This form should be used for all taxonomic proposals. Please complete all those modules that are applicable.

For guidance, see the notes written in blue and the separate document “Help with completing a taxonomic proposal”

Please try to keep related proposals within a single document.

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

|  |  |  |  |  |  |
| --- | --- | --- | --- | --- | --- |
| **Code assigned:** | ***2017.005P*** | | | | (to be completed by ICTV officers) |
| **Short title:** Two new species in the genus *Nepovirus*; two new species in the genus *Fabavirus*; one unassigned species in the family *Secoviridae.* | | | | | |
| **Modules attached**  (Modules 1, 4 and either 2 or 3 are required. | | **1**  **2  3  4** | | | |
| **Author(s):** | | | | | |
| |  |  | | --- | --- | | Jeremy R. Thompson (Chair) | [jrt36@cornell.edu](mailto:jrt36@cornell.edu) | | Alexander V. Karasev | [akarasev@uidaho.edu](mailto:akarasev@uidaho.edu) | | Hélène Sanfacon | [Helene.Sanfacon@agr.gc.ca](mailto:Helene.Sanfacon@agr.gc.ca) | | Indranil Dasgupta | [Indranil58@yahoo.co.in](mailto:Indranil58@yahoo.co.in) | | Ioannis Tzanetakis | [itzaneta@uark.edu](mailto:itzaneta@uark.edu) | | Karel Petrzik | [petrzik@umbr.cas.cz](mailto:petrzik@umbr.cas.cz) | | Marc Fuchs | [mf13@cornell.edu](mailto:mf13@cornell.edu) | | Nobu Yoshikawa | [yoshikawa@iwate-u.ac.jp](mailto:yoshikawa@iwate-u.ac.jp) | | René van der Vlugt | [Rene.vanderVlugt@wur.nl](mailto:Rene.vanderVlugt@wur.nl) | | Thierry Wetzel | [thierry.wetzel@agroscience.rlp.de](mailto:thierry.wetzel@agroscience.rlp.de) | | Toru Iwanami | [tiwsw37@affrc.go.jp](mailto:tiwsw37@affrc.go.jp) | | | | | | |
| **Corresponding author with e-mail address:** | | | | | |
| |  |  | | --- | --- | | Jeremy R. Thompson | [jrt36@cornell.edu](mailto:jrt36@cornell.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) | | | ***Secoviridae*** | | |
| **ICTV Study Group comments (if any) and response of the proposer:** | | | | | |
|  | | | | | |
|  | | | | | |
| Date first submitted to ICTV: | | | |  | |
| Date of this revision (if different to above): | | | |  | |

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

**Part 2**: **PROPOSED TAXONOMY**

|  |
| --- |
| Present the proposed new taxonomy on accompanying spreadsheet |
| **Name of accompanying spreadsheet: 2017.005P.N.v1.Secoviridae\_5sp** |

Please display the taxonomic changes you are proposing on the accompanying spreadsheet module 2017\_TP\_Template\_Excel\_module. Submit both this and the spreadsheet to the appropriate ICTV Subcommittee Chair.

**Part 3:** **NON-STANDARD**

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

|  |
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| non-standard proposal |
| **Title of proposal:** |
| **Text of proposal:** |
|  |

**Part 4:** **APPENDIX**: supporting material

Table 1. Summary of the evidence published for each novel virus.

|  |  |  |  |  |  |  |
| --- | --- | --- | --- | --- | --- | --- |
| **Acronym** | **Name** | **RNA1** | **RNA2** | **Sequencing Method** | **Biological support** | **Reference** |
| GFabV | grapevine fabavirus | KX241482 | KX241485 | total RNA, Illumina NextSeq 500, 50nt reads | grafting confirmed by RT-PCR | Al Rwahnih et al (2016) |
| PrVF | Prunus virus F | KX269865 | KX269871 | Plant Ribo-Zero, 50 bp single-end read Illumina HiSeq 2000 platform, RACE | grafting confirmed by RT-PCR | Villamor et al (2017) |
| PVB | potato nepovirus B | KX656670 | KX656671 | total RNA, Illumina Hiseq 2000 platform in 50 bp single end read, RACE | field isolates | De Souza et al (2017) |
| SLSV | soybean latent spherical virus | KX424571 | KX424572 | total RNA & rRNA depleted, Illumina HiSeq 2500 | infectious clones reported | Yasmin et al (2017) |
| DMaV | Dioscorea mosaic associated virus | KU215538 | KU215539 | total RNA, Illumina HiSeq 2000, 100-base paired-end reads, RACE | none | Hayashi et al (2017) |

Species demarcation criteria in the family Secoviridae as outlined in the Tenth Report (Thompson et al, 2017)

Useful criteria to demarcate species are:

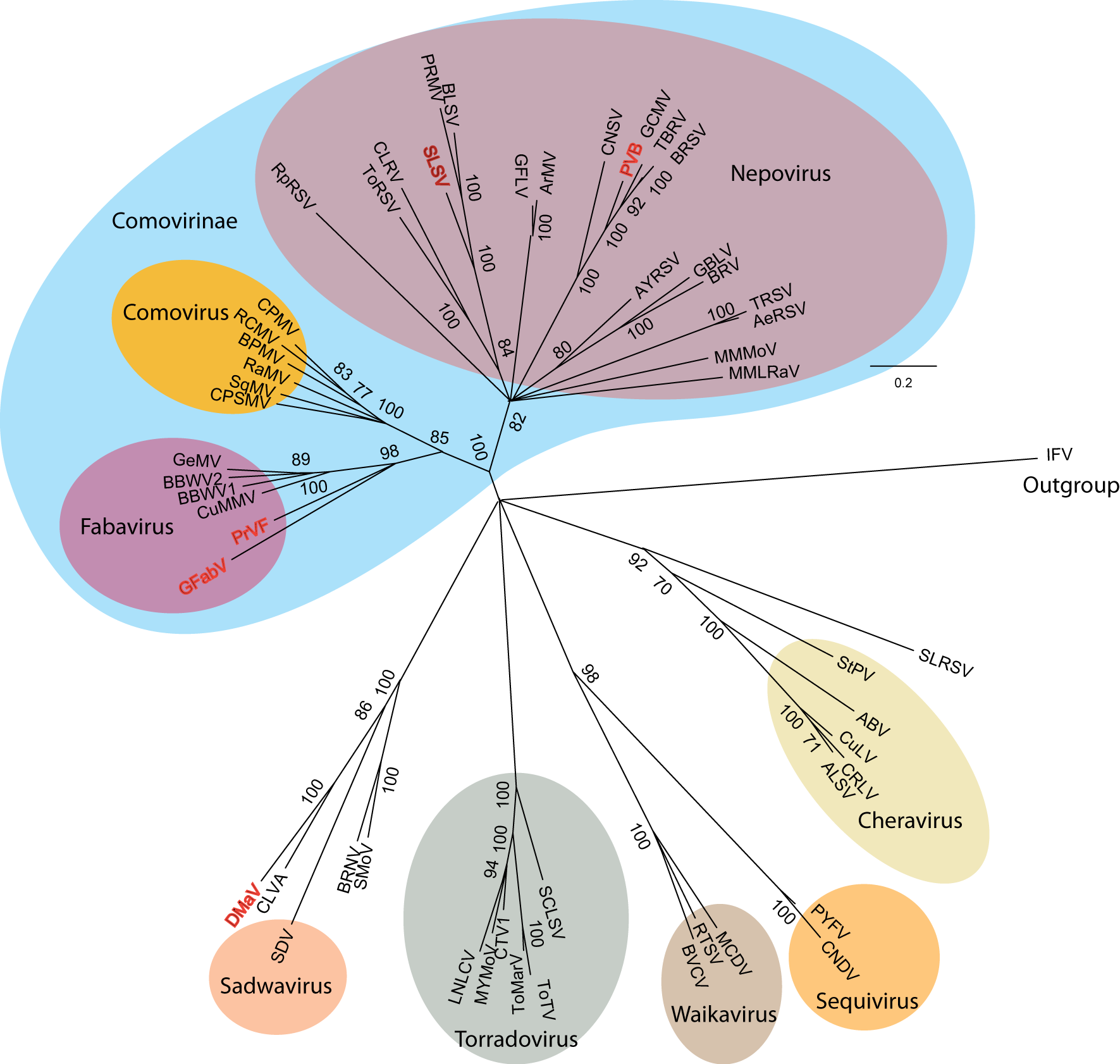
* CP aa sequence with less than 75% identity (for viruses with two or three CPs, combined CP sequences are considered)
* Conserved Pro-Pol region aa sequence (defined as the region between the conserved CG motif in the protease and GDD motif in the RNA-dependent RNA polymerase) with less than 80% identity
* Differences in antigenic reactions
* Distinct host range
* Distinct vector specificity
* Absence of cross-protection
* For viruses with a bipartite genome, absence of reassortment between RNA1 and RNA2

**Sequence relationship of proposed new species compared to closest related species**

|  |  |  |  |  |
| --- | --- | --- | --- | --- |
| **Acronym** | **Name** | **Most closely related species (genus)** | **% aa sequence identity in the CP region** | **% aa sequence identity in the Pro-Pol region** |
| GFabV | grapevine fabavirus | Prunus virus F (fabavirus, proposed new species) | nd | 52 |
| PrVF | Prunus virus F | broad bean wilt virus 1 (CP): grapevine fabavirus (fabavirus, proposed new species) (Pro-Pol) | 27 | 52 |
| PVB | potato nepovirus B | tomato black ring virus (nepovirus) | 32 | 71 |
| SLSV | soybean latent spherical virus | blueberrry latent spherical virus (nepovirus) | 46 | 58 |
| DMaV | Dioscorea mosaic associated virus | chocolate lily virus A (unassigned) | 28 | 55 |

nd – not determined due to lack of information on cleavage sites

Based on the table above, all proposed new species meet the species demarcation criteria based on sequence relationships.



**Figure 1.** Maximum likelihood inferred phylogenetic tree of members of the family *Secoviridae* based on an alignment of amino acid sequences of the conserved domains between the “CG” motif of the 3C-proteinase and the “GDD” motif of the polymerase (Pro-Pol region) using MUSCLE (Edgar 2004) . The tree was generated with PhyML (Guindon et al., 2010) (1000 bootstrap replicates) in the TOPALi suite (Milne et al., 2009). Results are presented as an unrooted radial tree. The bar represents the genetic distance. Different genera within the family are shown within colored areas. The *Comovirinae* is shown with the light blue shading. For each species, the sequence of the exemplar isolate was used for the alignments. Branches with bootstrap values below 70% were collapsed. Virus names and abbreviations are listed below with the nucleotide (left) and protein (right) accession numbers of each exemplar isolate analyzed. The acronyms of newly proposed viruses are shown in red: Dioscorea mosaic associated virus (DMaV, KU215538 = ANV28173), grapevine fabavirus (GFaV, KX241482 = ANG55944.1), potato nepovirus B (PVB, KX656670), Prunus virus F (PrVF, KX269865 = ANH71247), soybean latent spherical virus (SLSV, KX424571 = APO15117).

Recognized species are in black: Aeonium ringspot virus (AeRSV, JX304792 = AFR67086), apple latent spherical virus (ALSV, AB030940 = BAA90870), Arabis mosaic virus (ArMV, AY303786 = AAQ73821), Arracacha virus B (AVB, JQ437415 = AFI74271), artichoke yellow ringspot virus (AYRSV, AM087671 = CAJ33467), bean pod mottle virus (BPMV, U70866 = U70866), beet ringspot virus (BRSV, D00322 = BAA00234), bellflower vein chlorosis virus (BVCV, KT238881 = ALF36838), black raspberry necrosis virus (BRNV, DQ344639 = ABC71319), blackcurrant reversion virus (BRV, AF368272= AAL36026), blueberry latent spherical virus (BLSV, AB649296 = BAL04700), broad bean wilt virus 1 (BBWV1, AB084450 = BAD00183), broad bean wilt virus 2 (BBWV2, AF225953 = AAK27841), carrot necrotic dieback virus (CNDV, EU980442 = ACJ04421), carrot torradovirus 1 (CaTV1, KF533719 = AHA85556), cherry leaf roll virus (CLRV, FR851461 = CCA64538), cherry rasp leaf virus (CRLV, AJ621357 = CAF21713), chocolate lily virus A (CLVA, JN052073 = AEV45821) cowpea mosaic virus (CPMV, X00206 = CAA25029), cowpea severe mosaic virus (CPSMV, M83830), cucurbit mild mosaic virus (CuMMV, FJ194941 = ACK76423), currant latent virus (CuLV, KT692952 = ALT45950), Cycas necrosis stunt virus (CNSV, AB073147 = BAB89369), gentian mosaic virus (GeMV, AB084452 = BAD99001), grapevine Bulgarian latent virus (GBLV, FN691934= CBL43395), grapevine chrome mosaic virus (GCMV, X15346 = CAA33405), grapevine fanleaf virus (GFLV, D00915 = BAA00761), lettuce necrotic leaf curl virus (LNLCV, KC855266 = AGR55590), maize chlorotic dwarf virus (MCDV, U67839 = AAB58882), melon mild mottle virus (MMMoV, AB518485 = BAJ16223), motherwort yellow mottle virus (MYMoV, KM229700 = AIT59085), mulberry mosaic leaf roll associated virus (MMLRaV, KC904083 = AGY34703), parsnip yellow fleck virus (PYFV, D14066 = BAA03151), peach rosette mosaic virus (PRMV, AF016626 = AAB69867), radish mosaic virus (RaMV, AB295643 = BAF75830), raspberry ringspot virus (RpRSV, AY303787 = AAQ73822), red clover mottle virus (RCMV, X64886 = CAA46104), rice tungro spherical virus (RTSV, M95497 = AAA66056), satsuma dwarf virus (SDV, AB009958 = BAA76746), squash chlorotic leaf spot virus (SCLSV, KU052530 = AMN91910), squash mosaic virus (SqMV, AB054688 = BAB62139), stocky prune virus (StPV, DQ143874 = AAZ76594), strawberry latent ringspot virus (SLRSV, AY860978 = AAW63128), strawberry mottle virus (SMoV, AJ311875 = CAC86396), tobacco ringspot virus (TRSV, U50869 = AAB03785), tomato black ring virus (TBRV, AY157993 = AAN72830), tomato marchitez virus (ToMarV, EF681764 = ABV44416), tomato ringspot virus (ToRSV, L19655 = AAA78254), tomato torrado virus (ToTV, DQ388879 = ABD38934). Outgroup: infectious flacherie virus (IFV, AB000906 = NP\_620559) (Family *Iflaviridae*; Genus *Iflavirus*).

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| **References:** |
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| Al Rwahnih, M., Alabi, O.J., Westrick, N.M., Golino, D., and Rowhani, A. 2016. Near-Complete genome sequence of grapevine fabavirus, a novel putative member of the genus *Fabavirus*. Genome Announcements 4: e00703-16.  De Souza, J., Muller, G., Perez, W., Cuellar, W., and Kreuze, J. 2017. Complete sequence and variability of a new subgroup B nepovirus infecting potato in central Peru. Archives of Virology 162:885-889.  Edgar, R. C. 2004. MUSCLE: multiple sequence alignment with high accuracy and high throughput. Nucleic Acids Research 32:1792-1797.  Hayashi, E. A. I., Blawid, R., de Melo, F. L., Andrade, M. S., Pio-Ribeiro, G., de Andrade, G. P., and Nagata, T. 2017. Complete genome sequence of a putative new secovirus infecting yam (*Dioscorea*) plants. Archives of Virology 162:317-319.  Guindon, S., Dufayard, J.F., Lefort, V., Anisimova, M., Hordijk, W., and Gascuel, O. 2010. New algorithms and methods to estimate maximum-likelihood phylogenies: assessing the performance of PhyML 3.0. Systematic Biology 59:307-321.  Milne, I., Lindner, D., Bayer, M., Husmeier, D., McGuire, G., Marshall, D. F., and Wright, F. 2009. TOPALi v2: a rich graphical interface for evolutionary analyses of multiple alignments on HPC clusters and multi-core desktops. Bioinformatics 25:126-127.  Thompson J. R., Dasgupta, I., Fuchs, M., Iwanami, T., Karasev A.V., Petrzik K., Sanfaçon H., Tzanetakis I., van der Vlugt R., Wetzel T., Yoshikawa N. and ICTV Report Consortium (2017) ICTV Virus Taxonomy Profile: *Secoviridae*. Journal of General Virology 98:529-531.  Villamor, D. E. V., Pillai, S. S., and Eastwell, K. C. 2017. High throughput sequencing reveals a novel fabavirus infecting sweet cherry. Archives of Virology 162:811-816.  Yasmin, T., Nelson, B. D., Hobbs, H. A., McCoppin, N. K., Lambert, K. N., and Domier, L. L. 2017. Molecular characterization of a new soybean-infecting member of the genus *Nepovirus* identified by high-throughput sequencing. Archives of Virology 162:1089-1092. |

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| **Annex:**  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. |