

The International Committee on Taxonomy of Viruses

Taxonomy Proposal Form, 2025

**Part 1a: Details of taxonomy proposals**

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| **Title:** | Create twenty-two [22] new species in the genus *Polerovirus (Sobelivirales:Solemoviridae)* |
| **Code assigned:** | 2025.022P.Solemoviridae\_Polerovirus\_22nsp | |

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**Part 1b: Taxonomy Proposal Submission**

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| **ICTV Subcommittee:** | | | |
| Animal DNA Viruses and Retroviruses |  | Bacterial viruses |  |
| Animal minus-strand and dsRNA viruses |  | Fungal and protist viruses |  |
| Animal positive-strand RNA viruses |  | Plant viruses | **X** |
| Archaeal viruses |  | General |  |

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| **List the ICTV Study Group(s) that have seen or have been involved in creating this proposal:** |
| Solemoviridae SG |

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| **Submission date:** | 16/06/2025 |

**Part 1c: Feedback from ICTV Executive Committee (EC) meeting**

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| **Executive Committee Meeting Decision code:** | **X** |
| A – Accept |  |
| Ac – Accept subject to revision by relevant subcommittee chair. No further vote required |  |
| U – Accept without revision but with re-evaluation and email vote by the EC |  |
| Uc – Accept subject to revision and re-evaluation and email vote by the EC |  |
| Ud – Deferred to the next EC meeting, with an invitation to revise based on EC comments |  |
| J - Reject |  |
| W - Withdrawn |  |

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| **Comments from the Executive Committee:** |
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**Part 1d: Revised Taxonomy Proposal Submission**

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| **Response of proposer:** |
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| **Revision date:** |  |

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

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| **Taxonomic changes proposed:** | | | |
| Establish new taxon | **X** | Split taxon |  |
| Abolish taxon |  | Merge taxon |  |
| Move taxon |  | Promote taxon |  |
| Rename taxon |  | Demote taxon |  |
| Move and rename |  |

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| **Etymology (origin) of proposed taxonomic names:** | |
| **Taxon name** | **Etymology of the term** |
| *Polerovirus ACTPV* | Epithet from the virus name acronym |
| *Polerovirus AGV* | Epithet from the virus name acronym |
| *Polerovirus ARMOV* | Epithet from the virus name acronym |
| *Polerovirus BYCV* | Epithet from the virus name acronym |
| *Polerovirus CALRV* | Epithet from the virus name acronym |
| *Polerovirus CAPV1* | Epithet from the virus name acronym |
| *Polerovirus CAPV2* | Epithet from the virus name acronym |
| *Polerovirus CHVD* | Epithet from the virus name acronym |
| *Polerovirus CYMAV* | Epithet from the virus name acronym |
| *Polerovirus FEQPV* | Epithet from the virus name acronym |
| *Polerovirus GLPV* | Epithet from the virus name acronym |
| *Polerovirus IXYMAV* | Epithet from the virus name acronym |
| *Polerovirus MUSPV* | Epithet from the virus name acronym |
| *Polerovirus NBPV* | Epithet from the virus name acronym |
| *Polerovirus PAPV* | Epithet from the virus name acronym |
| *Polerovirus PEVYV10* | Epithet from the virus name acronym |
| *Polerovirus RDPV* | Epithet from the virus name acronym |
| *Polerovirus SLBPV* | Epithet from the virus name acronym |
| *Polerovirus SPRPV* | Epithet from the virus name acronym |
| *Polerovirus TONYV* | Epithet from the virus name acronym |
| *Polerovirus VPPV* | Epithet from the virus name acronym |
| *Polerovirus WCRLV* | Epithet from the virus name acronym |

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| **Abstract of Taxonomy Proposal:** |
| *Taxonomic rank(s) affected*: Species  *Description of current taxonomy*: Currently, the genus *Polerovirus* consists of 77 species.  *Proposed* *taxonomic change(s):* Create 22 new species in the genus *Polerovirus*  *Justification*: The recent high-throughput sequencing projects have revealed 23 putative novel poleroviruses that have not yet been assigned to species. The assembled genomes share the highest sequence identites with poleroviruses. Phylogenetic analysis of their genome nucleotide sequences and the amino acid sequences of their RdRPs confirmed clustering within the genus *Polerovirus*. The putative novel candidate viruses are: Actinidiapolerovirus, Ageratumvirus 3, arachis mottle-associated virus, bitter apple aphid-borne yellows virus, bitter gourd yellowing crumple virus, cacao leafroll virus, carrot polerovirus 1, carrot polerovirus 2, Chrysanthemum virus D, Cynanchumyellow mottle-associated virus, Ficus esquiroliana polerovirus, gladiolus polerovirus, Ixeridium yellow mottle virus, Musa polerovirus, noble dendrobium polerovirus, parsley polerovirus, pepper vein yellows virus 10, rice dwarf polerovirus, spruce polerovirus, sweet leaf bush polerovirus, tomato necrotic yellowing virus, Viola philippica polerovirus, We propose that all could be recognized as members of species in the genus *Polerovirus*, except bitter apple aphid-borne yellows virus. |

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| **Text of Taxonomy proposal:** |
| *Taxonomic rank(s) affected*: Species.  *Description of current taxonomy*: *Sobelivirales:Solemoviridae:Polerovirus*  *Proposed* *taxonomic change(s)*: Create 22 new species in the genus *Polerovirus*.  *Demarcation criteria:*  The following novel species demarcation criteria for the genus *Polerovirus* were set in 2023 (accepted in 2024 by the ICTV):  • 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 RdRPs > 10%;  • Differences in nucleotide sequence identity of genomes around or > 25%.  *Justification*:  Poleroviruses are a genetically diverse group of viruses transmitted by aphids (or more rarely, by whiteflies) in a persistent circulative and non-propagative manner, being highly dependent on interactions between the virus and the vector. Poleroviruses are phloem limited. Their virions are isometric, 25 to 30 nm in size. The genome is a single-stranded (ss) positive-sense RNA molecule of approximately 5.6 to 6.2 kb with a small genome-linked protein (VPg) covalently attached to the 5′ end of the genomic RNA.  Polerovirus genomes have seven common major open reading frames (ORFs) designated as ORF0, 1, 2, 3, and 5. ORF0 encodes a viral RNA silencing suppressor protein (P0), ORF1 encodes the P1 protein that has a serine protease activity, ORF2 encodes a viral RNA-directed RNA polymerase (RdRP; P2) which is involved in replication, ORF3 encodes the major coat protein (CP; P3), ORF3a encodes the P3a needed for systemic infection, ORF4 encodes a cell-to-cell movement protein (P4), and ORF5 encodes an aphid-transmission factor (P5). Additional minor ORFs are present only in a few poleroviral genomes. Translation of P3a is directed from a non-AUG start codon. The RdRP is synthesized by translational fusion with P1 (P1-P2) via a -1 ribosomal frameshift in ORF1. The P5 is expressed as a readthrough protein with P3 (P3-P5).  The current list of poleroviruses includes seventy-seven species. Our research in the literature and NCBI GenBank database has revealed additional tentative species that could belong to the genus *Polerovirus* but are not yet recognized by ICTV. Complete or coding-complete genomes have been sequenced for the new viruses considered in this proposal, and these genomes show a genome organization characteristic of poleroviruses.  To support the proposal, we have calculated the sequence identity between the viral genome nucleotide sequences, and between the amino acid sequences of viral RdRPs of putative novel and recognized members of the genus *Polerovirus* (Tables 1 and2) and performed phylogenetic analysis based on their RdRPs (Fig.1).  **Ageratum virus 3 (AgV3**) was identified from symptomless *Ageratum conyzoides* plant collected in Fuding, China in 2019 by the transcriptome data analysis. The genome sequences were confirmed by sequencing of PCR and RACE products. The genome of 5,652 nucleotides (**PQ675349**) shared the highest nucleotide sequence identity (65.7%) with that of cucurbit aphid-borne yellows virus (CABYV). Maximum-likelihood phylogenetic trees based on the P1-P2 and CP clustered AgV3 with members of the genus *Polerovirus* [1]. **We propose the recognition of AgV3 as member of a new species in the genus *Polerovirus,* “*Polerovirus AGV”.***  **Arachis mottle-associated virus (ArMoV)** was identified in the symptomatic Pinto peanut (*Arachis pintoi*) plants collected from the Active Germplasm Bank (BGA) at the Embrapa Acre Institute in Rio Branco, Brazil by high-throughput sequencing (HTS). The genome assembly was confirmed by sequencing of PCR and RACE products. The genome sequence (**LC818997**) consisted of 5775 nucleotides and shared the highest nucleotide sequence identity (49.2%)  to chickpea chlorotic stunt virus (CpCSV). Maximum-likelihood phylogenetic trees based on the P1-P2 and CP clustered ArMoV with members of the genus *Polerovirus* [2] . **We propose the recognition of ActPV as member of a new species in the genus *Polerovirus*, “*Polerovirus ArMoV”.***  **Bitter gourd yellowing crumple virus (BYCV**) was identified from bitter gourd (*Momordica charantia*) plants showing yellowing and crumple symptoms in the field of Haikou, Hainan province of China in 2021 by HTS and confirmed by sequencing of PCR products. The viral genome (**OQ448155**) of 5665 nucleotides shared the highest nucleotide sequence identity (79.8%) with that of CABYV. Phylogenetic analysis showed that this virus was closely related to CABYV [3]. In our analysis, the genome sequence of BYCV shared 78% of identity with that of CABYV, and BYCV RdRP shared 75% of identity with that of CABYV (Tables 1 and2). According to the species demarcation criteria, the genomes of BYCV and CABYV shared slightly more identities than recommended but their RdRPs were under 10% aa divergence cut, being appropriate to be considered as a new species. Therefore, **we propose the recognition of BYCV as member of a new species in the genus *Polerovirus,* “*Polerovirus BYCV”.***  **Cacao leafroll virus (CaLRV)** was characterized from symptomatic cacao *Theobroma cacao* plants received by the USDA-ARS54 SHRS, Miami, FL quarantine greenhouse. The complete genome sequence was determined by high-throughput sequencing (HTS) and the genome ends were confirmed by RACE. The CaLRV genome sequences ranged from 5,976 to 5,997 nucleotides (nt) in length. The genome of exemplar isolate (**OR423049**) shared the highest nt sequence identity of 62% with that of potato leafroll virus (PLRV) [4]. The nearly complete genome sequence of the same species (sharing 99% of identity), referred to as **cacao polerovirus** (OR605721), was assembled from publicly available transcriptome datasets of *T. cacao* originating from the germplasm held at International Cocoa Quarantine Centre, Reading, UK (ICQC-R), imported from the International Cacao Collection (IC3) at Centro Agronómico Tropical de Investigación y Enseñanza (CATIE), Costa Rica, between 1988 and 2021 [5]. **We propose the recognition of CaLRV as member of a new species in the genus *Polerovirus*,“*Polerovirus CALRV”.***  **Carrot polerovirus 1 (CAPV1)** and **carrot polerovirus 2 (CAPV2)** were identified from several wild carrot (*Daucus carota* ssp*. carota*) populations collected in Nouvelle Aquitaine, France in 2019 by HTS. In Blast searches, CaPV1 (**OP886450**) was most closely related to Trachyspermum ammi polerovirus (TAPV) with 89% aa identity in the RdRP, being under the 10% aa divergence species cut-off. CaPV2 (**OP886451**) was most closely related to Torilis crimson leaf virus (TorCLV) and carrot red lead virus (CtRLV) sharing with them respectively 72% and 71% aa identity in the RdRP amino acid sequences [6]. In our analysis, the genome sequence of CAPV1 shared the highest nucleotide sequence identity with that of parsley polerovirus (PaPV, another polerovirus candidate) (79%), and TAPV (77%); and CAPV1 RdRP shared 94% and 90% of aa sequence identity with their RdRPs, respectively. Although CAPV1 shares a high rate of sequence identity with PaPV both at nucleotide and aa sequence level, it could be considered as a distinct species as PaPV possibly evolved through a recombination event between CAPV1 and TCLV (see below); also, these viruses have identified from different continents. CAPV2 genome sequence shared the highest nucleotide sequence identity with the genome sequences of TCLV (64%); and CAPV2 RdRP shared 80% of aa sequence identity with the RdRPs of CAPV1, CtRLV, TCLV and wild carrot red leaf virus (WCRLV), and 79% of aa sequence identity with the RdRPs of PaPV and TAPV (Table 1-2). **We propose the recognition of CAPV1 and CAPV2 as members of two new species in the genus *Polerovirus,* “*Polerovirus CAPV1”* and *“Polerovirus CAPV2”.***  **Chrysanthemum virus D (ChVD)** was identified from symptomatic *Chrysanthemum morifolium* in Seongju County, South Korea in 2021 by HTS. The genome (**OR453957**) of 5,963 nucleotides shared the highest nucleotide sequence identity (66.8%; with a query coverage of 48%), with artemisia virus B (ArtVB). Maximum-likelihood phylogenetic trees based on the P1-P2 and CP clustered ChVD with members of the genus *Polerovirus* [7]. **We propose the recognition of ChVD as member of a new species in the genus *Polerovirus,*“*Polerovirus CHVD”.***  **Cynanchum yellow mottle-associated virus (CYMaV)** was identified from *Cynanchum rostellatum* leaves showing yellow mottle symptoms, found in Tokyo, Japan in 2017 by HTS. The genome assembly was confirmed by sequencing of PCR and RACE products. The complete sequence of the virus genome (**LC699794**) was 5,878 nucleotides in length. Maximum-likelihood phylogenetic trees based on the P1-P2 and CP clustered CYMaV with members of the genus *Polerovirus* [8]. The second finding of CYMaV (OR290115) originates from China, done in 2021 [9]. The Japanese and Chinese isolates share 93.3% of nucleotide sequence identity. **We propose the recognition of CYMaV as member of a new species in the genus *Polerovirus*, *“Polerovirus CYMAV”.***  **Ixeridium yellow mottle virus 1 (IxYMaV-1)**, a putative novel polerovirus, was identified in a complex with a novel umbravirus IxYMAV-2 from an *Ixeridium dentatum* plant with yellow mottle symptoms collected from Bonghwa, South Korea in 2013. The genome sequence was assembled from the HTS data and confirmed by sequencing of PCR and RACE products. The IxYMaV-1 genome sequence (**KT8689495**) of 6017 nt shared 56.4% sequence identity with CABYV. Maximum-likelihood phylogenetic trees based on the P1-P2 and CP clustered IxYMaV-1 in a clade with members of the genus *Polerovirus* [10]. **We propose the recognition of IxYMaV-1 as member of a new species in the genus *Polerovirus*, “*Polerovirus IXYMAV”.***  **Parsley polerovirus (PaPV)**, was identified from parsley (*Petroselinum crispum*) samples collected in Ventura County, California, U.S. in 2020. The sequenced genome indicated a natural recombination between carrot polerovirus 1 (CAPV1), sharing 92% amino acid (aa) identity with the RdRP in the 5' gene block, and torilis crimson leaf virus (TorCLV), sharing >98% aa identity with the capsid protein in the 3 gene block. To confirm that these virus sequences were not artifactual assemblies, nearly full-length sequences were RT-PCR amplified, and Sanger sequenced from two separate parsley samples. RACE was performed to obtain two full length (5,741 nt) isolates of this putative new polerovirus: PaPV\_1 (**PP683457**), and PaPV\_2 (PP683458) [11]). In our analysis, the genome sequence of PaPV shared 80% of identity with that of TorCLV, and 79% of identity with that of CAPV1, whereas the PaPV RdRP aa sequence shared 94% of identity with that of CAPV1, and 90% of identity with that of Trachyspermum ammi polerovirus (TAPV) (Tables 1 and2). According to the species demarcation criteria, the genomes of PaPV, TorCLV, and CAPV1 shared slightly more identities than recommended but their RdRPs were different enough to be considered as the new species. Also, the recombinant origin of PaPV supports its recognition as a distinct species. Therefore, **we propose the recognition of PaPV as member of a new species in the genus *Polerovirus*, “*Polerovirus PAPV”.***  **Pepper vein yellows virus 10 (PeVYV-10)** is represented by three isolates: Ita-7, 5357, and  J4702 were discovered from garlic, chickpea, and tomato samples collected in three different locations in Queenland, Australia. Their genome sequences shared 88-96% nt sequence identity with each other. These three isolates were divergent from the other described pepper vein yellows viruses (PeVYV) 1-9, sharing only 69-74% nt sequence identity with those. Their P2 amino acid sequences shared 84-87% aa sequence identity with other PeVYVs [12]). The exemplar isolate 5357 (**OR225495**) genome sequence indicates the highest identity (79.1%) with PeVYV2. **We propose the recognition of PeVYV-10 as member of a new species in the genus *Polerovirus*, “*Polerovirus PEVYV10”.***  **Rice dwarf polerovirus (RDPV)** isolate 1 was identified from symptomatic rice plants showing dwarfing and fewer tillering symptoms collected from paddy fields in Hainan Province, China in 2023. It was shown to be transmitted both by bird cherry oat aphids (*Rhopalosipum padi*) and rice whiteflies (*Bemisia formosana*). The RDPV genome (**PP925870**) was determined by HTS and RACE procedures. It consisted of 5832 nt and shared the highest identity (75%) with panicum distortion mosaic virus (PDMV). Phylogenetic analyses based on the full-length genome sequence and P2 amino acid sequence revealed that RDPV with members of the *Polerovirus* genus [13]. The second example of RPDV (isolate GX-53-7) was sequenced from wild rice (*Oryza rufipogon*) in China in 2019 and deposited in NCBI GenBank nucleotide database under the name of **rice polerovirus 2** (OM835626). In BLASTN analysis, it shared 93% of nucleotide sequence identity with RPDV. In addition, the third isolate of RPDV collected from *O. rufipogon* in Rwere Guangxi Zhuang Autonomous Region, China in 2023, sharing 92% of nucleotide sequence identity, was characterized under the name of **rice tiller less virus** (the sequence was published in Yan et al 2025; PRJNA956225). **We propose the recognition of RDPV as member of a new species in the genus *Polerovirus* , “*Polerovirus RDPV”.***  **Tomato necrotic yellowing virus (ToNYV)** was recently discovered by metagenomic sequencing of tomato virome in Saint-Philippe, Reunion Island [12]4. In our analysis, ToNYV genome nt sequence (**PV289033**) of 5955 nt indicated the highest identity (79%) with that of African eggplant yellowing virus (AeYV) while their RdRP aa sequences shared the identity of 81%. According to the species demarcation criteria, the genomes of ToNYV and AeYV shared slightly more identities than recommended but their RdRPs were under 10% aa divergence cut, being appropriate to be considered as the new species. Therefore, **we propose the recognition of ToNYV as member of a new species in the genus *Polerovirus*,“*Polerovirus TONYV”.***  **Viola philippica polerovirus (VPPV)** was identified from *Viola philippica* plant showing symptoms of yellowing, mottling, and vein chlorosis in 2021, sampled in the Summer Palace in Beijing, China. The genome (**PP770488**) consisted of 5535 nt. The highest identity (56.1%) to the genome sequence was observed with chickpea chlorotic stunt virus (CpCSV). Phylogenetic trees based on the P1-P2 and CP clustered VPPV in with members of the genus *Polerovirus* [15]. **We propose the recognition of VPPV as member of a new species in the genus *Polerovirus*, “*Polerovirus VPPV”.***  **Wild carrot red leaf virus (WCRLV)** was identified from wild carrot (*Daucus carota* spp*. carota*) sampled in Thessaloniki, Greece in 2003 by HTS. Recently, it was found to be widely spread in wild carrot populations in France [6]. The complete genome of IL2 isolate (**LT615231**) consisted of 5688 nt and it had a genome organization characteristic of poleroviruses [16]. In our analysis, WCRLV nucleotide sequence shared the highest identity (82%) with that of carrot red leaf virus (CtRLV), while their RdRPs (P2) shared 96% of aa sequence identity. With that the identity with CtRLV was exceeding divergence cut both at genome sequence and protein sequence level. However, WCtRLV was identified as recombinant with CtRLV as major parent and carrot polerovirus 1 (CaPV1) as minor parent, the recombined region concerning part of the CP readthrough (P5). The recombinant origin of WCRLV supports its recognition as a distinct species. Co-infections likely explain that several tentative recombination events could be detected among members of the *Polerovirus* genus. Recognition of species risen from recombination in genus *Polerovirus* has been already accepted for the group of pepper vein yellow viruses, and could be also reliable for carrot-infecting poleroviruses. Therefore, **we propose the recognition of WCRLV as member of a new species in the genus Polerovirus, *“Polerovirus WCRLV”.***  In addition to the mentioned novel polerovirus candidates, seven putative novel poleroviruses were revealed by the analysis of plant transcriptome data deposited in public databases. These viruses showed the genomic organization characteristic of poleroviruses and clustered with the members of *Polerovirus* in phylogenetic analysis [17]).  **Actinidia polerovirus (ActPV)** genome sequence (**BK068684**) was assembled from the transcriptome data (DDBJ/EMBL/GenBank entry SRR8446737; PRJNA514180) of the kiwifruit (*Actinidia*) germplasm resources repository of the Zhengzhou Fruit Research Institute, Henan province, China. The assembled near-complete genomic sequence spanned 5980 nt. **We propose the recognition of ActPV as member of a new species in the genus *Polerovirus*, “*Polerovirus ACTPV”.***  **Ficus esquiroliana polerovirus (FeqPV)** genome sequence (**BK068690**) was assembled from the transcriptome data (DDBJ/EMBL/GenBank entry DDBJ/EMBL/GenBank entry SRR7892351; PRJNA492455) of *Ficus triloba* (syn. *F. esquiroliana*) grown in South China Botanical Garden, Guangzhou, China. The assembled near-complete genomic sequence spanned 5891 nt. **We propose the recognition of FeqPV as member of a new species in the genus *Polerovirus*, “*Polerovirus FEQPV”.***  **Gladiolus polerovirus (GlPV)** genome sequence (**BK068697**) was assembled from the transcriptome data (DDBJ/EMBL/GenBank entry DDBJ/EMBL/GenBank entry SRR7849283; PRJNA491310) of *Gladiolus x hybridus* cv ‘Rose Supreme’ in the Science Research Garden at China Agricultural University, Beijing, China. The assembled near-complete genomic sequence spanned 5863 nt. **We propose the recognition of GlPV as member of a new species in the genus *Polerovirus*, “*Polerovirus GLPV”.***  **Musa polerovirus (MusPV)** genome sequence (**BK068683**) was assembled from the transcriptome data (DDBJ/EMBL/GenBank entry DDBJ/EMBL/GenBank entry SRR16881676; PRJNA777477) of banana germplasm maintained at Gembloux, University of Liege, Belgium. The assembled near-complete genomic sequence spanned 5439 nt. **We propose the recognition of MusPV as member of a new species in the genus *Polerovirus*, “*Polerovirus MUSPV”.***  **Noble dendrobium polerovirus (NbPV)** genome sequence (**BK068693**) was assembled from the transcriptome data (DDBJ/EMBL/GenBank entry DDBJ/EMBL/GenBank entry SRR15036785; PRJNA725550) of wild *Dendrobium nobile* plant collected from evergreen broad-leaf forest in Yunnan province, China. The assembled near-complete genomic sequence spanned 5545 nt. **We propose the recognition of NbPV as member of a new species in the genus *Polerovirus*, “*Polerovirus NBPV”.***  **Spruce polerovirus (SprPV)** genome sequence (**BK068705**) was assembled from the transcriptome data (DDBJ/EMBL/GenBank entry DDBJ/EMBL/GenBank entry SRR11565954; PRJNA622085) from spurce (*Picea abies*) roots collected from Maridalen valley, Oslo, Norway. The assembled near-complete genomic sequence spanned 5557 nt. **We propose the recognition of SpPV as member of a new species in the genus *Polerovirus*, “*Polerovirus SPRPV”.***  **Sweet leaf bush polerovirus (SlbPV)** genome sequence (**BK068689**) was assembled from the transcriptome data (DDBJ/EMBL/GenBank entry DDBJ/EMBL/GenBank entry SRR7983122; PRJNA494978) from sweet leaf (*Breynia androgyna*) collected in Bangi, Selangor, Malaysia. The assembled near-complete genomic sequence spanned 5943 nt. **We propose the recognition of SlbPV as member of a new species in the genus *Polerovirus*,“*Polerovirus SLBPV”.***  **Bitter apple aphid-borne yellows virus (BaABYV)** genome was sequenced from leaf samples of wild bitter apple plants (*Citrullus colocynthis*) exhibiting symptoms such as dwarfing, leaf crinkling, and chlorosis, collected from a desert area in the Jiroft region in Kerman province, Iran in 2021. BaABYV isolate IR-1 (GenBank Acc. No. **OR266512**) has a nucleotide length of 5,816. It exhibited 90% of the identity with the pepo aphid-borne yellows virus (PABYV) and 88.8% of identity with the pumpkin polerovirus (PuPV). However, recombination detection analysis revealed evidence of recombination in ORF5 indicating a rise of possible new species [2]. Our calculation showed 88% and 87% of the identity with the PABYV and PuPV genome sequences, respectively; and 94%, and 91% of the identity with their translated RdRP sequences (Table 1-2). According to the species demarcation criteria for genus *Polerovirus*, **BaABYV cannot be recognized as the novel species now but as the isolate of PABYV**. However, several closely related viruses in *Polerovirus*, sharing the recombinant origin have recognized as the separate species earlier, the status of BaABYV may change after additional findings in future. |
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| **References:** |
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| **Accompanying files:** | |
| **Filename** | **Description of contents** |
| 2025.022P.N.v2.Polerovirus\_22nsp.xlsx | Excel module |

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| **Tables, Figures:** Table 1; Table 2; Fig. 1. |

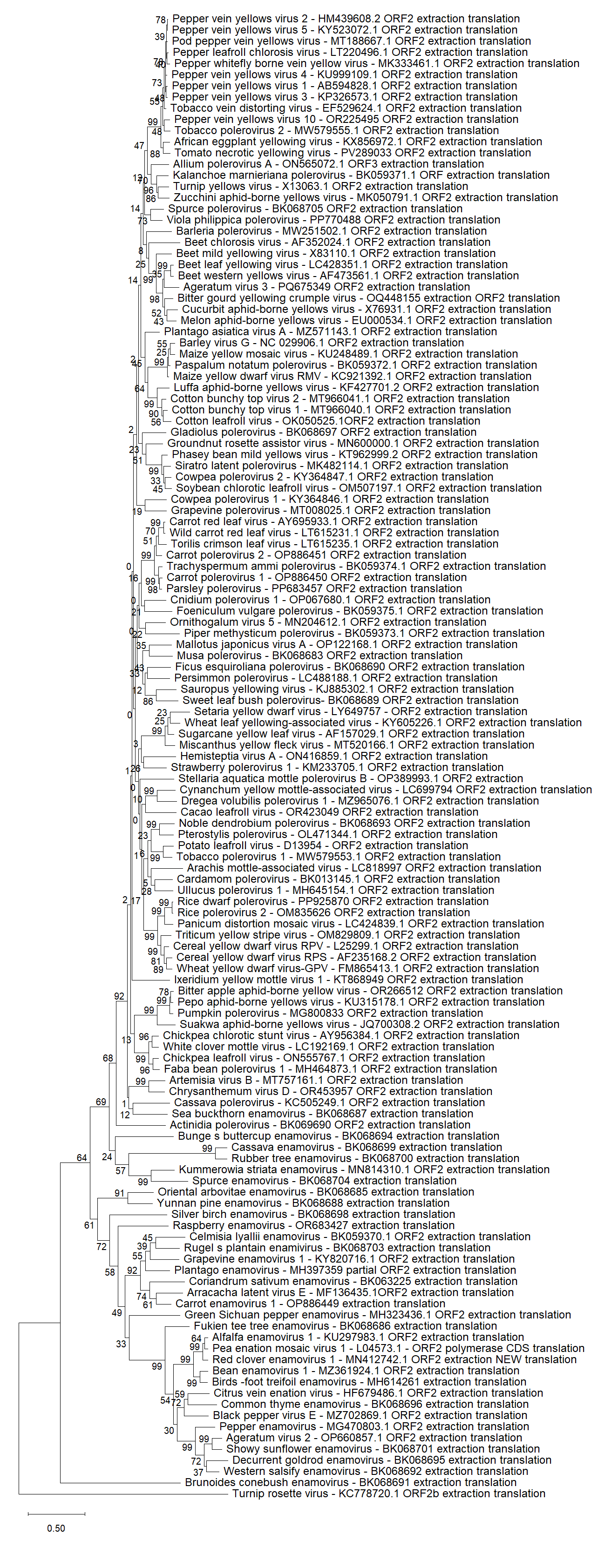
Table 1. Identity percentages between nucleotide sequences\* of putative novel and recognized polerovirus genomes retrieved from NCBI GenBank. Multiple sequence alignment was performed using MUSCLE algorithm in the Geneious Prime ver. 2025.1.2.



\*Actinidia polerovirus - BK069690.1; African eggplant yellowing virus - KX856972.1; Ageratum virus 3 - PQ675349.1; Allium polerovirus A - ON565072.1; Arachis mottle-associated virus - LC818997.1; Artemisia virus B - MT757161.1; Barleria polerovirus - MW251502.1; Barley virus G - KT9962089.1; beet chlorosis virus - AF352024.1; beet leaf yellowing virus - LC428351.1; beet mild yellowing virus - X83110.1; beet western yellows virus - AF473561.1; bitter apple aphid-borne yellow virus - OR266512.1; bitter gourd yellowing crumple virus - OQ448155.1; cacao leafroll virus - OR423049.1; cardamom polerovirus - BK013145.1; carrot red leaf virus - AY695933.1; carrot polerovirus 1 – OP886450.1; carrot polerovirus 2 – OPO886451.1; cassava polerovirus - KC505249.1; cereal yellow dwarf virus RPS - AF235168.2; cereal yellow dwarf virus RPV - L25299.1; chickpea chlorotic stunt virus - AY956384.1; chickpea leafroll virus - ON555767.1; Chrysanthemum virus D - OR453957.1; Cnidium polerovirus 1 - OP067680.1; cotton bunchy top virus 1 - MT966040.1; cotton bunchy top virus 2 - MT966041.1; cotton leafroll virus - OK050525.1; cowpea polerovirus 1 - KY364846.1; cowpea polerovirus 2 - KY364847.1; cucurbit aphid-borne yellows virus - X76931.1; Cynanchum yellow mottle-associated virus - LC699794.1; Dregea volubilis polerovirus 1 - MZ965076.1; faba bean polerovirus 1 - MH464873.1; Ficus esquiroliana polerovirus - BK068690.1; Foeniculum vulgare polerovirus - BK059375.1; Gladiolus polerovirus - BK068697.1; Grapevine polerovirus - MT008025.1; groundnut rosette assistor virus - MN600000.1; Hemisteptia virus A - ON416859.1; Ixeridium yellow mottle virus 1 - KT868949.1; Kalanchoe marnieriana polerovirus - BK059371.1; luffa aphid-borne yellows virus - KF427701.2; maize yellow dwarf virus RMV - KC921392.1; maize yellow mosaic virus - KU248489.1; Mallotus japonicus virus A - OP122168.1; melon aphid-borne yellows virus - EU000534.1; Miscanthus yellow fleck virus - MT520166.1; Musa polerovirus - BK068683; noble dendrobium polerovirus - BK068693; Ornithogalum virus 5 - MN204612.1; Panicum distortion mosaic virus - LC424839.1; parsley polerovirus - PP683457; Paspalum notatum polerovirus - BK059372.1; pepo aphid-borne yellows virus - KU315178.1; pepper leafroll chlorosis virus - LT220496.1; pepper vein yellows virus 1 - AB594828.1; pepper vein yellows virus 2 - HM439608.2; pepper vein yellows virus 3 - KP326573.1; pepper vein yellows virus 4 - KU999109.1; pepper vein yellows virus 5 - KY523072.1; pepper vein yellows virus 6 - LT559483.1; Pepper vein yellows virus 10 - OR225495.1; Pepper whitefly borne vein yellow virus - MK333461.1; Persimmon polerovirus - LC488188.1; phasey bean mild yellows virus - KT962999.2; Piper methysticum polerovirus - BK059373.1; Plantago asiatica virus A - MZ571143.1; pod pepper vein yellows virus - MT188667.1; potato leafroll virus - D13954.1; Pterostylis polerovirus - OL471344.1; pumpkin polerovirus - MG800833.1; rice dwarf polerovirus - PP925870; rice polerovirus 2 - OM835626; Sauropus yellowing virus - KJ885302.1; Setaria yellow dwarf virus - LY649757.1; Siratro latent polerovirus - MK482114.1; soybean chlorotic leafroll virus - OM507197.1; spurce polerovirus - BK068705.1; Stellaria aquatica mottle polerovirus B - OP389993.1, strawberry polerovirus 1 - KM233705.1; Suakwa aphid-borne yellows virus - JQ700308.2; sugarcane yellow leaf virus - AF157029.1; sweet leaf bush polerovirus- BK068689.1; tobacco polerovirus 1 - MW579553.1; tobacco polerovirus 2 - MW579555.1; tobacco vein distorting virus - EF529624.1; tomato necrotic yellowing virus - PV289033.1; Torilis crimson leaf virus - LT615235.1; Trachyspermum ammi polerovirus - BK059374.1; Triticum yellow stripe virus - OM829809.1; turnip yellows virus - X13063.1; Ullucus polerovirus 1 - MH645154.1; Viola philippica polerovirus - PP770488.1; wheat leaf yellowing-associated virus - KY605226.1; wheat yellow dwarf virus-GPV - FM865413.1; white clover mottle virus - LC192169.1; wild carrot red leaf virus - LT615231.1; zucchini aphid-borne yellows virus - MK050791.1.

Table 2. Identity percentages between amino acid sequences of putative novel and recognized polerovirus RdRPs translated from ORF2 of exemplar isolate sequences (indicated in Table 1), starting at ribosomal frameshift signal. Multiple sequence alignment was performed using MUSCLE algorithm in the Geneious Prime ver. 2025.1.2.



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**Fig. 1. Phylogenetic analysis of RdRPs amino acid sequences of poleroviruses and enamoviruses by the Maximum Likelihood method. RdRP of turnip rosette virus (sobemovirus) was used as an outgroup. Putative new polerovirus sequences were marked with blue diamonds and putative new enamoviruses were marked with yellow diamonds. RdRPs grouping within polerovirus-like aa sequences were marked with rounded rectangle.**

The phylogeny was inferred using the Maximum Likelihood method and Le-Gascuel (2008) LG model (+Freq) of amino acid substitutions. The tree with the highest log likelihood (-71 207,36) is shown. The percentage of replicate trees in which the associated taxa clustered together, where the number of replicates (127) was determined adaptively, is shown. The initial tree for the heuristic search was selected by choosing the tree with the superior log-likelihood between a Neighbor-Joining (NJ) tree and a Maximum Parsimony (MP) tree. The NJ tree was generated using a matrix of pairwise distances computed using the Le-Gascuel (2008) LG model (+Freq). The MP tree had the shortest length among 10 MP tree searches, each performed with a randomly generated starting tree. The evolutionary rate differences among sites were modeled using a discrete Gamma distribution across 5 categories (+G, parameter = 0,4380), with 6,50% of sites deemed evolutionarily invariant (+I). The analytical procedure encompassed 130 amino acid sequences with 923 positions in the final dataset. Evolutionary analyses were conducted in MEGA12 (Kumar S., Stecher G., Suleski M., Sanderford M., Sharma S., and Tamura K. 2024. Molecular Evolutionary Genetics Analysis Version 12 for adaptive and green computing. Molecular Biology and Evolution 41:1-9).