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:	***2009.015a,bV***	(to be completed by ICTV officers)

Short title: Create a new virus species, *Spring viraemia of carp virus*, in the genus *Vesiculovirus*, in the family *Rhabdoviridae*, in the order *Mononegavirales*
(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:

David Stone
david.stone|@cefas.co.uk

Has this proposal has been seen and agreed by the relevant study group(s)? Please select answer in the box on the right	**Yes**

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

Checked by SGS, waiting for SG confirmation

Date first submitted to ICTV:	26.05.09
Date of this revision (if different to above):	22.06.09

MODULE 2: **NEW SPECIES**

Part (a) to create and name one or more new species.

If more than one, they should be a group of related species belonging to the same genus (see Part b)

Code	***2009.015aV***	(assigned by ICTV officers)

To create 1 new species with the name(s):

Spring viraemia of carp virus

Part (b) assigning new species to higher taxa

All new species must be assigned to a higher taxon. This is usually a genus although it is also permissible for species to be "unassigned" within a subfamily or family.

Code	***2009.015bV***	(assigned by ICTV officers)

To assign the species listed in section 2(a) as follows:

Genus:	***Vesiculovirus***
Subfamily:	
Family:	***Rhabdoviridae***
Order:	***Mononegavirales***

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.

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.
- Provide Genbank accession numbers (not RefSeq accessions) for genomic sequences
- Further material in support of this proposal may be presented in the Appendix, Module 9

The complete genome sequence of *Spring viraemia of carp virus* (SVCV) has been deposited with Genbank (AJ318079) and it shares sufficient organisational and sequence similarities to VSIV and the other recognised Vesiculoviruses to justify recognition as a species within the genus, *Vesiculovirus*. SVCV has five major structural proteins designated N, P M, G and L. The genome is approximately 11.1kb in length with a short leader sequence that preceeds the N gene and a short non translated region following the L gene. The genome does not have the Nv protein gene found in the Novirhabdoviruses.

SVCV is considered a separate species within the genus based on genetics, host range and replication characteristics.
Phylogenetic analysis based on the complete N , P and G proteins of the rhabdoviruses assigns SVCV to the *Vesiculoviruses* genus (module 9) and separated from the *Novirhabdovirus and Sinichuvirus,* the two rhabdovirus genera containing fish viruses.
Similar to viruses assigned to the genus, *Novirhabdovirus* and the newly proposed genus, *Sinichuvirus* (proposal submitted in May 2009), the replication temperature range of SVCV is typically lower than those of other rhabdoviruses; reflecting the aquatic poikilothermic nature of the host species. The viruses are typically isolated on cultured fish cell lines at 15-25ºC.

Partial L-gene and G gene sequences are available for a range of SVCV isolates from different geographical areas and for a number of viruses that it is proposed are considered tentative species within the genus (Stone *et al* 2003; Betts *et al* 2003). Phylogenetic analysis based on partial G-gene sequences has identified four subtypes of SVCV that are separated based on geographical origins (Stone *et al.* 2003). These viruses shared 82.7%-100% nucleotide identity. Similar subgroups of SVCV are observed when analysing partial L or complete P gene sequences (Miller et al. 2007, Sheppard et al. 2007)

MODULE 9: **APPENDIX**: supporting material

additional material in support of this proposal

References:

Dikkeboom, A., Radi, C., Toohey Kurth, K., Marcquenski S., Engel, M., Goodwin, A., Way, K., Stone, D and Longshaw C. (2004). First Report of Spring Viremia of Carp Virus in wild North American Common Carp (Cyprinus carpio) from Cedar Lake, Wisconsin. Journal of Aquatic Health 16:169-178

Hoffmann,B., Schutze,H. and Mettenleiter,T.C. Determination of the complete genomic sequence and analysis of the gene products of the virus of Spring Viremia of Carp, a fish rhabdovirus. Virus Res. 84 (1-2), 89-100 (2002)],

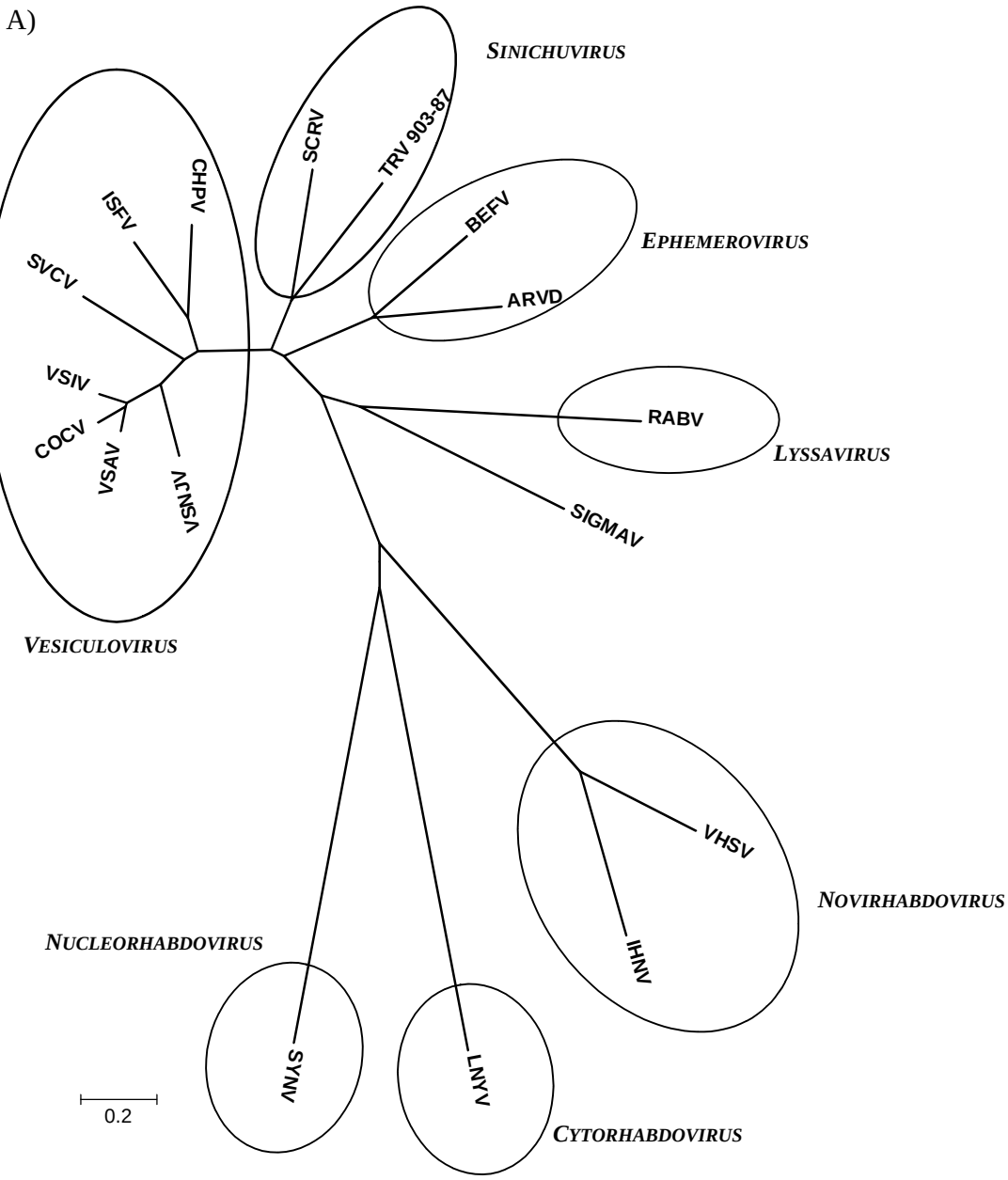
Miller, O. , Fuller, F. J.,Gebreyes, W.A., Lewbart, G.A., Shchelkunov, I.S., Shivappa, R.B.,Joiner, C., Woolford, G. Stone , D.M., Dixon, P.F., Raley , M.E., and Levine, J.F. (2007)Phylogenetic Analysis of Phosphoprotein and Gylcoprotein Gene Sequences of Recent Isolates of Spring Viremia of Carp Reveals Common Origins for Viruses Isolated in theUnited States and the United Kingdom. Dis Aquat. Org 76; 193-204

Sheppard A. M., LeDeuff R. M., Way K., and Stone D. M., (2007). Genotyping spring vireamia of carp virus and other piscine vesiculotype viruses using reverse hybridisation Dis Aquat. Org.76 (2) 163-168

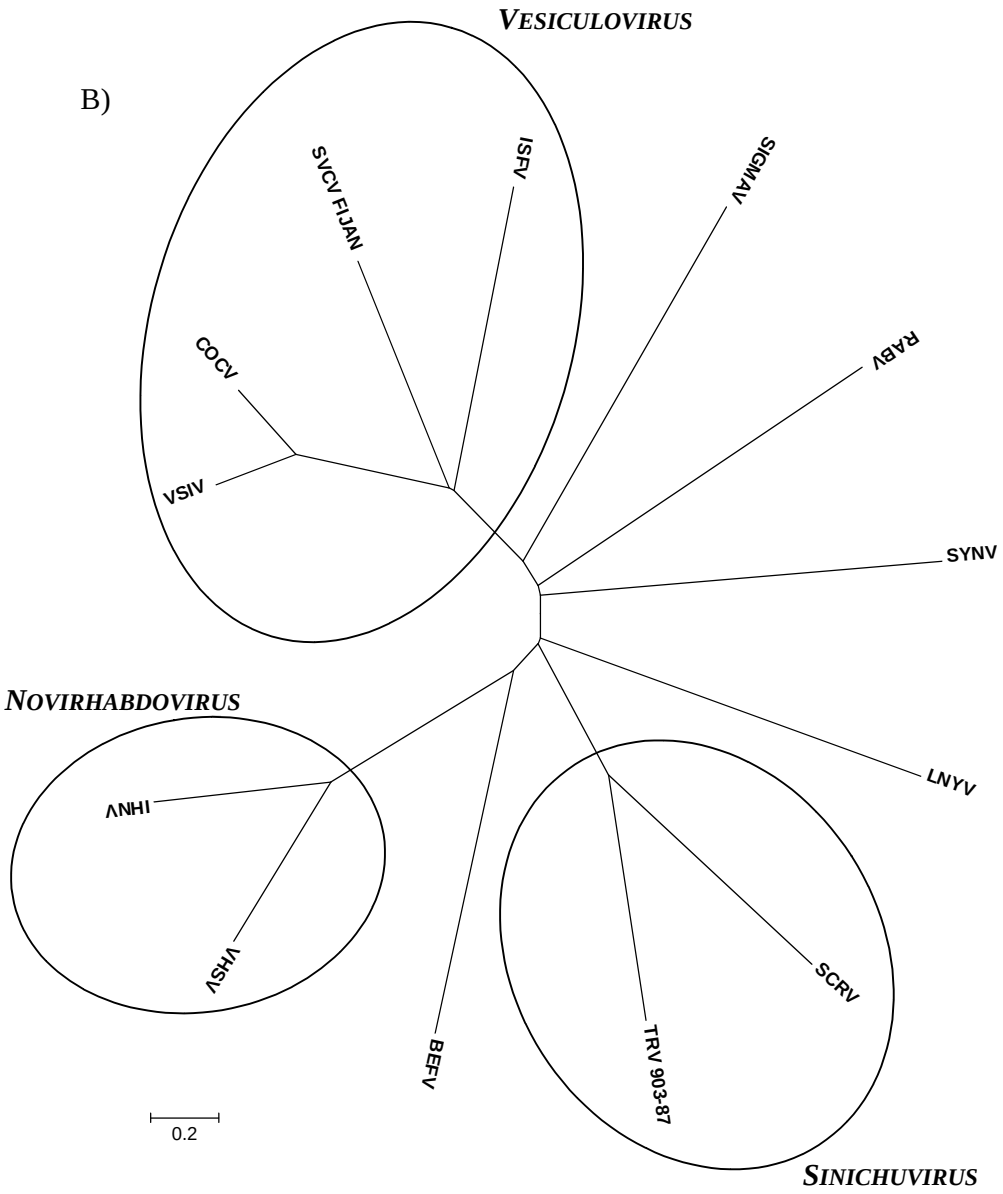
Stone, D.M., Ahne, W., Sheppard, A.M., Tsin-yee Liu, C. T-Y., Taylor, G.R., Denham, K. D., Dixon P.F. and Way K. (2003). Nucleotide sequence analysis of the glycoprotein gene of putative spring viraemia of carp viruses and pike fry rhabdovirus isolates reveals four distinct piscine vesiculovirus genogroups. Dis Aquat. Org. 53:203-210.

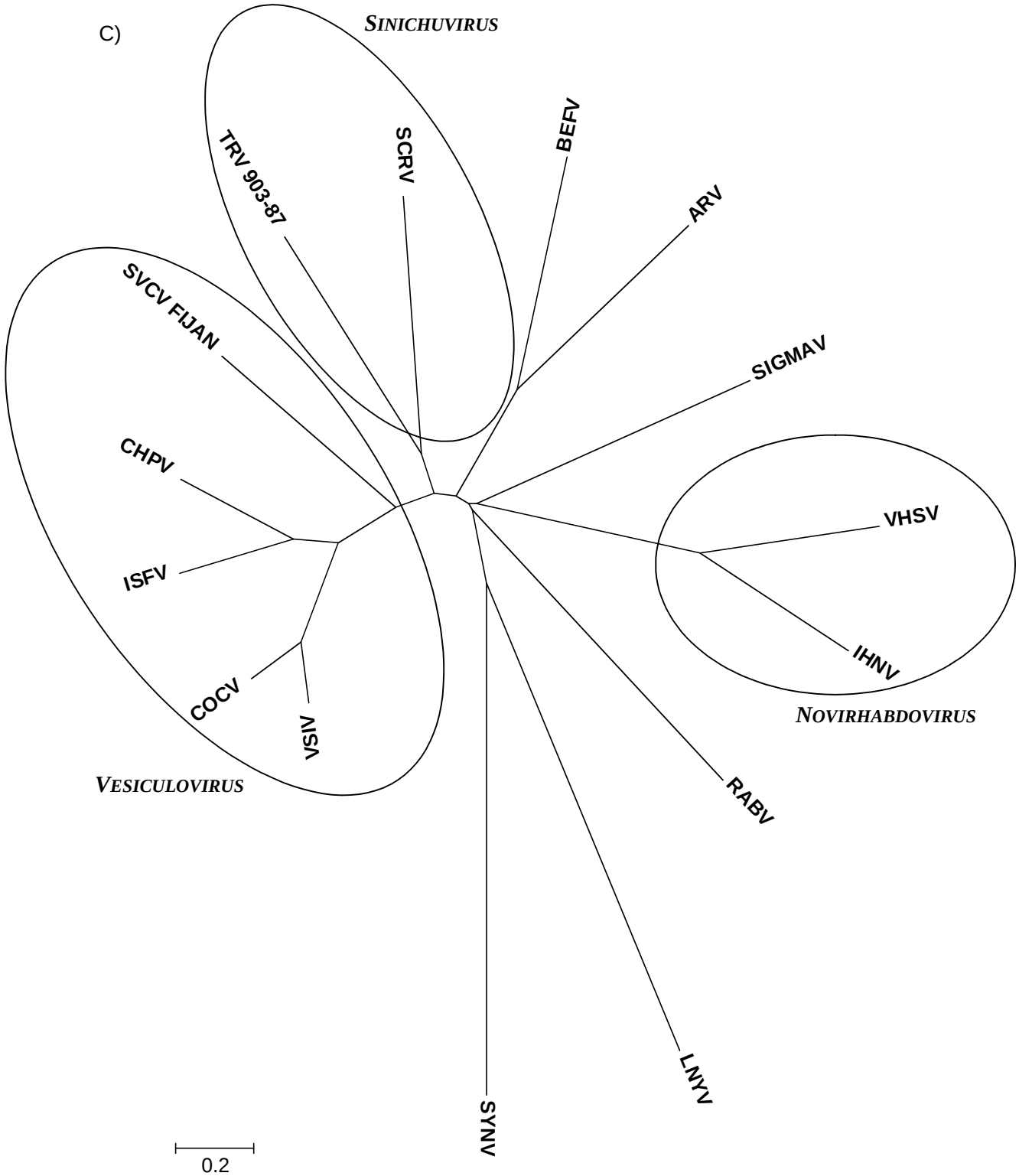
Annex:

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.


A)
SINICHUVIRUS
SCRV
TRV 903-87
BEFV
EPHEMEROVIRUS
ARVD
CHPV
ISFV
SVCV
VSIV
COCV
VSAV
VSNJV
VESICULOVIRUS
RABV
LYSSAVIRUS
SIGMAV
VHSV
NOVIRHABDOVIRUS
IHNV
NUCLEORHABDOVIRUS
SYNV
LNYV
CYTORHABDOVIRUS
0.2

B)


VESICULOVIRUS
SVCV FIJAN
ISFV
SIGMAV
COCV
RABV
VSIV
SYNV
NOVIRHABDOVIRUS
LNYV
IHNV
VHSV
SCRV
BEFV
TRV 903-87
0.2
SINICHUVIRUS



Neighbor-Joining trees based on the complete (A) N protein (B) P protein and (C) G protein sequences of a range of rhabdoviruses, highlighting the genetic relationship of SVCV to the V*esiculoviruses* and the two genera containing fish viruses.