

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

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| **Code assigned:** | **2020.026P** |  |
| **Short title:** Abolish the family *Luteovirida*e (*Tolivirales*) and move its genera to the familes *Tombusviridae* (*Tolivirales*) and *Solemoviridae* (*Sobelivirales*) | | |
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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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| *Tombusviridae* Study Group, *Luteoviridae* Study Group, *Solemoviridae* Study Group |

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

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| Minor typos were found/corrected by *Tombusviridae* study group members, and MS. This is a minor revision of the previously submitted proposal, and all SGs consider this version acceptable. |

**Submission dates**

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| Date first submitted to SC Chair | 31 July 2020 |
| Date of this revision (if different to above) | 3 December 2020 |

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

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| Figure 5 (tree for RdRp region only) was reanalyzed and MBV (U07551) removed. Note that this figure shows *Gammacarmovirus* split, but the genus criteria for tombusvirids is based on differential branching of the complete RdRp, so this is not a problem. Also, I had trouble finding some PMIDs, so not all references have them included. |

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

**Name of accompanying Excel module**

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| 2020.026P.R.Abolish\_Leoteoviridae.xlsx |

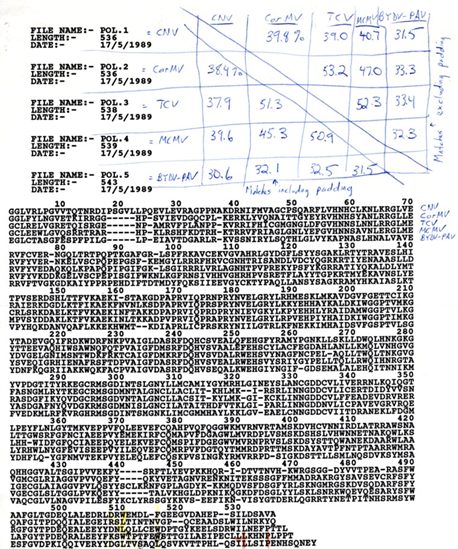
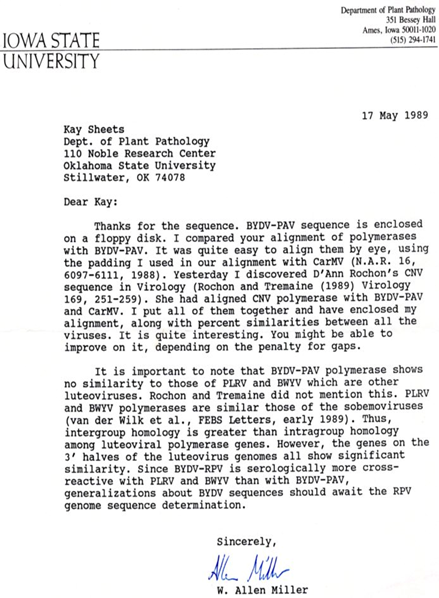
**Abstract**

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| The proposal 2019.006G.N.v4.Riboviria [1] listed the hallmark genes for viral replication (RdRps and RTs) as the basis for its large-scale organization. Current luteovirids fit into 2 different RdRp superfamilies (flavivirus-like and picornavirus-like) and are only united by their distinctive single-jellyroll CPs that produce virions occasionally decorated with small peptides that allow aphid transmission. We propose that family *Luteoviridae* be dissolved, and Genus *Luteovirus* be moved into Family *Tombusviridae*, while Genera *Polerovirus* and *Enamovirus* be moved into Family *Solemoviridae*. This rearrangement will group the genera by RdRp-type with their closest relatives. All tombusvirids, luteovirids, and solemovirids are encapsidated in similar sized virions with T=3 structures, so rearrangements based on RdRp phylogeny do not produce major differences in virion structure categorization. |

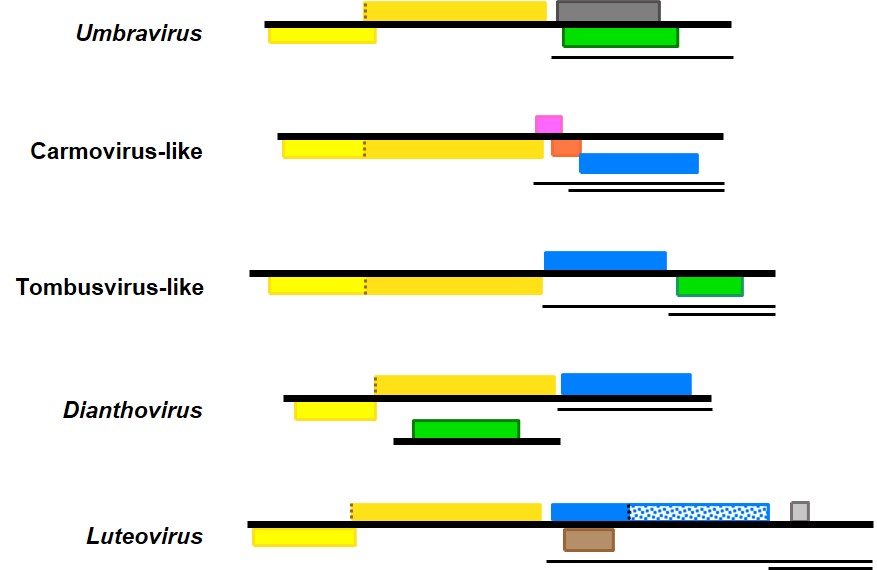
**Text of proposal**

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| |  | | --- | | Plant viruses were initially classified in “groups”, and all relationships were based on physical characteristics: type of nucleic acid, virion particles, virion shape (EM), vectors, and immunological cross-reactivity of virion particles or their virion components. When ICTV was formed [2], the “groups” were eventually reorganized into the current or similar taxonomic hierarchy. Thus, 7 members of the current family *Luteoviridae* were placed together as “Luteovirus Group”, with BYDV**MAV** as type species based on plant hosts, virion structure, some immunological cross-reactions, their requirement for aphid transmission [3], and similar sized ssRNA genomes [2, 4]. It was noted that the sequence of PLRV, type species for Genus *Polerovirus*, was not highly similar to the sequences of two luteoviruses [5]. In 1989 two proposal authors (WAM and KS) discussed the lack of similarity of the RdRp of BYDV-PAV with RdRps of two other luteovirus group species, PLRV and BWYV (currently poleroviruses), while it showed high similarity to four viruses that are currently included in the family *Tombusviridae* and have genomes that fit into two of the four general genome organizations of tombusvirids (Figs. 1 & 2).  The differences between "luteovirus" RdRps (BYDVPAV, BWYV, PLRV) was noted in 1989 [5] and 1991 [6], since BWYV and PLRV clustered in supergroup 1 while BYDVPAV was in supergroup 2 along with 6 tombusvirids that are now type species for 6 tombusvirid genera. Miller et al. [7] pointed out the dichotomous nature of luteoviruses when using the ICTV species definition of "a polythetic class of viruses that constitute a replicating lineage and occupy a particular ecological niche" [8] since the ecological niche of luteoviruses grouped them with poleroviruses and enamoviruses, while molecular biology characteristics indicate their much closer similarity to tombusvirids. This proposal aims to "ungroup/regroup" current luteovirids to better fit ICTV criteria:  **A**) Dissolve family *Luteoviridae* and reassign members to families *Tombusviridae* and *Solemoviridae*  **B**) Add genus *Luteovirus* to subfamily *Regressovirinae* in family *Tombusviridae*  **C**) Add all current unassigned luteovirids, and genera *Enamovirus* and *Polerovirus* to family *Solemoviridae*.  **Parts A&B)** The sequence/molecular biology data clearly suggest that early luteoviruses arose by recombination between a tombusvirid similar to a dianthovirus and another member/precursor of the family *Luteoviridae* resulting in a virus with a polerovirus-type CP but a tombusvirid-like replicase region. Similarly, the polemovirus poinsettia latent virus (PnLV) arose from a recombination event that replaced a polerovirus CP ORF with a sobemovirus CP ORF [9]. Similar recombination events between species from different tombusvirid genera have also expanded the number of genera within that family [10], and led to the creation of three subfamilies [11]. The similarity of luteoviruses to tombusvirids includes sequence similarity of the complete RdRp (Figs. 2 and 3), uncapped RNA that uses RNA secondary/tertiary structure to form 5' "kissing loops", 3' cap-independent translational enhancers, structural signals for sgRNA synthesis [12, 13], and regulation of replication via long distance RNA-RNA interactions [14]. Additionally, relatively large structures within the RdRp ORF just downstream of the -1FS or RT junction mediate the rates of RT or ‑1FS for RdRp production [15].  Since the ICTV uses virion content/replication strategy as the chief criteria for taxonomic organization, the current family *Luteoviridae* should be dissolved, and its members reassigned to reflect an emphasis on those criteria. This rearrangement also more accurately reflects what their relationship should be within realm *Riboviria*.  Current members of Genus *Luteovirus* will remain in a genus of the same name, but the genus will be moved into family *Tombusviridae* since the sum of their characteristics distinguishes them from other genera in the family when using the family's revised genus demarcation criteria [16]:  • Structural criteria: spherical virions with either a smooth or granular appearance.  • Genomic criteria: genome organization, number of genome segments, size of genome,  number of subgenomic RNAs.  • Polymerase criteria: gene interrupted by a termination codon or a -1 ribosomal  frameshifting element that is periodically read through  • Differential branching of phylogenetic trees based on complete RdRp.  The species demarcation criteria for Genus *Luteovirus* and type species will remain the same as that given in the 9th Report [4], but in the near future the *Tombusviridae* Study Group will consider whether species criteria should be revised so they are more in line with the criteria for other tombusvirid genera.  **Part C)** The remaining viruses of current family *Luteoviridae* are more closely related to current members of the family *Solemoviridae* (VPg decorating 5'-end, protease gene partially overlapping RdRp active site domain, -1FS enabled by small stem loop or small pseudoknot, homology of RdRps, no polyA tail). The downstream RdRp domains are also more closely related to sobemoviruses and polemovirus. This relationship has been recently reviewed/described [17], and these similarities indicate that genera *Polerovirus* and *Enamovirus* should be moved into family *Solemoviridae*. The remaining unassigned members of family *Luteoviridae* also have characteristics most similar to poleroviruses, so those species should be transferred as unassigned solemovirids. | |

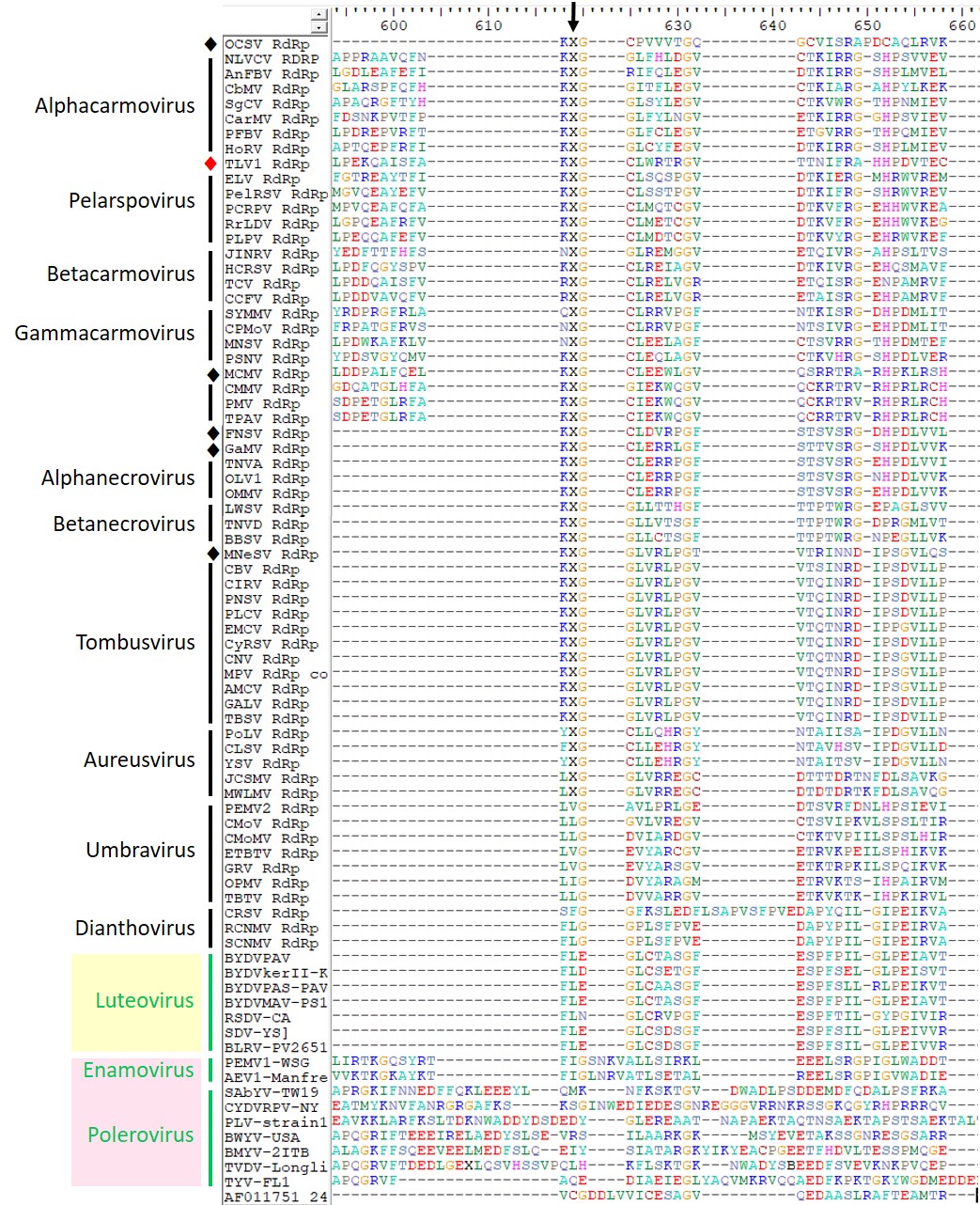
**Supporting evidence**



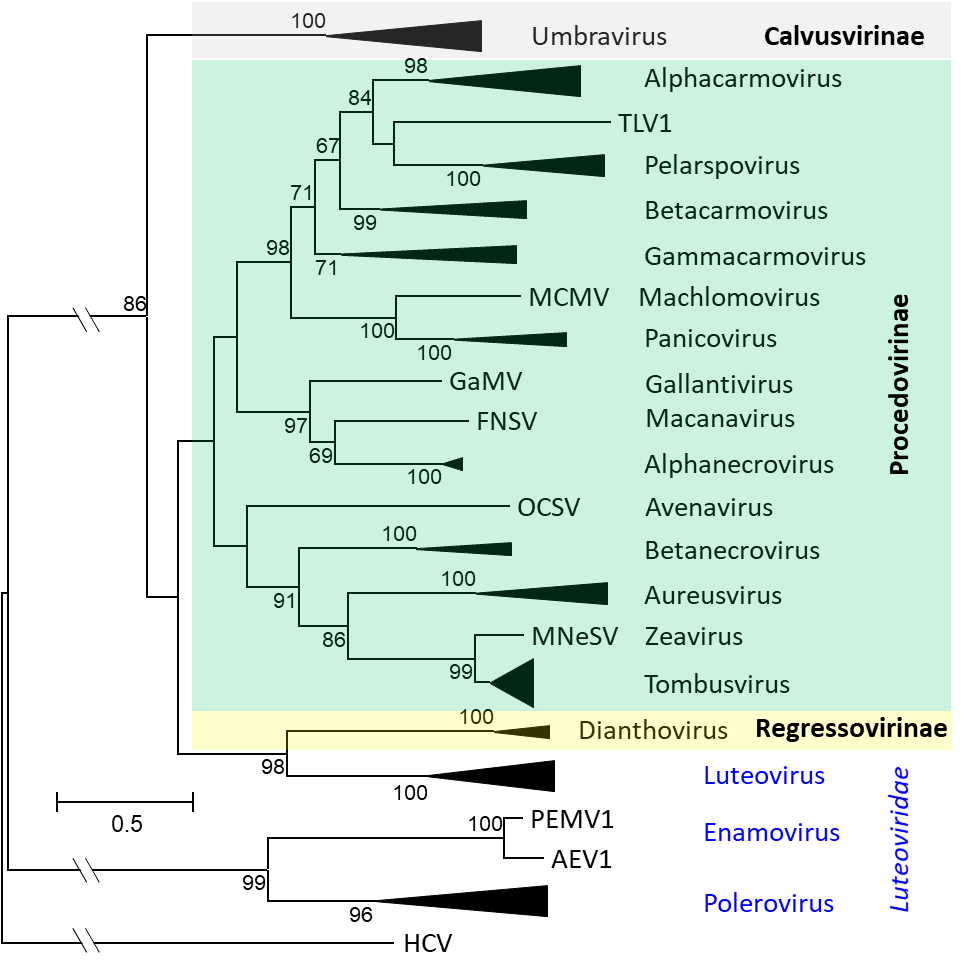
**Fig. 1** 1989 letter from WA Miller to K Scheets where the relationships between known luteoviruses, tombusviruses and sobemoviruses is discussed.



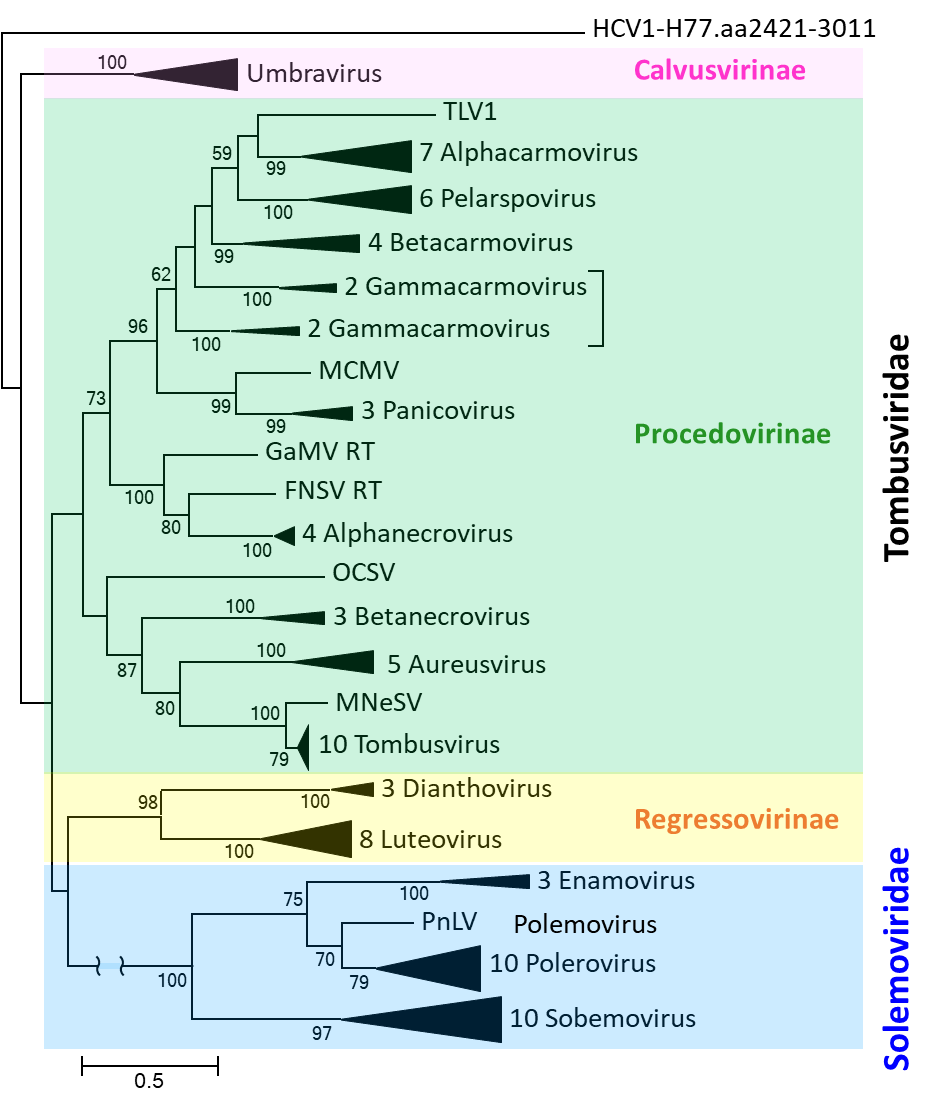
**Fig. 2.** General genome organizations for current and proposed members of family *Tombusviridae*: umbravirus, 10 carmovirus-like genera, four tombusvirus-like genera, dianthoviruses, and luteoviruses. ORFs encoding proteins with yellow and gold boxes mark the replicase-associated proteins (RAPs) and downstream portion of complete RdRps. Vertical dashed lines mark RT and -1FS locations. Blue boxes mark CP ORFs, and the aphid-transmission domain of luteovirus CP is stippled. Additional ORFs are required for either cell-to-cell movement, long distance movement, or act as suppressors of silencing. Thin lines below genomes mark sgRNAs that function as mRNAs for downstream ORFs. Note that four carmovirus-like and one tombusvirus-like genera have smaller CP ORFs than represented by these sketches.



**Fig. 3**. Black arrow marks the readthrough (X=nonsense-coded aa) and -1 frameshift (-1FS) region for complete RdRps in the MUSCLE alignment of 61 tombusvirids, 7 of 8 luteoviruses of ICTV-recognized species with complete or coding-complete sequences in GenBank. The -1FS for enamoviruses (2 of 4) and poleroviruses (7 of 19) do not align at the arrow. The outgroup was hepatitus C virus replicase (AF011751\_2421..3011 [591 aa]). Monotypic genera have a black diamond and TLV1 is unassigned (red diamond). Green font and lines mark genera in current family *Luteoviridae*. Sequence sources and virus names are in **Table 1 of [11].**



**Fig. 4**. Phylogenetic (distance) analysis of the **complete RdRps** for all tombusvirids, with selected viruses from family *Luteoviridae* as shown in **Fig. 3** and used in **2018.001P.N.v2.Tombusviridae\_3subfam** [10]. Alignments of the 78 sequences were made using MUSCLE while trees were generated in Mega 7 [18] with the Maximum Likelihood (ML) algorithm using 1000 bootstrap replicates (showing values >50%). Positions with <50% site coverage were eliminated, leaving 809 positions in the final dataset. Condensed triangles or brackets mark monophyletic lineages. Brackets connecting tombusvirid branching, enamovirus plus polerovirus branching, and HCV RdRp (aa 2421-3011) were proportionately shortened. *Tombusviridae* genera and subfamily names are on the right, and colored boxes enclose current member genera.

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**Fig. 5**. Phylogenetic (distance) analysis of the **RdRp functional domains** for viruses from families *Tombusviridae, Luteoviridae, Solemoviridae* using the RdRp (aa 2421-3011) of hepatitis C virus 1 as the outgroup. Sequences from three genera with more than 10 members were limited to 10 (*Tombusvirus* lacks cucumber Bulgarian latent virus; for *Polerovirus*, and *Sobemovirus*, see Table 1). Stop-codon readthrough regions begin with "X" for the suppressor codon residue, and the last residue preceding the frameshift were included. Analyses were performed the same as for Fig. 4. There were 95 sequences and 523 positions in the final dataset. Condensed triangles and bracket mark ICTV genera. The bracket connecting tombusvirids and luteoviruses to current and proposed solemovirids was shortened to save space. Tombusvirid subfamily names are on the right, and colored boxes enclose current and proposed member genera. Sequence sources and virus names are in **Table 1** or [11].

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| **Table 1: Abbreviations used in Figs. 4 & 5** | | | | |
| and species IDs from families *Luteoviridae* and *Solemoviridae* | | | | |
|  |  |  | | |
|  |  | **GenBank** | | |
| **Abbr.** | **Species** | | **Genome ID** | |
| TLV1 | Trailing lespedeza virus 1 | | | HM640935 |
| MCMV | Maize chlorotic mottle virus | | | X14736 |
| GaMV | Galinsoga mosaic virus | | | Y13463 |
| FNSV | Furcraea necrotic streak virus | | | FJ768020 |
| OCSV | Oat chlorotic stunt virus | | | X83964 |
| MNeSV | Maize necrotic streak virus | | | AF266518 |
|  | Luteovirus | | |  |
|  | Barley yellow dwarf virus kerII | | | KC571999 |
|  | Barley yellow dwarf virus kerIII | | | KC559092 |
| BYDVMAV | Barley yellow dwarf virus MAV | | | D11028 |
|  | Barley yellow dwarf virus PAS | | | AF218798 |
| BYDVPAV | Barley yellow dwarf virus PAV | | | X07653 |
|  | Bean leafroll virus | | | AF441393 |
|  | Rose spring dwarf-associated virus | | | EU024678 |
|  | Soybean dwarf virus | | | AB038147 |
|  | Enamovirus | | |  |
| AEV1 | Alfalfa enamovirus 1 | | | KU297983 |
| PEMV1 | Pea enation mosaic virus 1 | | | HM439775 |
|  | Citrus vein enation virus | | | HF679486 |
|  | Polerovirus | | |  |
| BWYV | Beet chlorosis virus  Beet western yellows virus | | | AF352024  AF473561 |
|  | Carrot red leaf virus | | | AY695933 |
| CYDVRPS | Cereal yellow dwarf virus RPS | | | AF235168 |
|  | Chickpea chlorotic stunt virus | | | AY956384 |
|  | Cucurbit aphid-borne yellows virus | | | X76931 |
|  | Maize yellow dwarf virus RMV | | | KC921392 |
|  | Melon aphid-borne yellows virus | | | EU000534 |
| PLRV | Potato leafroll virus | | | D00530 |
|  | Sugarcane yellow leaf virus | | | AF157029 |
|  | Tobacco vein distorting virus | | | EF529624 |
|  | Polemovirus | | |  |
| PnLV | Poinsettia latent virus | | | AJ867490 |
|  | Sobemovirus | | |  |
|  | Blueberry shoestring virus | | | LC081344 |
|  | Cocksfoot mottle virus | | | Z48630 |
|  | Cymbidium chlorotic mosaic virus | | | LC019764 |
|  | Imperata yellow mottle virus | | | AM990928 |
|  | Papaya lethal yellowing virus | | | JX123318 |
|  | Rice yellow mottle virus | | | L20893 |
|  | Ryegrass mottle virus | | | AB040446 |
|  | Southern bean mosaic virus | | | AF055887 |
|  | Soybean yellow common mosaic virus | | | JF495127 |
|  | Velvet tobacco mottle virus | | | HM754263 |
|  |  | | |  |
| HCV | Hepatitis C virus H77 | | | AF011751 |

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