This Word module should be used for all taxonomic proposals.

Please complete **Part 1** and:

either **Part 3** for proposals to create new taxa or change existing taxa

or **Part 2** for proposals of a general nature.

Submit the completed Word module, together with the accompanying Excel module named in Part 3, to the appropriate ICTV Subcommittee Chair.

For guidance, see the notes written in blue, below, and the help notes in file Taxonomic\_Proposals\_Help\_2018.

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

|  |  |  |  |
| --- | --- | --- | --- |
| **Code assigned:** | ***2018.001P*** | | (to be completed by ICTV officers) |
| **Short title:** (e.g. “6 new species in the genus *Zetavirus”*)  Create three subfamilies in family *Tombusviridae* | | | |
|  | | | |
| **Author(s):** | | | |
| Kay Scheets for *Tombusviridae* study group, Kanakala Surapathrudu, and W. Allen Miller | | | |
| **Corresponding author with e-mail address:** | | | |
| Kay Scheets kay.scheets@okstate.edu | | | |
| **List the ICTV study group(s) that have seen this proposal:** | | | |
| A list of study groups and contacts is provided at <http://www.ictvonline.org/subcommittees.asp> . If in doubt, contact the appropriate subcommittee chair (there are six virus subcommittees: animal DNA and retroviruses, animal ssRNA-, animal ssRNA+, fungal and protist, plant, bacterial and archaeal) | | *Luteoviridae***,** *Tombusviridae* | |
| **ICTV Study Group comments (if any) and response of the proposer:** | | | |
|  | | | |
|  | | | |
| Date first submitted to ICTV: | | | 31-May-2018 |
| Date of this revision (if different to above): | | |  |

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| **ICTV-EC comments and response of the proposer:** |
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**Part 2:** **NON-STANDARD**

Template for any proposal regarding ICTV procedures, rules or policy, not involving the creation of new taxonomy.

| **Text of proposal:** |
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|  |

**Part 3:** **PROPOSED TAXONOMY**

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| **Name of accompanying Excel module:** 2018.001P.N.v3.Tombusviridae\_subfam.xlsx |

The taxonomic changes you are proposing should be presented on an accompanying Excel module, 2017\_TP\_Template\_Excel\_module. Please enter the file name of the completed module in this box.

**Supporting material:**

| additional material in support of this proposal |
| --- |
| Please explain the reasons for the taxonomic changes you are proposing and provide evidence to support them. The following information should be provided, where relevant:   * **Species demarcation criteria**: Explain how new species differ from others in the genus and demonstrate that these differences meet the criteria previously established for demarcating between species. If no criteriahave previously been established, and if there will now be more than one species in the genus, please state the demarcation criteria you are proposing. * **Higher taxa**:   + There is no formal requirement to state demarcation criteria when proposing new genera or other higher taxa. However, a similar concept should apply in pursuit of a rational and consistent virus taxonomy.   + Please indicate the **origin of names** assigned to new taxa at genus level and above.   + For each new genus a **type species** must be designated to represent it. Please explain your choice. * **Supporting evidence**: The use of Figures and Tables is strongly recommended (note that copying from publications will require permission from the copyright holder). For phylogenetic analysis, try to provide a tree where branch length is related to genetic distance. |

Family *Tombusviridae* bases its criteria for inclusion in the family and separation into genera on virion morphology, the type of viral nucleic acid, and the encoded RNA dependent RNA polymerase (RdRp) (Scheets et al., 2015). Most tombusvirid genera use stop codon readthrough (RT) to produce the RdRp while dianthoviruses and umbraviruses use a -1 frameshift (-1FS) mechanism to synthesize phylogenetically related RdRps. Viruses from many genera in the family *Tombusviridae* use a variety of 3' cap-independent translational enhancers (3'CITEs) and simpler RNA base-pairing structures in either the 5' UTR or within the RdRp ORF of their gRNAs, and in the 5’UTR of their sgRNAs to circularize the RNA and initiate translation (Simon and Miller, 2013). Additionally, structures within the RdRp ORF just downstream of the -1FS or RT junction, mediate the rates of RT or -1FS for RdRp production (Miras et al., 2017).

The family *Tombusviridae* currently includes 16 genera, with enough varying characteristics that subfamilies would be highly useful for further organization. Comparing the RdRp expression mechanism and the general gene order of the family *Tombusviridae* shows that there are four basic formats (Fig. 1). For genera that use a RT mechanism for expression of the RdRp, the capsid protein (CP) ORF of carmo-like viruses is located at the 3' end of the genome, while the CP ORF for tombus-like viruses immediately follows the RdRp ORF. For genera that use a -1FS mechanism, umbraviruses lack a CP ORF, and dianthoviruses have a split genome. An RdRp tree of all sequenced tombusvirids and viruses from the family *Luteoviridae* places umbraviruses outside all CP-coding tombusvirids, clusters all RT genera on one branch, and groups dianthoviruses with luteoviruses (Fig. 2).

We propose the following subfamily names derived from Latin roots:

*Procedovirinae*, from the verb *procedo* (go ahead, advance, continue, go forward), which includes all genera using a RT mechanism for RdRp;

*Regressovirinae,* from *regressus* (step back), for genera encoding CPs and using a -1FS mechanism for RdRp (genus *Dianthovirus*). In the future, this subfamily could also include genus *Luteovirus* (see below);

*Calvusvirinae*, from *calvus* (bare or naked), for genus *Umbravirus*.

Five viruses with partial sequence data (*Ahlum waterborne virus*, *Bean mild mosaic virus*, *Chenopodium necrosis virus*, *Cucumber soil-borne virus*, and *Weddel waterborne virus*) were "orphaned" when genus *Necrovirus* (Rochon, 2011) and genus *Carmovirus* (Scheets et al., 2015) were divided. These viruses, along with *Trailing lespedeza virus 1* will be unassigned within the subfamily *Procedovirinae.*

For future reference, it should be noted that the phylogeny depicted in Fig. 2 indicates that members of the genus *Luteovirus* (family *Luteoviridae*) have a closer relationship with members of other genera in the *Tombusviridae* than with those in the two other genera in the family *Luteoviridae*. As a matter of fact, many researchers have observed the similarities between the molecular biology of viruses in the genus *Luteovirus* and members of the family *Tombusviridae* (such as Miller et al., 2002). For example, members of genus *Luteovirus* have undecorated RNA termini like tombusvirids while poleroviruses and enamoviruses have a 5' terminal genome-linked peptide (VPg); the RT and -1FS junctions of tombusvirid and luteovirus RdRps but not enamovirus and poleroviruses align; the type of 3' CITE first described in a luteovirus is also found or predicted for many currently recognized tombusvirids; unlike enamoviruses and poleroviruses, which use an H-type pseudoknot, luteoviruses have a long stem-loop which interacts with a 3' UTR sequence, a mechanism also found in tombusvirids. Together, these factors indicate that genus *Luteovirus* should be moved into family *Tombusviridae*.

**Tombusvirus-like**

***Dianthovirus***

***Umbravirus***

**Carmovirus-like**

**Figure 1 -** General genome organizations for umbraviruses, 11 carmovirus-like genera, 3 tombusvirus-like genera, and dianthoviruses. ORFs encoding proteins with yellow and gold boxes mark the replication-associated proteins (RAPs) and carboxyl regions of RdRps. A vertical dashed line marks RT and -1FS locations. Blue boxes mark CP ORFs. Additional ORFs are required for either cell-to-cell movement, long distance movement, or act as suppressors of silencing (tan). Thin lines below genomes mark sgRNAs that function as mRNAs for downstream ORFs. Notethat four carmovirus-like and one tombusvirus-like genera have smaller CP ORFs than represented by these genome sketches.

Umbravirus

Alphacarmovirus

TLV1

Pelarspovirus

Betacarmovirus

Gammacarmovirus

MCMV

Panicovirus

GaMV

FNSV

Alphanecrovirus

OCSV

Betanecrovirus

Aureusvirus

MNeSV

Tombusvirus

Dianthovirus

PEMV1

AEV1

Polerovirus

HCV

100

96

100

100

99

99

100

100

100

100

100

100

100

97

69

98

98

99

86

91

86

71

98

71

67

84

0.5

Luteovirus

Machlomovirus

Avenavirus

Gallantivirus

Macanavirus

Zeavirus

Enamovirus

**Procedovirinae**

**Regressovirinae**

**Calvusvirinae**

*Luteoviridae*

**Figure 2 -** Phylogenetic (distance) analysis of the RdRps for all tombusvirids plus viruses from family *Luteoviridae*. Alignments of the 78 sequences were made using MUSCLE while trees were generated 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. Proposed *Tombusviridae* subfamily names are on the right, and colored boxes enclose member genera. Sequence sources and virus names are in Table 1.

**Table 1 -** Sequence IDs used for phylogenetic analyses of RdRps. For each genus, the type species is listed first. Some viruses in the current family *Tombusviridae* and family *Luteoviridae* are annotated incorrectly in the databases. **Bold** sequence IDs were the source for RdRps. Black or blue font indicates the entry has the correct RdRp annotation. Red font has incorrect annotation and **bold red** font indicates the more correct RdRp was used. Note that all polerovirus RefSeqs (as of 28May2018) are annotated inaccurately at their -1FS site (X XXY YY**Z**), and those sequences were used "as is". Additional changes corrected two tombusvirid RdRps: \* join RAP & RT with "X"; \*\* insert "X" at RT site.

|  |  |  |  |
| --- | --- | --- | --- |
| **Virus abbreviation(s)** | **Species name** | **Exemplar RefSeq #** | **Exemplar Virus GB #** |
| **genus *Alphacarmovirus*** | | | |
| CarMV-B | ***Carnation mottle virus*** | **X02986** | NC\_001265 |
| AFBV-FL | *Angelonia flower break virus* | **DQ219415** | NC\_007733 |
| CbMV-CA | *Calibrachoa mottle virus* | **GQ244431** | NC\_021926 |
| HoRSV-CA | *Honeysuckle ringspot virus* | **HQ677625** | NC\_014967 |
| NLVCV-AK | *Nootka lupine vein clearing virus* | **\*EF207438** | **NC\_009017** |
| PFBV-MZ10 | *Pelargonium flower break virus* | **AJ514833** | NC\_005286 |
| SgCV-MRN | *Saguaro cactus virus* | **U72332** | NC\_001780 |
| **genus *Alphanecrovirus*** | | | |
| TNVA-FM1B | ***Tobacco necrosis virus A*** | **M33002** | NC\_001777 |
| OLV1-citrus | *Olive latent virus 1* | **X85989** | NC\_001721 |
| OMMV-GP | *Olive mild mosaic virus* | **AY616760** | NC\_006939 |
| **genus *Aureusvirus*** | | | |
| PoLV | ***Pothos latent virus*** | **X87115** | NC\_000939 |
| CLSV | *Cucumber leaf spot virus* | **EU127904** | NC\_007816 |
| JCSMV-Iran | *Johnsongrass chlorotic stripe mosaic virus* | **AJ557804** | NC\_005287 |
| MWLMV-OH | *Maize white line mosaic virus* | **EF589670** | NC\_009533 |
| YSV-DMSZ:PV0517 | *Yam spherical virus* | **KF482072** | NC\_022895 |
| **genus *Avenavirus*** | | | |
| OCSV-Llanwern | ***Oat chlorotic stunt virus*** | **X83964** | NC\_003633 |
| **genus *Betacarmovirus*** | | | |
| TCV-B | ***Turnip crinkle virus*** | **M22445** | NC\_003821 |
| CCFV-CL | *Cardamine chlorotic fleck virus* | **L16015** | NC\_001600 |
| HCRSV-Singapore | *Hibiscus chlorotic ringspot virus* | **X86448** | NC\_003608 |
| JINRV | *Japanese iris necrotic ring virus* | **D86123** | NC\_002187 |
| **genus *Betanecrovirus*** | | | |
| TNVD-Hungary | ***Tobacco necrosis virus D*** | **U62546** | NC\_003487 |
| BBSV-Ningxia | *Beet black scorch virus* | **AF452884** | NC\_004452 |
| LWSV | *Leek white stripe virus* | **X94560** | NC\_001822 |
| **genus *Dianthovirus*** | | | |
| CRSV | ***Carnation ringspot virus*** | **L18870** | NC\_003530 |
| RCNMV-Australia | *Red clover necrotic mosaic virus* | **J04357** | NC\_003756 |
| SCNMV-59 | *Sweet clover necrotic mosaic virus* | L07884 | **NC\_003806** |
| **genus *Gallantivirus*** | | | |
| GaMV | ***Galinsoga mosaic virus*** | **Y13463** | NC\_001818 |
| **genus *Gammacarmovirus*** | | | |
| MNSV-Dutch | ***Melon necrotic spot virus*** | **M29671** | NC\_001504 |
| CPMV-ATCC:PV955 | *Cowpea mottle virus* | **U20976** | NC\_003535 |
| PSNV-Wakayama | *Pea stem necrosis virus* | **AB086951** | NC\_004995 |
| SYMMV-Gunwi | *Soybean yellow mottle mosaic virus* | **FJ457015** | NC\_011643 |
| **genus *Macanavirus*** | | | |
| FNSV-Cauca | ***Furcraea necrotic streak virus*** | **FJ768020** | NC\_020469 |
| **genus *Machlomovirus*** | | | |
| MCMV-KS1 | ***Maize chlorotic mottle virus*** | **X14736** | NC\_003627 |
| **genus *Panicovirus*** | | | |
| PMV-109S | ***Panicum mosaic virus*** | **U55002** | NC\_002598 |
| CMMV-Scotland | *Cocksfoot mild mosaic virus* | **EU081018** | NC\_011108 |
| TPAV-05TGP00369 | *Thin paspalum asymptomatic virus* | **JX848617** | NC\_021705 |
| **genus *Pelarspovirus*** | | | |
| PelRSV-DMSZ:PV0304 | ***Pelargonium ringspot virus*** | **AY038068** | NC\_026240 |
| ELV-ATCC:PV522 | *Elderberry latent virus* | **AY038066** | NC\_026239 |
| PCRPV-GR57 | *Pelargonium chlorotic ring pattern virus* | **AY038069** | NC\_005985 |
| PLPV-DMSZ:PV0193 | *Pelargonium line pattern virus* | **AY613852** | NC\_007017 |
| RrLDV-MN-3 | *Rosa rugosa leaf distortion virus* | **KC166238** | NC\_020415 |
| **genus *Tombusvirus*** | | | |
| TBSV-cherry | ***Tomato bushy stunt virus*** | **M21958** | NC\_001554 |
| AMCV-Bari | *Artichoke mottled crinkle virus* | **X62493** | NC\_001339 |
| CIRV | *Carnation Italian ringspot virus* | **X85215** | NC\_003500 |
| CBV-Bulgaria | *Cucumber Bulgarian virus* | **AY163842** | NC\_004725 |
| CNV | *Cucumber necrosis virus* | **M25270** | NC\_001469 |
| CyRV | *Cymbidium ringspot virus* | **X15511** | NC\_003532 |
| EMCV-Israel | *Eggplant mottled crinkle virus* | **JQ864181** | NC\_023339 |
| GALV-nipplefruit | *Grapevine Algerian latent virus* | **AY830918** | NC\_011535 |
| MPV-PM75 | *Moroccan pepper virus* | **\*\*JX197071** | **NC\_020073** |
| PLCV-T46 | *Pelargonium leaf curl virus* | **KU187189** | NC\_030452 |
| PNSV-UPEV | *Pelargonium necrotic spot virus* | **AJ607402** | NC\_005285 |
| **genus *Umbravirus*** | | | |
| CMoV-Weddel | ***Carrot mottle virus*** | **FJ188473** | NC\_011515 |
| CMoMV-Australia | *Carrot mottle mimic virus* | **U57305** | NC\_001726 |
| ETBTV-18-2 | *Ethiopian tobacco bushy top virus* | **KJ918748** | NC\_024808 |
| GRV-MC1 | *Groundnut rosette virus* | **Z69910** | NC\_003603 |
| OPMV-PHEL 5235 | *Opium poppy mosaic virus* | **EU151723** | NC\_027710 |
| PEMV2-WSG | *Pea enation mosaic virus 2* | U03563 | **NC\_003853** |
| TBTV-Ch | *Tobacco bushy top virus* | **AF402620** | NC\_004366 |
| **genus *Zeavirus*** | | | |
| MNeSV-AZ | ***Maize necrotic streak virus*** | **AF266518** | NC\_007729 |
| TLV1-06TGP01091 | *Trailing lespedeza virus 1* | **HM640935** | NC\_015227 |
| **genus *Luteovirus*** | | | |
| BYDVPAV | ***Barley yellow dwarf virus PAV*** | X07653.1 | **NC\_004750.1** |
| BLRV-PV2651 | *Bean leafroll virus* | **AF441393.1** | NC\_003369.1 |
| BYDVkerII-K439 | *Barley yellow dwarf virus kerII* | **KC571999.1** | NC\_021481.1 |
| BYDVMAV-PS1 | *Barley yellow dwarf virus MAV* | D11028.1 | **NC\_003680.1** |
| BYDVPAS-PAV129 | *Barley yellow dwarf virus PAS* | **AF218798.2** | NC\_002160.2 |
| RSDaV-CA | *Rose spring dwarf-associated virus* | **EU024678.1** | NC\_010806.1 |
| SDV-YS | *Soybean dwarf virus* | AB038147.1 | **NC\_003056.1** |
| **genus *Enamovirus*** | | | |
| PEMV1-WSG | ***Pea enation mosaic virus 1*** | L04573 | **NC\_003629.1** |
| AEV1-Manfredi | *Alfalfa enamovirus 1* | KU297983 | **NC\_029993.1** |
| **genus *Polerovirus*** | | | |
| PLV-strain1 | ***Potato leafroll virus*** | D00530.1 | **NC\_001747.1** |
| BMYV-2ITB | *Beet mild yellowing virus* | X83110 | **NC\_003491.1** |
| BWYV-USA | *Beet western yellows virus* | AF473561 | **NC\_004756.1** |
| CYDVRPV-NY | *Cereal yellow dwarf virus RPV* | L25299 | **NC\_004751.1** |
| SAbYV-TW19 | *Suakwa aphid-borne yellows virus* | JQ700308 | **NC\_018571.2** |
| TVDV-Longlin | *Tobacco vein distorting virus* | EF529624 | **NC\_010732.1** |
| TYV-FL1 | *Turnip yellows virus* | X13063 | **NC\_003743.1** |
| **genus *Hepacivirus*** | | | |
| HCV-H77 | *Hepacivirus C* | **AF011751.1** |  |

| **References:** |
| --- |
| Miller, W.A., Liu, S., Beckett, R., 2002. Barley yellow dwarf virus: *Luteoviridae* or *Tombusviridae*? Mol Plant Pathol 3, 177-183.  Miras, M., Miller, W.A., Truniger, V., Aranda, M.A. 2017. Non-canonical translation in plant RNA viruses. Front Plant Sci 8, 494.  Rochon, D’A. 2011. Divide the genus *Necrovirus* into 2 new genera, *Alphanecrovirus* and *Betanecrovirus*. <https://talk.ictvonline.org/ICTV/proposals/2011.009a-mP.A.v3.split_Necrovirus.pdf>  Scheets, K., White, K.A., Rubino, L., Martelli, G., Rochon, D.A. 2015. ICTV taxonomic proposal 2015.007a-rP.A.v1.split\_Carmovirus. Divide the genus *Carmovirus* (family *Tombusviridae*) into three new genera: *Alphacarmovirus*, *Betacarmovirus*, and *Gammacarmovirus.*<https://talk.ictvonline.org/files/ictv_official_taxonomy_updates_since_the_8th_report/m/plant-official/5841>  Simon, A.E., Miller, W.A. 2013. 3' cap-independent translation enhancers of plant viruses. Annu Rev Microbiol 67, 21-42. |