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:** | ***2017.013P*** | | | | (to be completed by ICTV officers) |
| **Short title: 3 new species in the genus *Ilarvirus*** | | | | | |
| **Modules attached**  (Modules 1, 4 and either 2 or 3 are required. | | **1**  **2  3  4** | | | |
| **Author(s):** | | | | | |
| Bujarski, J., Gallitelli, D, Reddy, M.K., Garcia-Arenal, F, Wang, A., Scott, S.W | | | | | |
| **Corresponding author with e-mail address:** | | | | | |
| Simon W. Scott sscott@clemson.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) | | | ***Bromoviridae*** | | |
| **ICTV Study Group comments (if any) and response of the proposer:** | | | | | |
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| 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:** |
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**Part 2**: **PROPOSED TAXONOMY**

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| Present the proposed new taxonomy on accompanying spreadsheet |
| **Name of accompanying spreadsheet: 2017.013P.N.v1.Ilarvirus\_3sp** |

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

| additional material in support of this proposal |
| --- |
| **References:** |
| 1) Pallas, V., Aparicio F, Herranz, M.C., Sanchez-Navarro, J.A., Scott, S.W. (2013) The Molecular Biology of Ilarviruses. Advances in Virus Research, 87: 139-181.  2) Scott SW, Zimmerman MT, Ge X (2003) Viruses in subgroup 2 of the genus *Ilarvirus* share properties at the molecular level. Arch. Virol. 148:2063–2075  3) Tzanetakis, I.E., Martin, R.R., Scott, S.W. 2010 Genomic sequences of blackberry chlorotic ringspot virus and strawberry necrotic shock virus and the phylogeny  of viruses in subgroup 1 of the genus *Ilarvirus*. Arch. Virol. 155:557–561  3) Adkins S, Baker CA, Badillo-Vargas IE, Frantz G, Mellinger HC, Roe N, Funderburk JE, 2015. Necrotic streak disease of tomato in Florida caused by a new ilarvirus species related to *Tulare apple mosaic virus*. New Disease Reports 31:16. [[http://dx.doi.org/10.5197/j.2044-0588.2015.031.01](http://dx.doi.org/10.5197/j.2044-0588.2015.031.016)  4) Badillo-Vargas, I. E., Baker, C. A., Turechek, W. W., Frantz, G., Mellinger, H. C., Funderburk, J. E., and Adkins, S. 2016. Genomic and biological characterization of Tomato necrotic streak virus, a novel subgroup 2 ilarvirus infecting tomato in Florida. Plant Dis. 100:1046-1053. 5) Batuman, O., Miyao, G. Y.-W. Kuo,Y-W, Chen,L-F, Davis, R.M.and Gilbertson, R.L. (2009) An outbreak of a necrosis disease of tomato in California in 2008 was caused by a new ilarvirus species related to Parietaria mottle virus Plant Disease 93: 546 6) Sharman, M. and Thomas, J.E. (2013) Genetic diversity of subgroup 1 ilarviruses from eastern Australia. Arch Virol. 158:1637–1647 7) Aboughanem-Sabanadzovic, N., Tzanetakis, I.E., Lawrence, A. Stephenson, R.C and Sabanadzovic, S. (2016) A Novel Ilarvirus Is Associated with Privet Necrotic Ringspot Disease in the Southern United States. Phytopathology 106: 87-93 |

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| **Annex:**  In the 9th report of the ICTV, criteria accepted for demarcation of species within the genus *Ilarvirus* are: serology, host range, and sequence similarity (specific levels of sequence similarity were not defined).  Ilarviruses had been grouped on the basis of serological relationships (1). The report of a “new ilarvirus” (isometric virus, tripartite genome, characteristic size of genomic molecules, recalcitrant in inoculation and purification) in a previously unreported plant host typically led to the creation of a new species with a corresponding name. However, panels of virus isolates and antibodies that would allow rigorous comparisons between a previously unreported virus and all accepted species do/did not exist.  As both nucleotide sequence data and putative amino acid sequence data for the members of this genus have accumulated, it has become clear that some of these earlier assignations were erroneous and changes have been made to the taxonomy. Some of the groupings have been confirmed, whereas some of them have been shown to be inappropriate. For example, Hydrangea mosaic virus, described in 1983, was later shown by comparative sequencing of type isolates of both viruses to be elm mottle virus which had been described originally in the 1960s and 1970s (2).  Phylogenetic trees produced using either nucleotide sequence data or putative amino acid sequence data clearly support 4 subgroups and two additional species (*American plum line pattern virus* [APLPV] and *Humulus japonicas latent virus* [HJLV] that do not cluster within these groups (3).  The complete genomes for three new viruses have been described:  Ageratum latent virus (AgLV) JX463340, JX463341, JX463342  Privet ringspot virus (PrRSV) KT290039, KT290040, KT290041  Tomato necrotic streak virus (TomNSV) KT779204, KT779205, KT779206  Ageratum latent virus (AgLV) was isolated from a previously unreported host species and shows less than 75% amino acid identity with the p1 protein, p2 protein and CP of tobacco streak virus (TSV)*,* type species of the genus and a member of subgroup 1, (6). In the phylogenetic tree based on concatenated aa sequences of all viral proteins (Fig. 1), it is distant from TSV.  Privet ringspot virus (PrRSV) (7) was reported in a host never previously associated with infection by members of the genus. It is also a subgroup 1 virus. It shows less than 70% amino acid identity with the p1 protein, p2 protein and CP of tobacco streak virus (TSV) but in Fig. 1 clusters with isolates of three ilarviruses [TSV, strawberry necrotic shock virus (SNSV), and blackberry chlorotic ringspot virus (BCRV)].  Tomato necrotic streak virus (TomNSV) (4,5), is clearly related to members of subgroup 2 of the genus *Ilarvirus*, with its CP sharing 84% aa identity with TAMV. The only previous report (5) of an ilarvirus named from a disease observed in tomato (tomato necrotic spot virus reported from the US) clusters with Parietaria mottle virus, a virus in subgroup 1 reported to cause disease problems in tomato in Europe. No direct comparison of the isolates from the US and Europe has yet been published.  Based on the isolation of these viruses from previously unreported hosts, the percentage aa identity with accepted members, and the groupings within the phylogenetic tree it is proposed that tomato necrotic streak virus, Ageratum latent virus and privet ringspot virus be accepted as members of new homonymous species (*Tomato necrotic streak virus, Ageratum latent virus and Privet ringspot virus,* respectively) in the genus *Ilarvirus*. |
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Figure 1. An unrooted tree for accepted and putative members of the family *Bromoviridae* based on concatenated amino acid sequences of the four products encoded by all members.

The putative aa sequences of each of products of the four ORFs common to all members of the *Bromoviridae* were aligned using Clustal Omega [9] on the EMBL-EBI web service [6]. Geneious v6.1.8 [3] was used to concatenate the four genes for a final length of 3,049 amino acids. To identify the optimal partitioning strategy and model of evolution for each partition, a ‘greedy’ analysis in PartitionFinder v2.0.0 [4,[5](#_ENREF_5)] using RAxML was completed. The optimal partitioning scheme was determined using the Bayesian information criterion (BIC; [[8](#_ENREF_8)]).

The evolutionary relationships among the viruses were reconstructed using maximum likelihood methods. The maximum likelihood analysis of each dataset was conducted using RAxML-HPC2 on XSEDE v8.2.9 [[10](#_ENREF_10)] with the default settings on the CIPRES Science Gateway [[7](#_ENREF_7)]. The PROTCAT+I+G model was applied to all partitions based on the results of the PartitionFinder analysis that demonstrated the lowest BIC score was achieved with the gamma and invariable sites model of rate heterogeneity. Support for each of the topologies was determined using 1,000 bootstrap pseudoreplicates [[1](#_ENREF_1)]. The most likely trees were visualized using FigTree v1.4.2 (<http://tree.bio.ed.ac.uk/software/figtree/>).

The subgroups of the ilarviruses are delineated using blue boxes.

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Table 1. List of currently accepted species in the family *Bromoviridae* with acronyms for typical virus isolate(s) for each species and corresponding sequence Accession Numbers used for constructing the phylogenetic tree along with those discussed in this proposal: Ageratum latent virus (AgLV), privet ringspot virus (PrRSV) and tomato necrotic streak virus (TomNSV) .

Genbank accessions of genomic molecules

Virus acronym RNA 1 RNA2 RNA3

Genus: *Alfamovirus*

*Alfalfa mosaic virus* AMV L00163 X01572 K02703

Genus: *Anulavirus*

*Pelargonium zonate spot virus* PZSV AJ272327 AJ272328 AJ272329

*Amazon lily mild mottle virus* ALiMMV AB724113 AB72414 AB724115

*Cassava Ivorian bacilliform virus* CIBV KF742519 KF742520 KF742521

Genus: *Bromovirus*

*Brome mosaic virus* BMV X02380 X01678 J02042

*Broad bean mottle virus* BBMV M65138 M64713 M60291

*Cassia Yellow blotch virus* CYBV AB194806 AB194807 AB194808

*Cowpea chlorotic mottle virus* CCMV M65139 M28817 M298818

*Melandrium yellow fleck virus* MYFV AB444583 AB444584 AB444585

*Spring beauty latent virus* SBLV AB080598 AB080599 AB080600

Genus: *Cucumovirus*

*Cucumber mosaic virus* CMVFny D00356 D00355 D10538

CMVQ X02733 D00985 M21464

*Peanut stunt virus* PSV U15728 U15729 U15730

*Tomato aspermy virus* TAV D10044 D10663 AJ277268

*Gayfeather mild mottle virus* GMMV FM881899 FM881900 FM881901

Genus: *Ilarvirus*

Subgroup 1

*Tobacco streak virus* TSV U80934 U75538 X00435

*Blackberry chlorotic ringspot virus* BCRV DQ091193 DQ091194 DQ091195

*Parietaria mottle virus* PMoV AY496068 AY496069 U35145

*Strawberry necrotic shock virus* SNSV DQ318818 AY743591 AY363228

Subgroup 2

*Asparagus virus-2* AV-2 EU919666 EU919667 X86352

*Citrus leaf rugose virus* CiLRV U23715 U17726 U17390

*Citrus variegation virus*  CVV EF584664 EF584865 U17389

*Elm mottle virus* EMoV U57047 U34050 U85399

*Lilac ring mottle virus*  LiRMV EU919669**†** EU919668 U17391

*Spinach latent v irus* SpLV U93192 U93193 U93194

*Tulare apple mosaic virus* TAMV AF226160 AF226161 AF226162

Subgroup 3

*Apple mosaic virus* ApMV AF174584 AF174585 U15608

*Bluberry shock virus* BLShV [KF031037](https://www.ncbi.nlm.nih.gov/nuccore/KF031038) [KF031038](https://www.ncbi.nlm.nih.gov/nuccore/KF031038) KF031039

*Lilac leaf chlorosis virus*  LLCV HE572565 FN669168 FN669169

*Prunus necrotic ringspot virus* PNRSV AF278534 AF278535 U57046

Subgroup 4

*Fragaria chiloensis virus* FCiLV AY682102 AY707771 AY707772

*Prune dwarf virus* PDV U57648 AF277662 L28145

Ungrouped

*American plum line pattern virus* APLPV AF235033 AF235165 AF235166

*Humulus japonicus latent virus*  HJLV AY500236 AY500237 AY500238

Genus: *Oleavirus*

*Olive latent virus 2* OLV-2 X94346 X94347 X76993

***Viruses discussed in this proposal are highlighted in red***

Ageratum latent virus AgLV JX463340 JX463341 JX463342  
privet ringspot virus PrRSV KT290039 KT290040 KT290041

tomato necrotic streak virus TomNSV KT779204 KT779205 KT779206