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**

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| **Code assigned:** | ***2017.003P*** | | | | (to be completed by ICTV officers) |
| **Short title: Create a new family of positive-sense RNA viruses, *Solemoviridae***  (e.g. 6 new species in the genus *Zetavirus*) | | | | | |
| **Modules attached**  (Modules 1, 4 and either 2 or 3 are required. | | **1**  **2  3  4** | | | |
| **Author(s):** | | | | | |
| Merike Sõmera  Erkki Truve  Eugenie Hebrard | | | | | |
| **Corresponding author with e-mail address:** | | | | | |
| Merike Sõmera, merike.somera@ttu.ee | | | | | |
| **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) | | | **Sobemovirus study group** | | |
| **ICTV Study Group comments (if any) and response of the proposer:** | | | | | |
| Agree with a proposition | | | | | |
|  | | | | | |
| Date first submitted to ICTV: | | | | June 2017 | |
| 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**: **PROPOSED TAXONOMY**

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| Present the proposed new taxonomy on accompanying spreadsheet |
| **Name of accompanying spreadsheet: 2017.003P.N.v1.Sobemoviridae** |

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

| additional material in support of this proposal |
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| **References:** |
| Aus dem Siepen M, Pohl JO, Koo BJ, Wege C, Jeske H. Poinsettia latent virus is not a cryptic virus, but a natural polerovirus-sobemovirus hybrid. Virology 2005, 336:240-250  Sõmera M, Sarmiento C, Truve E. Overview on Sobemoviruses and a Proposal for the Creation of the Family Sobemoviridae. Viruses 2015, 7:3076-3115 |

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| **Annex:**  Genus *Sobemovirus*, unassigned to any family, consists of viruses with monopartite (+) ssRNA genomes and isometric particles. Sobemoviruses have uniform genome structure and expression strategies (Sõmera et al, 2015).  *Poinsettia latent virus* (PnLV), a single representative of the unassigned genus *Polemovirus*, is considered as naturally occurring recombinant between polero- and sobemoviral ancestors — showing a close relationship to poleroviruses within the first three quarters of its genome but the last quarter encoding viral CP is related to sobemoviruses (aus dem Siepen, 2005).  The polyprotein (consisting of serine protease and VPg, or serine protease, VPg and RdRp) of sobemo- and polemoviruses shows sequence similarity to that of viruses from the genera *Enamovirus* and *Polerovirus* belonging in the family *Luteoviridae* as well as to that of *Mushroom bacilliform virus* (MBV), a single representative of genus *Barnavirus*, family *Barnaviridae*.  The CP of sobemo- and polemoviruses is related to CP of betanecroviruses from the family *Tombusviridae*. MBV CP sequence is unique and it is only distantly related to that of carmoviruses from the family *Tombusviridae*.  The family *Luteoviridae* includes 3 genera (*Luteovirus*, *Polerovirus* and *Enamovirus*) of viruses that encode RdRp-s belonging into two completely different lineages but have CP of common origin. Properties of the read-through region of their CP that determine exclusive transmission by aphid vectors has been used as the main argument to assign these viruses into the same family.  Classification into different genera within the family *Tombusviridae* is determined by the subtypes of RdRp, CP and MP. Common conserved feature of the members is a presence of flavivirus-like RdRp.  Family *Barnaviridae* was created for bacilliform viruses of fungi.  Here, we propose to create a new family *Solemoviridae* that would include the genera *Sobemovirus* and *Polemovirus* that do not fit into the previously mentioned evolutionary related families *Luteoviridae*, *Tombusviridae* and *Barnaviridae* but are phylogenetically related to each other both by their polyprotein and CP sequences (Figure 1).  The family name *Solemoviridae* is derived from the combination between *Sobemovirus* and *Polemovirus*.  Additional information: phylogenetic relationships of the sequences of the polyprotein, RdRp and coat protein of members of the genera *Sobemovirus*, *Polemovirus*, *Barnavirus*, *Polerovirus* and *Enamovirus* are shown in Figure 2.    Figure 1. Adapted from Sõmera et al (2015). Genome annotations of the type species of phylogenetically related families and genera. All genome annotations are shown to scale for size comparisons. RdRp genes are shown in the upper frame (frame 0); middle frame represents +1 frame and lower frame represents +2 frame. Non-canonical AUG start codon is marked with asterisk (\*). –1 ribosomal frameshifting is marked by long vertical dashed line. Read-through codon is shown by short vertical dashed line. Boxes with dashed borders: unique for the type species. Different protein functions are displayed with different colors and the homology is indicated by different tones. Color code: bright yellow—picornavirus-like RdRp; soft yellows and orange—flavivirus-like RdRp (three subgroups within *Tombusviridae* family are shown); red—serine protease; green—CP (CPs of *Tombusviridae* are presented in two different tones to distinguish CPs with protruding domains (shown in olive green) and without it (shown in dark green)); blue—movement protein (MP); lilac or purple—viral RNAi suppressor (VSR); brown—replication-associated protein (Rap); grey—no function found. VPg is depicted as a red dot at the 5’end of the genomic RNA. Virus name abbreviations: MBV—mushroom bacilliform virus (U07551); SBMV—southern bean mosaic virus (DQ875594); PnLV—poinsettia latent virus (AJ867490); PEMV-1—pea enation mosaic virus-1 (L0473); PLRV—potato leafroll virus (D00530); BYDV-PAV—barley yellow dwarf virus-PAV (X06753); CMoV—carrot mottle virus (FJ188473); CRSV—carnation ringspot virus (L18870; M88589); OCSV—oat chlorotic stunt virus (X83964); TBSV—tomato bushy stunt virus (M21958); PoLV—Pothos latent virus (X87115); MNeSV—maize necrotic streak virus (AF266518); CarMV—carnation mottle virus (X02986); FNSV—Furcraea necrotic streak virus (FJ768020); GaMV—Galinsoga mosaic virus (Y13463); TNV-A—tobacco necrosis virus-A (M33002); TNV-D—tobacco necrosis virus-D (U62546); PMV—Panicum mosaic virus (U55002); MCMV—maize chlorotic mottle virus (X14736).  C:\Users\Merike\Documents\MERIKE 2011 2012\ICTVproposal\rephylogenetictreesrelatedtoproposal\phylo Sobemoviridae final 1.tif  C:\Users\Merike\Documents\MERIKE 2011 2012\ICTVproposal\rephylogenetictreesrelatedtoproposal\phylo Sobemoviridae final 2.tif  C:\Users\Merike\Documents\MERIKE 2011 2012\ICTVproposal\rephylogenetictreesrelatedtoproposal\phylo Sobemoviridae final 3.tif  Figure 2. Phylogenetic trees inferred by maximum likelihood method from the sequences of the polyprotein (A), RdRp (B) and coat protein (C) of members of the genus *Sobemovirus* (red), *Barnavirus* (orange), *Polerovirus* (dark blue) and *Enamovirus* (light blue). The polemovirus is shown by a red arrow. Significant bootstrap values ( >0.75) are shown by a star. Virus name abbreviations: CfMV - cocksfoot mottle virus (NP941377.1); LTSV - lucerne transient streak virus (YP007438851.1); RYMV - rice yellow mottle virus (YP007438863.1); RGMoV - ryegrass mottle virus (YP007438855.1); SeMV - Sesbania mosaic virus (NP066394.1); SCPMV - southern cowpea mosaic virus (NP042303.1); SoMV - Sowbane mosaic virus (YP002158815.1); SCMoV - subterranean clover mottle virus (NP715629.1); TRoV - turnip rosette virus (YP008869288.1);  VTMoV - velvet tobacco mottle virus (YP003896040.1); ArtVA - Artemisia virus A (YP006331063.1); IYMV - Imperata yellow mottle virus (YP002308437.1); PLYV - papaya lethal yellowing virus (YP006589927.1); SYCMV - soybean yellow common mosaic virus (YP004869652.1); CyCMV - Cymbidium chlorotic mosaic virus (YP009140474.1);  RoMoV - Rottboellia yellow mottle virus (YP009142786.1); BSSV - blueberry shoestring virus (NC\_029578.1); SoNMV - Solanum nodiflorum mottle virus (YP009344993.1); AEV-1 - alfalfa enamovirus 1 (YP009249826.1); BChV -beet chlorosis virus (NP114362.1); BMYV - beet mild yellowing virus (NP612216.1); BWYV - beet western yellows virus (NP840099.1); CtLRV - carrot red leaf virus (YP077189.1); CYDV-RPS - cereal yellow dwarf virus – RPS (NP054688.1); CYDV-RPV - cereal yellow dwarf virus – RPV (NP840023.1); CCSV - chickpea chlorotic stunt virus (YP667841.1); CLRDV - cotton leafroll dwarf virus (YP003915151.1); CABYV - cucurbit aphid-borne yellows virus (NP620104.1); MYDV-RMV - maize yellow dwarf virus-RMV (YP008083742.1); MABYV - melon aphid-borne yellows virus (YP001949873.1); PeVYV - pepper vein yellows virus (YP004207919.1); SABYV - Suakwa aphid-borne yellows virus (YP006666509.1); SCYLV - sugarcane yellow leaf virus (NP050008.1); TVDV - tobacco vein distorting virus (YP001931933.1); TuYV - turnip yellows virus (NP620488.1).  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. |