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

Code assigned:	***2011.007a-dV***	(to be completed by ICTV officers)

Short title: Create genus named *Sigmavirus* containing 7 new species in the family *Rhabdoviridae*

Modules attached	**1** ☒	**2** ☒	**3** ☐	**4** ☐	**5** ☐
	6 ☐	**7** ☒	**8** ☐	**9** ☒	

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

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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)	Rhabdoviridae Study Group

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

Proposal supported by the Study Group with minor revisions.

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	***2011.007aV***	(assigned by ICTV officers)

To create 7 new species within:

Genus:	***Sigmavirus (new)***
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.

And name the new species:	**GenBank sequence accession number(s) of reference isolate:**
Drosophila melanogaster sigmavirus	GQ375258
Drosophila obscura sigmavirus	GQ410979
Drosophila affinis sigmavirus	GQ410980
Drosophila tristis sigmavirus	JF311399
Drosophila immigrans sigmavirus	JF311401
Drosophila ananassae sigmavirus	JF311400
Muscina stabulans sigmavirus	JF311402

Reasons to justify the creation and assignment of the new species:

Sigma virus of *Drosophila melanogaster* (DMelSV) was discovered in 1937 due to its unusual phenotype of causing infected flies to become paralysed and die on exposure to CO_2 [1]. The infectious agent was later identified as a rhabdovirus based on its bullet shaped morphology (of ~ 75 x 140–200 nm), antigenic profile and partial genome sequences [2,3,4,5,6].

The complete genome sequences of DMelSV (12.6 kb) and *Drosophila obscura* sigmavirus (DObsSV) (12.7 kb) are available, along with the partial L gene sequences for the other proposed sigmavirus species. DMelSV and DObsSV each have the canonical rhabdovirus genome organization, but with an additional gene (named the X gene) located between the P and M genes (3'- N-P-X-M-G-L- 5') [4,6,7]. The X gene is of unknown function but has structural similarities to viral RNA polymerases and contains a signal peptide [7,8].

DMelSV, DObsSV and *Drosophila affinis* sigmavirus (DAffSV) have been shown to be transmitted only vertically through both eggs and sperm [9,10]. It is therefore likely that sigmaviruses represent a clade of vertically transmitted viruses that are purely entomopathogenic [11], although there is evidence of host-switching within the genus *Drosophila* on an evolutionary time scale.

Phylogenetic analysis of these viruses shows they form a distinct novel clade of rhabdoviruses, which is most closely related to the ephemeroviruses and vesiculoviruses (Figure 1) [7,11,12]. Sigmaviruses are known in six *Drosophila* host species and one host from the genus *Muscina*.

Each virus forms a distinct lineage with the level of viral strain divergence within a host species being relatively low (Figure 1; HAP23 and AP30 are the two most divergent strains of DMelSV known, with amino acid identity = 0.98 and Ks = 0.4) [7,11]. The viruses are highly divergent from one another with the maximum amino acid sequence identity between any two sigmaviruses being 0.73 (DAffSV-DTriSV) [11].

Please see below for species demarcation criteria.

MODULE 3: **NEW GENUS**

creating a new genus

Code	***2011.007bV***	(assigned by ICTV officers)

To create a new genus within:

Subfamily:	
Family:	***Rhabdoviridae***
Order:	***Mononegavirales***

naming a new genus

Code	***2011.007cV***	(assigned by ICTV officers)

To name the new genus: ***Sigmavirus***

Assigning the type species and other species to a new genus

Code	***2011.007dV***	(assigned by ICTV officers)

To designate the following as the type species of the new genus

Drosophila melanogaster sigmavirus

The new genus will also contain any other new species created and assigned to it (Module 2) and any that are being moved from elsewhere (Module 7b). **Please enter here the TOTAL number of species (including the type species) that the genus will contain:**

7

Reasons to justify the creation of a new genus:

Additional material in support of this proposal may be presented in the Appendix, Module 9

Sigmaviruses are biologically, genetically and antigenically distinct from other known rhabdoviruses. They are the only rhabdoviruses described to date that have only an insect host, are transmitted vertically and confer CO_2 sensitivity on the host. Based on partial L gene sequences, the sigmaviruses form a well-supported clade that is distinct from the previously described rhabdovirus genera [7,11,12] and the divergence between these seven viruses that are proposed as new species in the new genus is equivalent to or greater than that seen within four of the six previously classified genera in the *Rhabdoviridae* (Figure 1). Both DMelSV and DObSV (the only two sigmaviruses for which complete genome sequences are yet available) have an additional gene (X) of unknown function located between the P and M genes [7], suggesting this may be a common distinguishing feature of sigmaviruses. Furthermore, DMelSV has been shown to be antigenically distinct from other rhabdoviruses [5], and the pattern of cysteine residues that help define the folded structure of glycoprotein G is distinct from the genus-specific profiles of other rhabdoviruses [13].

Origin of the new genus name:

The genus name is taken from the naming of the original virus discovered in *Drosophila melanogaster* that was named virus “sigma” [14]

Reasons to justify the choice of type species:

DMelSV has been studied for over 70 years [1], and infects one of the most widely used model

organisms in biology [15]. It is the best studied of all the sigmaviruses, the complete genome sequence is available and its interactions with the host and dynamics in the field have been well studied [9,16,17,18,19,20,21].

Species demarcation criteria in the new genus:

Species demarcation criteria are based on the host species, supported by phylogenetic analysis and genetic diversity estimations to establish the species represents a distinct lineage.

Sigmaviruses found within different host species are likely to represent different virus species. The virus is transmitted only vertically, resulting in extreme host fidelity over ecological time scales. The currently known sigmaviruses form distinct lineages, with divergence between the viruses being equivalent to or greater than that seen between other rhabdovirus species. However, host switching does occur over evolutionary time scales and so it is possible that highly related viruses could be found in different host species. Nevertheless, as horizontal transmission and host switching events are likely to be rare, we propose species demarcation based upon the host species as the rapid accumulation of mutations in a novel host species (presuming host fidelity and vertical transmission following initial invasion) will lead to the formation of a distinct viral lineage. This should be supported by phylogenetic analysis based upon L gene sequences to indicate that the proposed virus species represents a distinct lineage and, if possible, estimates of genetic diversity to demonstrate much lower diversity within than between species. Typically, these will be <5% amino acid sequence diversity within species and >20% diversity between species.

MODULE 7: **REMOVE and MOVE**

Use this module whenever an existing taxon needs to be removed:
- *Either* to abolish a taxon entirely (when only part (a) needs to be completed)
- *Or* to move a taxon and re-assign it e.g. when a species is moved from one genus to another (when BOTH parts (a) and (b) should be completed)

Part (a) taxon/taxa to be removed or moved

Code		(assigned by ICTV officers)

To remove the following taxon (or taxa) from their present position:

The unassigned species *Sigma virus*

The present taxonomic position of these taxon/taxa:

Genus:	
Subfamily:	
Family:	***Rhabdoviridae***
Order:	***Monanegavirales***

If the taxon/taxa are to be abolished (i.e. not reassigned to another taxon) write "yes" in the box on the right

Reasons to justify the removal:

There is now sufficient information available to justify the creation of a new genus *Sigmavirus* containing 7 virus species. The currently unassigned species *Sigma virus* will be one of the 7 new species in the new grenus and renamed *Drosophila melanogaster sigmavirus.*

Part (b) re-assign to a higher taxon

Code		(assigned by ICTV officers)

To re-assign the taxon (or taxa) listed in Part (a) as follows:

Genus:	***Sigmavirus* (new)**
Subfamily:	
Family:	***Rhabdoviridae***
Order:	***Mononegavirales***

Reasons to justify the re-assignment:

The currently unassigned species *Sigma virus* will be one of the 7 new species in the new genus *Sigmavirus* and renamed as the species *Drosophila melanogaster sigmavirus* to distinguish it from other species in the genus. Other species in the genus will be named in the same fashion after their host species.

MODULE 9: **APPENDIX**: supporting material

References:

References:

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2. Berkalof A, Breglian J, Ohanessi A (1965) Mise En Evidence Des Virions Dans Des Drosophiles Infectees Par Le Virus Hereditaire Sigma. Pathologie Biologie 13: 976-&.
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14. L'Heritier P (1957) The hereditary virus of Drosophila. Advances in Virus Research 5: 195-245.
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17. Bangham J, Obbard DJ, Kim KW, Haddrill PR, Jiggins FM (2007) The age and evolution of an antiviral resistance mutation in Drosophila melanogaster. Proceedings of the Royal Society B-Biological Sciences 274: 2027-2034.
18. Carpenter J, Hutter S, Baines JF, Roller J, Saminadin-Peter SS, et al. (2009) The transcriptional response of Drosophila melanogaster to infection with the sigma virus (Rhabdoviridae). Plos One 4: e6838.
19. Carpenter JA, Keegan LP, Wilfert L, O'Connell MA, Jiggins FM (2009) Evidence for ADAR-induced hypermutation of the Drosophila sigma virus (Rhabdoviridae). BMC Genet 10: 75.
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References:

virus: University of Edinburgh.

21. Wilfert L, Jiggins FM (2010) Disease association mapping in Drosophila can be replicated in the wild. Biol Lett 6: 666-668.
22. Huelsenbeck JP, Ronquist F (2001) MRBAYES: Bayesian inference of phylogenetic trees. Bioinformatics 17: 754-755.
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Annex:

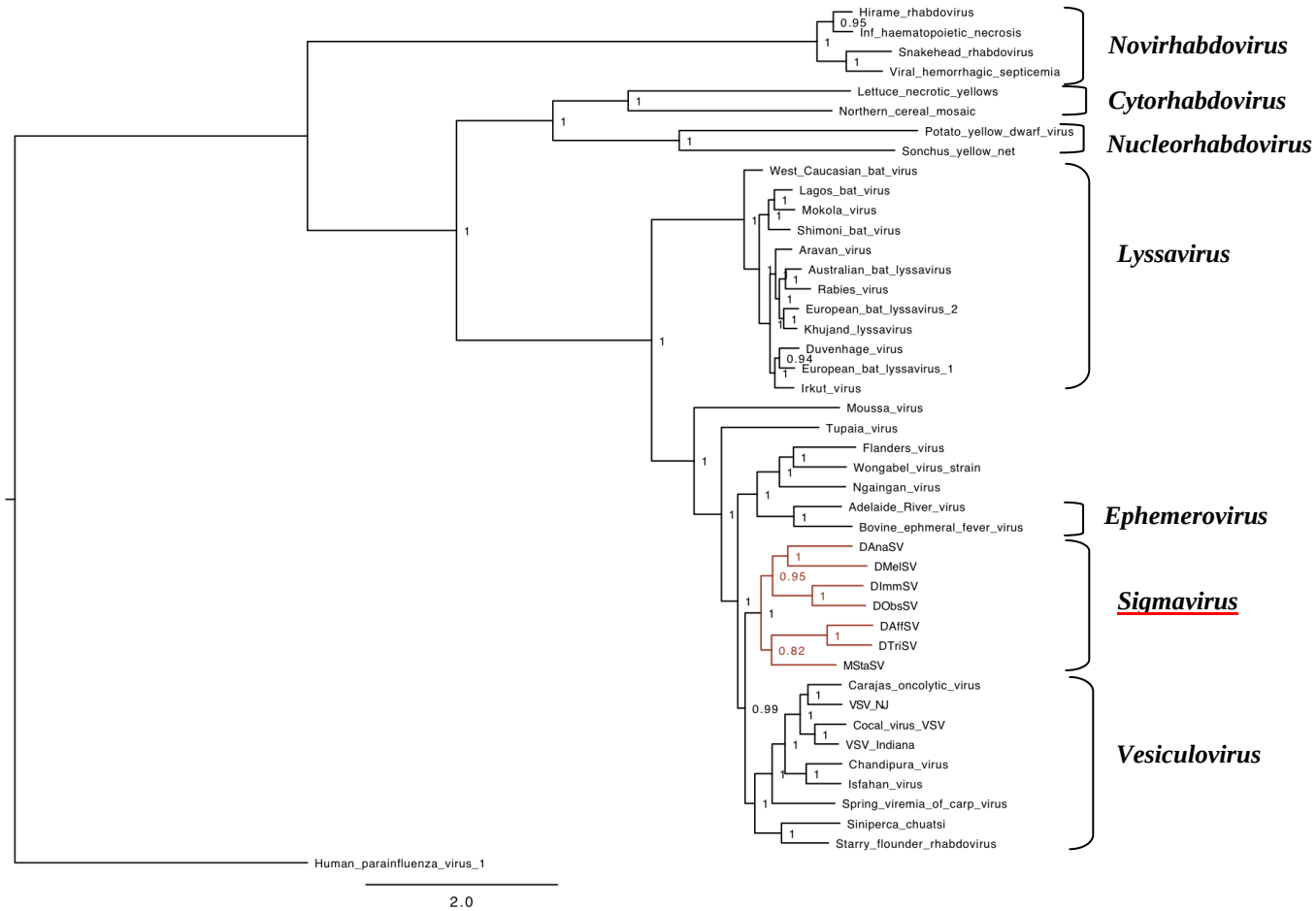

Figure 1. Rhabdovirus phylogeny based on partial L gene sequences, with the sigma virus clade highlighted in red. The results are robust to alignment and method of inference [7,11,12]. The analysis was run in MrBayes [22] and used a general time reversible model with a gamma distributed rate variation and a proportion of invariable sites, with parameters unlinked across codon positions. This model of sequence evolution was selected by comparing alternative models using Bayes Factors [23] in Tracer [24]. Node-supports are the posterior supports and the tree is rooted with human parainfluenza virus 1.