

The International Committee on Taxonomy of Viruses

Taxonomy Proposal Form, 2025

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

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| **Title:** | Create seventeen [17] new species in the genus *Polerovirus (Sobelivirales:Solemoviridae)* |
| **Code assigned:** | 2025.022P.Solemoviridae\_Polerovirus\_17nsp | |

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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 | **X** |
| 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| W - Withdrawn |  |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:** |
| The EC voted Uc for this proposal (see the table above for explanation).  Before the proposal can be accepted, the following points should be addressed:   * Three of the proposed new species do not meet the demarcation criteria established by the SG. Parsley polerovirus (PaPV) and carrot polerovirus 1 (CaPV1) maybe are the same species. The same applies to wild carrot red leaf virus (WCRLV). The EC suggests either to delete species or revise demarcation criteria to include recombinants. * A new tree should be prepared, to be clearer by including poleroviruses only. * The references should be updated to include the missing citations (highlighted in yellow in the figure legend). Citations should be replaced by numbers in the legend. * Please complete the description of the last seven proposed species, to show that they meet the requirements to create new species. * Please update the spreadsheet following the revision of the proposal.   Additional comments are reported in the text. Minor revisions mainly concerning style issues have been already included. |

**Part 1d: Revised Taxonomy Proposal Submission**

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| **Response of proposer:** |
| A new phylogenetic tree has been calculated for poleroviruses only. Sequence identity percentages revealed in MSA analyses have been added to the descriptions of ActPV, FeqPV, GlPV, MusPV, NbPV, SprPV, and SlbPV. The references and style have been updated.  We have changed part of proposal concerning the putative new recombinant species of carrot-infecting viruses (CaPV1, PaPV, WCRLV) that do not meet the current demarcation criteria. Also, two other viruses (BCYV and ToNYV) that were initially proposed as the novel members of genus *Polerovirus* (their RdRP aa sequences were appropriate with the species demarcation criteria) are now suggested to recognize as the isolates of already accepted species due their genome sequence identity rates that slightly exceed the species demarcation limit but also because of their overlapping host range. Therefore, the final number of proposed species is 17. |

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| **Revision date:** | 29.10.2025 |

**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 CALRV”* | Epithet from the virus name acronym |
| *“Polerovirus CAPV”* | 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 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 VPPV”* | Epithet from the virus name acronym |

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| **Abstract of Taxonomy Proposal:** |
| *Taxonomic rank(s) affected*:  Genus *Polerovirus* in the family *Solemoviridae*  *Description of current taxonomy*:  Currently, the genus *Polerovirus* consists of 77 species.  *Proposed* *taxonomic change(s):*  Create 17 new species in the genus *Polerovirus*  *Justification*: 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 identities 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, and wild carrot red leaf virus. We propose that 17 out of these 23 viruses could be recognized as members of species in the genus *Polerovirus*. |

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| **Text of Taxonomy proposal:** |
| *Taxonomic rank(s) affected*:  Genus *Polerovirus* in the family *Solemoviridae*  *Description of current taxonomy*:  *Sobelivirales:Solemoviridae:Polerovirus*  Currently, the genus *Polerovirus* consists of 77 species.  *Proposed* *taxonomic change(s)*:  Create 17 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, 3a, 3, 4, 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 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 and 2) and performed phylogenetic analysis based on their RdRPs (Fig.1).  **Ageratum virus 3 (AgV3**) was identified by transcriptome data analysis from a symptomless *Ageratum conyzoides* plant collected in Fuding, China in 2019. 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 using high-throughput sequencing (HTS) in symptomatic Pinto peanut (*Arachis pintoi*) plants collected from the Active Germplasm Bank (BGA) at the Embrapa Acre Institute in Rio Branco, Brazil by. 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 ArMoV as member of a new species in the genus *Polerovirus*, “*Polerovirus ARMOV”.***  **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 [3]. The single characterized 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) [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 a novel species but as isolate of PABYV**.  **Bitter gourd yellowing crumple virus (BYCV**) was identified by HTS from bitter gourd (*Momordica charantia*) plants showing yellowing and crumple symptoms in the field of Haikou, Hainan province of China in 2021 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 [4]. In our analysis, the genome sequence of BYCV shared 78% of identity with that of CABYV, and BYCV RdRP shared 75% identity with that of CABYV (Tables 1 and 2). According to the species demarcation criteria, the genomes of BYCV and CABYV shared slightly higher identity than recommended but their RdRPs were under the 10% aa divergence cut. Reports on CABYV indicate that it can also infect bitter gourd plants [5]. Therefore, **we propose not to recognize BYCV as member of a new species in the genus *Polerovirus* but as isolate of CABYV*.***  **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 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) [6]. The nearly complete genome sequence of the same species (sharing 99% 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 [7]. **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 by HTS from several wild carrot (*Daucus carota* ssp*. carota*) populations collected in Nouvelle Aquitaine, France in 2019. 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 [8]. 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%). CaPV1 RdRP shared 94% and 90% aa sequence identity with their RdRPs, respectively. Thus, **CaPV1** shares a high level of sequence identity with PaPV and TAPV both at nucleotide and aa sequence level. According to the species demarcation criteria for genus *Polerovirus*, **CaPV1 cannot be recognized as the novel species but as isolate of TAPV.** CaPV2 genome sequence shared the highest nucleotide sequence identity with the genome sequences of TCLV (64%); and CaPV2 RdRP shared 80% aa sequence identity with the RdRPs of CaPV1, CtRLV, TCLV and wild carrot red leaf virus (WCRLV), and 79%aa sequence identity with the RdRPs of PaPV and TAPV (Table 1-2). **We propose the recognition of CaPV2 as member of a new species in the genus *Polerovirus,* *“Polerovirus CAPV”.***  **Chrysanthemum virus D (ChVD)** was identified by HTS from symptomatic *Chrysanthemum morifolium* in Seongju County, South Korea in 2021. 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* [9]. **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 by HTS from *Cynanchum rostellatum* leaves showing yellow mottle symptoms, found in Tokyo, Japan in 2017. 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* [10]. In our MSA analysis, the genome nt sequence of CYMaV shared the highest identity (46%) with that of persimmon polerovirus, and the RdRP aa sequence shared the highest identity (57%) with that of carrot polerovirus 2 (Table 1-2). The second finding of CYMaV (OR290115) originates from China, done in 2021 [11]. 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* [12]. **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 several 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 which should be considered an isolate of Trachyspermum ammi polerovirus, TAPV, as indicated herein before), 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) [13]). 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 Trachyspermum ammi polerovirus (TAPV) RdRP (Tables 1 and 2). According to the current species demarcation criteria (>25% difference at genome sequence level and >10% difference at the RdRP aa sequence level), the genomes of PaPV, and TorCLV cannot be considered as separate species although the recombinant origin of PaPV supports its recognition as a distinct species. Therefore, **we propose the recognition of PaPV as isolate of TorCLRV.**  **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 Queensland, 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 [14]). 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 reduced 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 clusters with members of the *Polerovirus* genus [15]. 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% 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% nucleotide sequence identity, was characterized under the name of **rice less tiller virus** (PRJNA956225) [16]. **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 [17]. 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 an identity of 81%. According to the species demarcation criteria, the genomes of ToNYV and AeYV shared slightly higher identity than recommended but their RdRPs were under the 10% aa divergence cut. Reports on AeYV indicate that it can also infect tomato plants. Therefore, **we propose not to recognize ToNCV as member of a new species in the genus *Polerovirus* but as isolate of AeYV*.***  **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 with members of the genus *Polerovirus* [18]. **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 by HTS from wild carrot (*Daucus carota* spp*. carota*) sampled in Thessaloniki, Greece in 2003. Recently, it was found to be widely spread in wild carrot populations in France [7]. The complete genome of IL2 isolate (**LT615231**) consisted of 5688 nt and it had a genome organization characteristic of poleroviruses . 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) [19]. 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. Therefore, **we propose the recognition of WCRLV as isolate of CtRLV*.***  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 [20]). All seven candidates meet the demarcation criteria (>25% difference at genome sequence level and >10% difference at the RdRP aa sequence level) to be classified into new species. The descriptions of these seven species are following:  **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. In our MSA analysis, the genome nt sequence of ActPV shared the highest identity (40%) with that of turnip yellows virus, and the RdRP aa sequence shared the highest identity (51%) with that of turnip yellows virus, Allium polerovirus A, Barleria polerovirus, and zucchini aphid-borne yellows virus (Table 1-2). **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. In our MSA analysis, the genome nt sequence of FeqPV shared the highest identity (46%) with that of persimmon polerovirus, and the RdRP aa sequence shared the highest identity (58%) with that of persimmon polerovirus and Plantago asiatica virus A (Table 1-2). **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. In our MSA analysis, the genome nt sequence of GlPV shared the highest identity (55%) with that of turnip yellows virus, and the RdRP aa sequence shared the highest identity (65%) with that of Viola philippica polerovirus (Table 1-2). **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 indexed at Gembloux, University of Liege, Belgium. The assembled near-complete genomic sequence spanned 5439 nt. In our MSA analysis, the genome nt sequence of MusPV shared the highest identity (48%) with that of persimmon polerovirus, and the RdRP aa sequence shared the highest identity (58%) with that of barley virus G (Table 1-2). **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. In our MSA analysis, NbPV shared the highest identity both at genome nt sequence and RdRP aa sequence levels with that of Pterostylis polerovirus (respectively, 61% and 68%) (Table 1-2). **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. In our MSA analysis, the genome nt sequence of SprPV shared the highest identity (54%) with that of turnip yellows virus, and the RdRP aa sequence shared the highest identity (71%) with that of Viola philippica polerovirus (Table 1-2). **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. In our MSA analysis, SlbPV shared the highest identity both at genome nt sequence and RdRP aa sequence levels with that of Sauropus yellowing virus (respectively, (60% and 53%) (Table 1-2). **We propose the recognition of SlbPV as member of a new species in the genus *Polerovirus*, “*Polerovirus SLBPV”.*** |
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| **References:** |
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| **Accompanying files:** | |
| **Filename** | **Description of contents** |
| 2025.022P.Uc.v1.Polerovirus\_17nsp.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 - MH898577.1; 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 dwarf virus – GU167940.1; 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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AI-generated content may be incorrect.

**Fig 1. Phylogenetic analysis of RdRPs amino acid sequences of poleroviruses only by the Maximum Likelihood method. The representatives of proposed species are marked in red font, viruses that should be considered as isolates of known or proposed species are marked in orange font.**

RdRP aa sequences were translated from the genomic sequences starting from a ribosomal frameshift site: Actinidia polerovirus - BK069690.1; African eggplant yellowing virus - KX856972.1; Ageratum virus 3 - PQ675349.1; Allium polerovirus A - MH898577.1; 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 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 dwarf virus – GU167940.1; 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.

The phylogeny was inferred using the Maximum Likelihood method and Le-Gascuel (LG) model (+Freq) [21] of amino acid substitutions and the tree with the highest log likelihood (-46 859.81) is shown. The percentage of replicate trees in which the associated taxa clustered together (500 replicates) is shown above the branches. 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 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 = 0.4682), with 14.27% of sites deemed evolutionarily invariant (+I). The analytical procedure encompassed 100 amino acid sequences with 750 positions in the final dataset. Evolutionary analyses were conducted in MEGA12 [22].