



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:	2010.005aP	(to be completed by ICTV officers)
Short title: 2 new species in the genus <i>Ilarvirus</i> (e.g. 6 new species in the genus <i>Zetavirus</i>)		
Modules attached (modules 1 and 9 are required)	1 <input checked="" type="checkbox"/> 2 <input checked="" type="checkbox"/> 3 <input type="checkbox"/> 4 <input type="checkbox"/> 5 <input type="checkbox"/> 6 <input type="checkbox"/> 7 <input type="checkbox"/> 8 <input type="checkbox"/> 9 <input checked="" type="checkbox"/>	

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	2010.005aP	(assigned by ICTV officers)
To create 2 new species within:		
Genus:	<i>Ilarvirus</i>	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.
Subfamily:		
Family:	<i>Bromoviridae</i>	
Order:		
And name the new species:		GenBank sequence accession number(s) of reference isolate:
<i>Blackberry chlorotic ringspot virus</i>		DQ091193, DQ091194, DQ091195
<i>Strawberry necrotic shock virus</i>		DQ318818, AY743591, AY363228

<p>Reasons to justify the creation and assignment of the new species:</p> <ul style="list-style-type: none"> • Explain how the proposed species differ(s) from all existing species. <ul style="list-style-type: none"> ○ 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 assignments may have been erroneous. Phylogenetic analyses and sequence comparisons indicate relationships between Blackberry chlorotic ringspot virus (BCRV) and Strawberry necrotic shock virus (SNSV) with Tobacco streak virus (TSV) -type species of the genus. However, there are significant differences between the sequences of TSV, BCRV and SNSV.

The name SNSV had previously been associated with the virus inducing the disease strawberry necrotic shock. A second ilarvirus, Black raspberry latent virus (BLRV) had also been reported. Later work indicated serological relationships between these two viruses and TSV (the type species of the genus) and the names BLRV and SNSV were subsequently relegated to the status of synonyms of TSV.

Molecular characterization of an ilarvirus isolated from both *Rubus* and *Fragaria* revealed that it was unique and the name strawberry necrotic shock virus (SNSV) was resurrected.

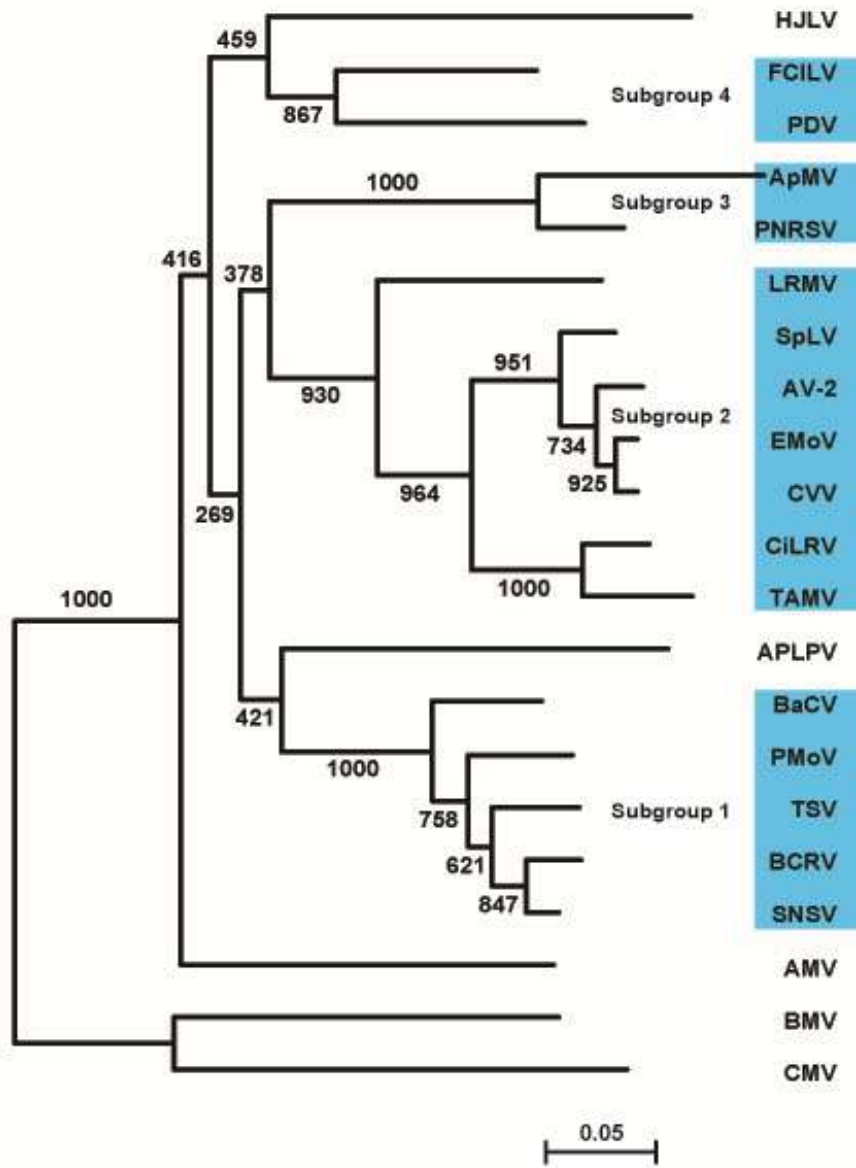
Blackberry chlorotic ringspot virus (BCRV) was described in *Rubus* and rose. This virus showed no serological relationship with either BRLV or SNSV using antisera that in previous work had shown relationships between these two viruses and TSV.

Even though there are conserved motifs in the 2b, 3a and CPs of these viruses, there are sufficient differences in these virus proteins that interact intimately with the host for these viruses to be considered distinct species. The amino acid sequences of the CPs of these three viruses share levels of identity of 50-60%.

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 *Iilarvirus* 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 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.

Figure 1



MODULE 9: **APPENDIX**: supporting material

additional material in support of this proposal

References:

Jones AT, McGavin WJ, Gepp V, Scott SW, Zimmerman MT (2006) Purification and properties of blackberry chlorotic ringspot, a new virus species in Subgroup 1 of the genus Ilarvirus found naturally infecting blackberry in the UK. *Ann Appl Biol* 149:125-135

Tzanetakis IE, Mackey IC, Martin RR, (2004) Strawberry necrotic shock virus is a distinct virus and not a strain of Tobacco streak virus. *Arch. Virol.* 149: 2001-2011.

Tzanetakis IE, Martin RR, Scott,SW (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

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.
