This form should be used for all taxonomic proposals. Please complete all those modules that are applicable (and then delete the unwanted sections). 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; you can copy the modules to create more than one genus within a new family, for example.

MODULE 1: **TITLE, AUTHORS, etc**

Code assigned:	***2010.016aP***	(to be completed by ICTV officers)

Short title: 1 new species in the genus Ilarvirus
(e.g. 6 new species in the genus *Zetavirus*)

Modules attached (modules 1 and 9 are required)	**1** ☒	**2** ☒	**3** ☐	**4** ☐	**5** ☐
	6 ☐	**7** ☐	**8** ☐	**9** ☒	

Author(s) with e-mail address(es) of the proposer:

Simon Scott(sscott@clemson.edu) on behalf of the Bromoviridae SG

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 (fungal, invertebrate, plant, prokaryote or vertebrate viruses)	Bromoviridae

ICTV-EC or Study Group comments and response of the proposer:

Date first submitted to ICTV:
Date of this revision (if different to above):

MODULE 2: **NEW SPECIES**

creating and naming one or more new species.

If more than one, they should be a group of related species belonging to the same genus. All new species must be placed in a higher taxon. This is usually a genus although it is also permissible for species to be “unassigned” within a subfamily or family. Wherever possible, provide sequence accession number(s) for one isolate of each new species proposed.

Code	***2010.016aP***	(assigned by ICTV officers)

To create new species within:

Genus:	***Ilarvirus***
Subfamily:	
Family:	***Bromoviridae***
Order:	

Fill in all that apply.
- If the higher taxon has yet to be created (in a later module, below) write “**(new)**” after its proposed name.
- If no genus is specified, enter “**unassigned**” in the genus box.

And name the new species:	**GenBank sequence accession number(s) of reference isolate:**
Lilac leaf chlorosis virus	`FN669168 (RNA2), FN669169 (RNA3)`

Reasons to justify the creation and assignment of the new species:
- Explain how the proposed species differ(s) from all existing species.
  - If species demarcation criteria (see module 3) have previously been defined for the genus, **explain how the new species meet these criteria**.
  - If criteria for demarcating species need to be defined (because there will now be more than one species in the genus), please state the proposed criteria.
- Further material in support of this proposal may be presented in the Appendix, Module 9

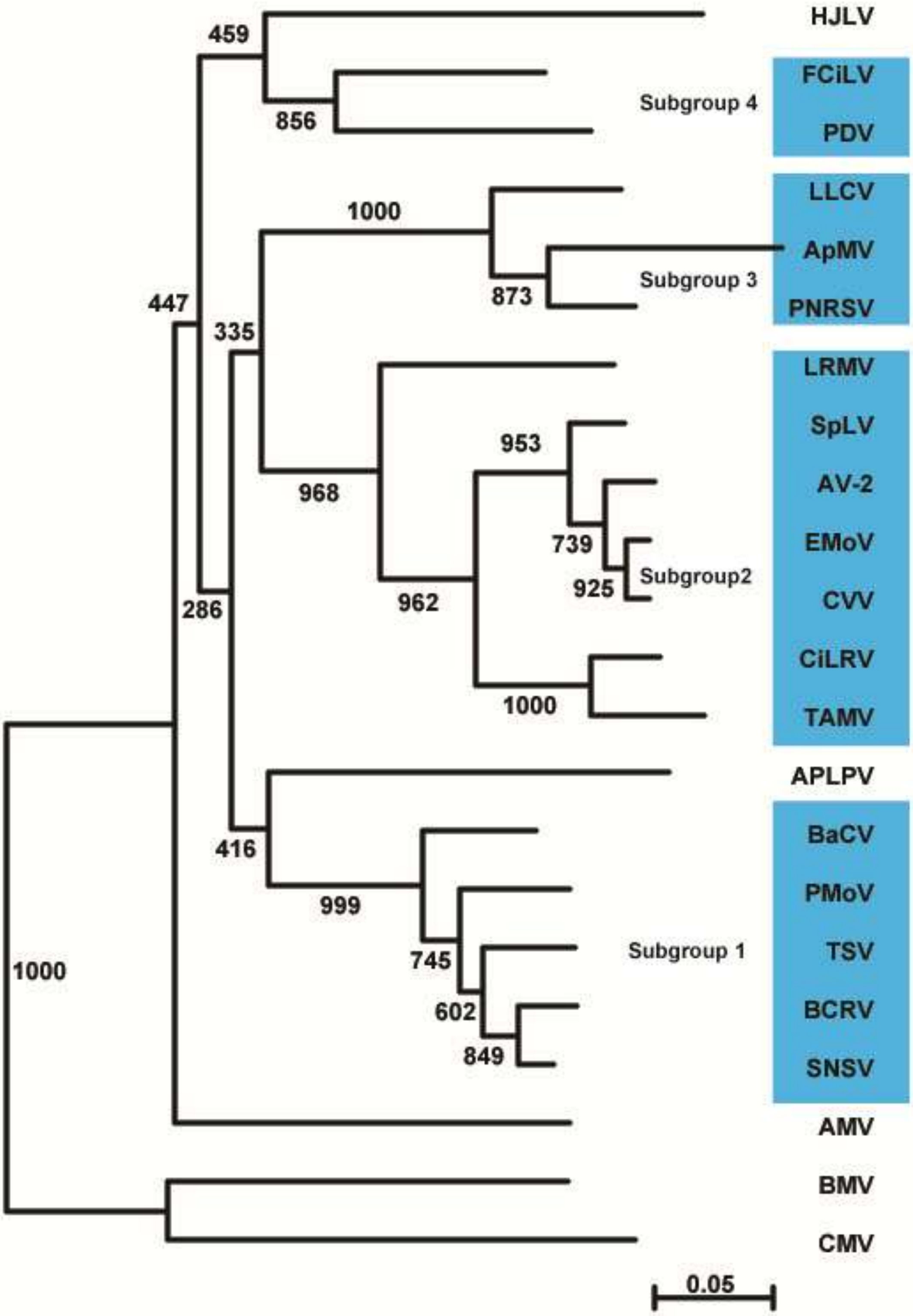
Species demarcation criteria at the molecular level do not currently exist for members within this genus. Previously, species have been assigned to subgroups (1-6) based on serological relationships (See 8th report). Sequence data suggest that some of these assignations may have been erroneous. Phylogenetic analyses and sequence comparisons indicate relationships between LLCV and Apple mosaic virus and Prunus necrotic ringspot virus the two members of subgroup 3 for which complete genomic sequence is available.

LLCV is unrelated to the other ilarvirus previously reported to infect Lilac (Lilac ring mottle virus) which is a member of subgroup 2.

LLCV is the first ilarvirus assigned to subgroup 3 for a number of years. Blueberry shock virus is assigned to subgroup 3 but there is no published sequence information. A preliminary sequence of the coat protein of this virus confirmed its relationship to PNRSV and ApMV. HJLV was assigned to subgroup 3 in the original description of the virus on the basis of a serological relationship. However, the genomic sequence does not support this as is shown in Figure 1.

Figure 1

A phylogenetic (NJ) tree constructed from a multiple alignment of the putative aa sequences of the polymerase signature defined by Candresse et al. (1990) Res Virol 141: 315-329 of members of the genus *Ilarvirus* and Alfalfa mosaic virus, using CLUSTAL X, and using Cucumber mosaic and Brome mosaic viruses as the outgroups. The acronyms of the viruses and the genomic sequences from which the polymerase signatures used in this comparison were extracted are: alfalfa mosaic virus (AMV), NC_002024; American plum line pattern virus (APLPV), NC_003452; apple mosaic virus (ApMV), NC_003465; asparagus virus 2 (AV-2), NC_011809; Bacopa chlorosis virus (BaCV), FJ607141; blackberry chlorotic ringspot virus (BCRV), NC_011554; brome mosaic virus (BMV), NC_002027; citrus leaf rugose virus (CiLRV), NC_003547; citrus variegation virus (CVV), NC_009538; cucumber mosaic virus (CMV), NC_002055; elm mottle virus (EMoV), NC003568; Fragaria chiloensis latent virus (FCILV), NC_006567; Humulus japonicus latent virus (HJLV), NC_ 006065; lilac leaf chlorosis virus (LLCV), FN669168; lilac ring mottle virus (LRMV), NC_003568; Parietaria mottle virus (PMoV), NC_005849; prune dwarf virus (PDV), NC_008037; Prunus necrotic ringspot virus (PNRSV), NC_004363; spinach latent virus (SpLV), NC_003809; strawberry necrotic shock virus (SNSV), NC_008707; tobacco streak virus (TSV), NC_003842; tulare apple mosaic virus (TAMV), NC_003834. Bootstrap values for individual branches are indicated using 1000 replicates. Bootstrap values of less than 70% are generally regarded as insignificant and the branches could be drawn as a polytomy but they are separated because of biological significance. The four currently accepted subgroups of ilarviruses are indicated.


HJLV
FCiLV
PDV
Subgroup 4
LLCV
ApMV
PNRSV
Subgroup 3
LRMV
SpLV
AV-2
EMoV
CVV
CiLRV
TAMV
Subgroup2
APLPV
BaCV
PMoV
TSV
BCRV
SNSV
Subgroup 1
AMV
BMV
CMV
459
856
1000
873
447
335
968
953
739
925
286
962
1000
416
999
745
602
849
1000
0.05

MODULE 9: **APPENDIX**: supporting material

additional material in support of this proposal

References:

James,D., Varga,A., Leippi,L., Godkin,S. and Masters,C. Sequence analysis of RNA 2 and RNA 3 of lilac leaf chlorosis virus: a putative new member of the genus Ilarvirus Arch. Virol. 155: 993-998 (2010)

Annex:

Include as much information as necessary to support the proposal, including diagrams comparing the old and new taxonomic orders. The use of Figures and Tables is strongly recommended but direct pasting of content from publications will require permission from the copyright holder together with appropriate acknowledgement as this proposal will be placed on a public web site. For phylogenetic analysis, try to provide a tree where branch length is related to genetic distance.