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: *2009.004a,bV* (to be completed by ICTV officers)

Short title: Create a species named Sigma virus to be unassigned 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:

Ralf Dietzgen, ralf.dietzgen@dpi.qld.gov.au

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:

Date first submitted to ICTV: 8 May 2009
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	***2009.004aV***	(assigned by ICTV officers)

To create 1 new species with the name:

Sigma 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	***2009.004bV***	(assigned by ICTV officers)

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

Genus:	**unassigned**
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:

Sigma virus (SIGMAV) is a rhabdovirus that naturally infects fruit flies (*Drosophila* spp.). It was discovered in 1937; flies exposed to carbon dioxide are irreversibly paralyzed (Contamine and Gaumer, 2008). In nature, SIGMAV transmission appears to be exclusively vertical. It is currently classified as an unassigned member of the family *Rhabdoviridae*.

Virion morphology, genome organization (Fig. 3) and sequence relationships of sequenced structural proteins (Fig. 1) are consistent with its classification as a rhabdovirus. SIGMAV is not closely related to other rhabdoviruses to be classified in an existing genus. Based on its genome organization, phylogenetic placement and pathobiology SIGMAV appears to be unique and not a member of any previously described genus.

Virions are spiked and enveloped bullet-shaped particles of ~ 75 x 140-200 nm, appear to be exclusively cytoplasmic and contain a helical nucleocapsid. The genome is a negative-sense, single-stranded RNA that contains six genes arranged in the same order as in other rhabdoviruses: 3’-N-P-X-M-G-L-5’. Unlike in vesiculoviruses, SIGMAV genome contains an additional gene between P and M genes (Fig. 1) like members in the genera *Cytorhabdovirus* and *Nucleorhabdovirus*; the encoded putative protein is of unknown function but contains conserved domains found in reverse transcriptases. Another unusual feature is that M and G mRNAs overlap by 33 nucleotides. Phylogenetic analysis based on N and G proteins indicate that SIGMAV clusters with vesiculoviruses (Fig.1).

The genome (approximately 12,000 nucleotides) has been sequenced with the exception of the L gene that is only partially sequenced at its 3’ end. A recent study showed low genetic diversity of SIGMAV isolates across Europe and North America (Carpenter et al., 2007).

GenBank accessions:
AM689308-AM689331 (variability study by Carpenter et al. 2007)
X06171, X77037, X77038, X91062, AM691026, AH004206-09

MODULE 9: **APPENDIX**: supporting material

additional material in support of this proposal

References:

Teninges D, Bras F, Dezelee S (1993) Genome organisation of the Sigma Rhabdovirus: Six genes with a gene overlap. Virology 193:1018-1023.

Bras F, Teninges D, Dezelee S (1994) Sequences of the N and M genes of the Sigma virus od Drosophila and evolutionary comparison. Virology 200:189-199.

Carpenter JA, Obbard DJ, Maside X, Jiggins FM (2007) The recent spread of a vertically transmitted virus through populations of Drosophila melanogaster. Molecular Ecology 16:3947-3954.

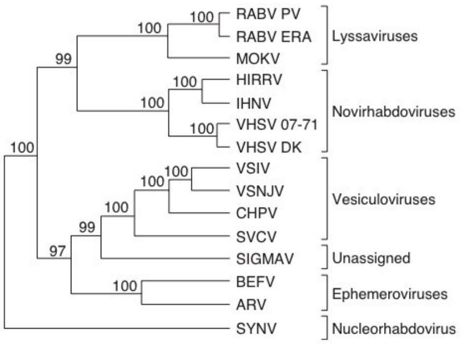
Condamine D, Gaumer S (2008) Sigma Rhabdoviruses. In: Encyclopedia of Virology, 3rd edition, BWJ Mahy and MHV Van Regenmortel, Eds., Oxford,: Elsevier.

Annex:

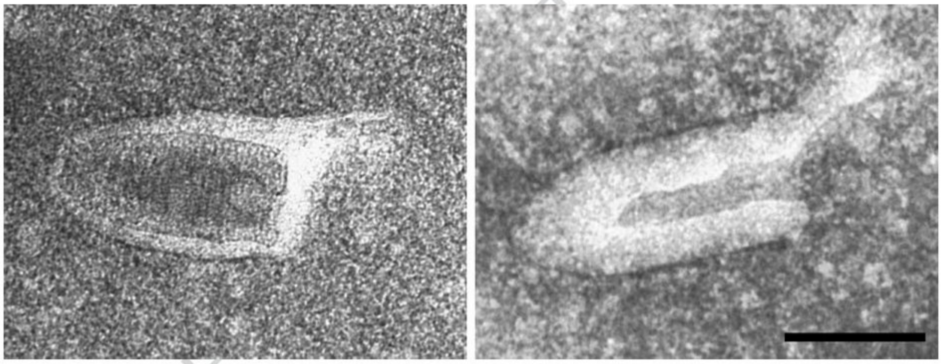
Include as much information as necessary to support the proposal, including diagrams comparing the old and new taxonomic orders.
The use of Figures and Tables is strongly recommended.

Figure 1: Phylogenetic tree of 15 rhabdovirus glycoproteins (from Condamine and Gaumer, 2008)

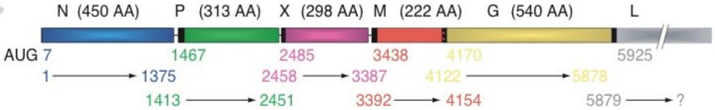
Figure 3: *Sigma virus* genome organization (from Condamine and Gaumer, 2008)



f0005 Figure 1 Phylogenetic tree of 15 rhabdovirus glycoproteins. The values next to the branches indicate the boostrapping confidence limits. Also sigma virus is unassigned to any group of rhabdoviruses: it's most conserved proteins (including protein G) are closer to vesiculoviruses. Reproduced from Bjòrklund HV, Higman KH, and Kurath G (1996) The glycoprotein genes and gene junctions of the fish rhabdoviruses spring viremia of carp virus and hirame rhabdovirus: Analysis of relationships with other rhabdoviruses. Virus Research 42: 65–80, with permission from Elsevier.



f0010 Figure 2 Sigma virus virions as observed by negative-contrast electron microscopy. The membrane fragment that is seen on the right side of the viral particles shown is frequently but not always observed. Scale ¼ 100 nm.



f0015 Figure 3 Genome organization of the sigma virus. The single-strand RNA genome of sigma virus encodes six proteins (N, P, X, M, G, and L) for which the size is indicated. The X protein is also named PP3 for protein product 3. The genome has been sequenced with the exception of the L gene that is only partially sequenced on its 3′ end. The length of the L gene is evaluated to approximately 6000 nucleotides and would encode a 2000-amino-acid long protein. The genome would thus be approximately 12 000 nucleotides long. The different mRNAs transcribed are indicated under the genome scheme as well as the position of the AUG sites. The arrows indicate the transcription direction for each gene and are in between the position numbers of the transcription starting and termination points. It is important to note that the M and G transcripts overlap from position 4122 to position 4154.