polerovirus*, the differences in amino acid sequence identity of any gene product should be greater than 10%, and thus, even more for the nucleotide sequence. Therefore, *Chickpea stunt disease associated virus* should be considered as an isolate of cotton leafroll dwarf virus (*Polerovirus CLDV*), the recognized member of the family *Polerovirus*.  (3) to move the unclassified species *Tobacco necrotic dwarf virus* (TNDV) to genus *Polerovirus* and name it *Polerovirus TNDV*, despite it is missing any sequencing data in public databases. TNDV was found in Japan in 1970-s, and it is closely related to potato leafroll virus (*Polerovirus PLRV*) as judged from its host range, distribution in plant tissues, transmissibility, physical properties of virus particles and serology. Like PLRV and tobacco vein distorting virus (*Polerovirus TVDV*), TNDV is transmitted by the aphid *Myzus persicae* in the persistent manner. However, the virus may be distinguished from potato leafroll, and tobacco vein-distorting viruses by their reactions of tobacco, *Physalis floridana*, and *Datura stramonium* plants (Kubo and Takanami 1979, Kubo 1981, Oshima et al 1989). TNDV antiserum is available at the ATCC collection.  (4) to move the unclassified species *Sweet potato leaf speckling virus* (SPLSV) to genus *Polerovirus* and name it *Polerovirus SPLSV.* A partial sequence of CP gene is available (DQ655700) and it shows the highest percentage of identities (76.7%) to the respective sequence of potato leafroll virus isolate PLRV165 (MG356502) with 99% of query coverage in BLASTN analysis performed at the NCBI website. SPLSV is transmitted in a persistent manner by the aphid *Macrosiphum euphorbiae* but not by *Myzus persicae* or *Aphis gossypii* (Fuentes et al 1996)*. M. persicae* is the primary vector of PLRV.  (5) to move the unclassified species *Groundnut rosette assistor virus* to genus *Polerovirus* and name it *Polerovirus GRAV.* Multiple alignment of poleroviral complete genome sequences reveals that GRaV (MN600000; Jones et al 2020) shares the highest identities with that of turnip yellows virus (TuYV; 52.0%). Multiple sequence alignments of translation products of the most conserved gene encoding a viral RdRP indicates 63.2% of identity to TuYV RdRP (Table 1). The genome organization of GRaV is characteristic of poleroviruses. Thus, the recognition of GRaV isolates as the representatives of *Polerovirus GRAV* is consistent with the species demarcation criteria in genus *Polerovirus*. A complex of GRaV, groundnut rosette umbravirus (GRV), and satellite RNA, is a cause of groundnut rosette disease in Sub-Saharan Africa, and is transmitted by *A. craccivora* (Taliansky et al 2000).  (6) to move the unclassified species *Barley yellow dwarf virus GPV* to genus *Polerovirus* and name it *Polerovirus WYDV-GPV*, using “wheat yellow dwarf virus GPV” as the common name*.* WYDV-GPV has been named as “barley yellow dwarf virus GPV”, “wheat yellow dwarf virus GPV” but also as “cereal yellow dwarf virus GPV” (Miller 1999, Du et al 2007, Zhang et al 2009, Miller and Lozier 2022)*.* Currently, all cereal-infecting barley yellow dwarf viruses belong to the genus *Luteovirus* family *Tombusviridae* whereas cereal-infecting poleroviruses belong to the family *Solemoviridae* have been renamed to “cereal”, “maize” or “wheat” yellow dwarf viruses. WYDV-GPV is spread in China, and it is persistently transmitted by the aphid *Schizaphis graminum*. The complete genome of wheat yellow dwarf virus GPV has been sequenced (FM865413; Zhang et al 2009). Multiple alignment of poleroviral genome sequences reveals it shares the highest identities with those of CYDV-RPS (74.8%) and CYDV-RPV (72.0%). Multiple sequence alignments of poleroviral RNA-directed RNA polymerases encoded by the most conserved gene indicates that WYDV-GPV shares 79.1% of identity to CYDV-RPS RdRP, and 81.4% of identity to CYDV-RPV RdRP (Table 1). The genome organization of WYDV-GPV is characteristic of poleroviruses. Thus, the recognition of WYDV-GPV isolates as the representatives of *Polerovirus WYDV-GPV* is consistent with the species demarcation criteria in genus *Polerovirus*.  (7) to move the unclassified species *Barley yellow dwarf virus SGV t*o genus *Luteovirus* subfamily *Regressovirinae* family *Tombusviridae* and name it *Luteovirus sgvhordei*, following the rules applied for the species names in the family *Tombusviridae*. The virus is primarily transmitted by the aphid *S. graminum*, and it has been reported to occur in the US (Lei et al 1995, Garrett et al 2004). A 1261 bp partial sequence of the New York isolate of BYDV-SGV containing the partial sequences of RdRP, CP and MP genes (AY541039; Malmstrom and Shu 2004) shows the highest percentage of identities (79.7%) to the sequence of barley yellow dwarf virus-PAV isolate 05WN1 (EU332315) with 94% of query coverage in BLASTN analysis performed at the NCBI website. The criteria used to demarcate species of the genera *Polerovirus* and *Enamovirus* were transferred from the criteria for the former family *Luteoviridae*, and those have been applied also for genus *Luteovirus*. As the criteria used to demarcate species of the genus *Luteovirus* have not been changed, the recognition of BYDV-SGV isolates as the representatives of *Luteovirus sgvhordei* is consistent with the species demarcation criteria in genus *Luteovirus.* | |

**Supporting evidence**

Table 1. Identity percentages revealed by multiple sequence alignment of poleroviral ORF2 translation products (RdRPs). The data related to groundnut rosette assistor virus (GRaV) and wheat yellow dwarf virus GPV (WYDV-GPV) RdRPs has been highlighted in yellow. The highest percentages are shown in orange background color.



**References**

Iwaki et al (1980) A Persistent Aphidborne Virus of Soybean, Indonesian Soybean Dwarf Virus. Plant Dis 64:1027-1030. DOI: 10.1094/PD-64-1027

Honda et al (1986) The occurrence of Indonesian soybean dwarf virus on soybean in Thailand. Technical bulletin of the Tropical Agriculture Research Center 21:126-131. <https://www.jircas.go.jp/en/publication/techtarc/21/126>

Naidu et al (1997) Diversity among the coat proteins of luteoviruses associated with chickpea stunt disease in India. Ann Appl Biol 130:37-47. DOI: 10.1111/j.1744-7348.1997.tb05781.x

Kubo S, Takanami Y (1979) Infection of Tobacco Mesophyll Protoplasts with Tobacco Necrotic Dwarf Virus, a Phloem-limited Virus. J Gen Virol 42:387-398. DOI: 10.1099/0022-1317-42-2-387

Kubo S (1981) CMI/AAB Descriptions of Plant Viruses No.234

Oshima et al (1989) Characterization of Monoclonal Antibodies against Tobacco Necrotic Dwarf Virus. Ann Phytopath Soc Japan 55:420-426. <https://www.jstage.jst.go.jp/article/jjphytopath1918/55/4/55_4_420/_pdf>

Fuentes et al (1996) A novel luteovirus from sweet potato, sweet potato leaf speckling virus. Ann Appl Biol 128:491-504. DOI: 10.1111/j.1744-7348.1996.tb07109.x

Jones S, Cowan G, MacFarlane S, Mukoye B, Mangeni BC, Were H, Torrance L (2020). RNA sequence analysis of diseased groundnut (*Arachis hypogaea*) reveals the full genome of groundnut rosette assistor virus (GRAV). Virus Res 277:197837. DOI: 10.1016/j.virusres.2019.197837. PMID: 31836513.

Taliansky ME, Robinson DJ, Murant AF (2000) Groundnut rosette disease virus complex: biology and molecular biology. Adv Virus Res 55:357-400. DOI: 10.1016/s0065-3527(00)55008-8. PMID: 11050947

Du et al (2007) Evaluation of aphid transmission abilities and vector transmission phenotypes of barley yellow dwarf viruses in China. J Plant Pathol 89:251-259. <https://www.jstor.org/stable/41998385>

Zhang W, Cheng Z, Xu L, Wu M, Waterhouse P, Zhou G, Li S (2009) The complete nucleotide sequence of the barley yellow dwarf GPV isolate from China shows that it is a new member of the genus *Polerovirus*. Arch. Virol 154:1125-1128. DOI: 10.1007/s00705-009-0415-8

Miller WA (1999) *Luteovirus* (*Luteoviridae*). Encyclopedia of Virology, pp.901–908. DOI: 10.1006/rwvi.1999.0170. PMCID: PMC7150254.

Miller WA, Lozier Z (2022) Yellow Dwarf Viruses of Cereals: Taxonomy and Molecular Mechanisms. Ann Rev Phytopathol 60:121-141. DOI: 10.1146/annurev-phyto-121421-125135

Lei et al (1995) SGV serotype isolates of barley yellow dwarf virus differing in vectors and molecular relationships. Phytopathol 85:820-826. DOI:10.1094/PHYTO-85-820

Garrett KA, Dendy SP, Power AG, Blaisdell GK, Alexander HM, McCarron JK (2004) Barley Yellow Dwarf Disease in Natural Populations of Dominant Tallgrass Prairie Species in Kansas. Plant Dis 88:574. DOI: 10.1094/PDIS.2004.88.5.574B. PMID: 30812673.

Malmstrom CM, Shu R (2004) Multiplexed RT-PCR for streamlined detection and separation of barley and cereal yellow dwarf viruses. J Virol Methods 120:69-78. DOI: 10.1016/j.jviromet.2004.04.005.