



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:	2015.009a-gM	(to be completed by ICTV officers)			
Short title: Establishment of one (1) new family (<i>Sunviridae</i>) including one (1) new genus (<i>Sunshinevirus</i>) including one new species (<i>Reptile sunshinevirus 1</i>) within the order <i>Mononegavirales</i>					
Modules attached (modules 1 and 10 are required)	1 <input checked="" type="checkbox"/>	2 <input checked="" type="checkbox"/>	3 <input checked="" type="checkbox"/>	4 <input type="checkbox"/>	5 <input checked="" type="checkbox"/>
	6 <input type="checkbox"/>	7 <input type="checkbox"/>	8 <input type="checkbox"/>	9 <input type="checkbox"/>	10 <input checked="" type="checkbox"/>

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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)

ICTV *Bornaviridae*, *Filoviridae*, *Nyamiviridae*, and *Rhabdoviridae* Study Groups

ICTV Study Group comments (if any) and response of the proposer:

Date first submitted to ICTV:

June 15, 2015

Date of this revision (if different to above):

ICTV-EC comments and response of the proposer:

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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	2015.009aM	(assigned by ICTV officers)
To create 1 new species within:		
Genus:	<i>Sunshinevirus</i> (new)	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>Sunviridae</i> (new)	
Order:	<i>Mononegavirales</i>	
Name of new species:	Representative isolate: (only 1 per species please)	GenBank sequence accession number(s)
<i>Reptile sunshinevirus 1</i>	Sunshine Coast virus (formerly Sunshine virus)	NC_025345

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

Sunshine Coast virus was first isolated from a captive black-headed python (*Aspidites melanocephalus*) from the Sunshine Coast of Queensland, Australia. A number of snakes from this collection died with neurological signs of disease. Spongiosis of the white matter in the hindbrain appears to be a reliable histological change in affected animals. The virus was isolated in viper heart cells (VH2) and produced massive syncytial cell formation without significant cytolysis (Figure 1).

A coding-complete genome of this novel virus was 17,187 nucleotides in length and contains at least six non-overlapping open reading frames (ORFs): 3’ – Nucleocapsid (N) – a putative phosphoprotein (P) – Matrix (M) – Fusion (F) – a putative attachment protein (G) – RNA-dependent RNA polymerase (L) – 5’. There is also a 540 nucleotide ORF located between N and the putative P ORFs. The genome length and ORF organization are both consistent with those of mononegaviruses (Figure 3).

Phylogenetic analysis of the complete amino acid sequence of the F protein supports this virus as being distinct from paramyxoviruses and pneumoviruses, which are the only known mononegaviruses known to have F genes. Similar analyses for N, M, and L (Hyndman *et al.*, and Figure 2) support this virus clustering separately to all other established families of the order *Mononegavirales*. A BLASTp search of the non-redundant (nr) protein sequences of GenBank did not result in hits with similarities to the putative phosphoprotein (P) or attachment protein (G) of this new virus. Finally, infected VH2 cells showed no phenotypic evidence of neuraminidase or hemagglutinating activity.

These unique characteristics justify Sunshine Coast virus as a representative of a new species to be included in a new genus and family in *Mononegavirales*.

MODULE 3: **NEW GENUS**

creating a new genus

Ideally, a genus should be placed within a higher taxon.

Code	2015.009bM	(assigned by ICTV officers)
To create a new genus within:		
Subfamily:		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 family is specified, enter “ unassigned ” in the family box
Family:	<i>Sunviridae</i>	
Order:	<i>Mononegavirales</i>	

naming a new genus

Code	2015.009cM	(assigned by ICTV officers)
To name the new genus: <i>Sunshinevirus</i>		

Assigning the type species and other species to a new genus

Code	2015.009dM	(assigned by ICTV officers)
To designate the following as the type species of the new genus		
<i>Reptile sunshinevirus 1</i>	Every genus must have a type species. This should be a well characterized species although not necessarily the first to be discovered	
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:		
1		

Reasons to justify the creation of a new genus:

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

See Module 2

Origin of the new genus name:

Sunshinevirus: sigil of Sunshine virus and virus

Reasons to justify the choice of type species:

Only one species is proposed to be included in this new genus, making that the type species by default

Species demarcation criteria in the new genus:

If there will be more than one species in the new genus, list the criteria being used for species demarcation and explain how the proposed members meet these criteria.

See Module 2

MODULE 5: **NEW FAMILY**

creating and naming a new family

Code	2015.009eM	(assigned by ICTV officers)
<p>To create a new family containing the subfamilies and/or genera listed below within the Order: <i>Mononegavirales</i></p> <p>If there is no Order, write "unassigned" here. If the Order has yet to be created (in Module 6) please write "(new)" after the proposed name.</p>		

Code	2015.009fM	(assigned by ICTV officers)
<p>To name the new family: <i>Sunviridae</i></p>		

assigning subfamilies, genera and unassigned species to a new family

Code		(assigned by ICTV officers)
<p>To assign the following subfamilies (if any) to the new family: N/A</p>		
Code	2015.009gM	(assigned by ICTV officers)
<p>To assign the following genera to the new family: You may list several genera here. For each genus, please state whether it is new or existing.</p> <ul style="list-style-type: none"> • If the genus is new, it must be created in Module 3 • If the genus already exists, please state whether it is currently unassigned or is to be removed from another family. If the latter, complete Module 7 to 'REMOVE' it from that family 		
<i>Sunshinevirus</i>		
<p>The new family will also contain any other new species created and assigned to it (Module 3) and any that are being moved from elsewhere (Module 7b). Please enter here the TOTAL number of unassigned species that the family will contain (those NOT within any of the genera or subfamilies listed above):</p>		
N/A		
<p>Reasons to justify the creation of the new family: Additional material in support of this proposal may be presented in the Appendix, Module 9</p>		
See module 2		
Origin of the new family name:		
<i>Sunviridae</i> : sigil of <u>Sunshine virus</u> and the family-specific suffix <i>-viridae</i>		

MODULE 10: **APPENDIX**: supporting material

additional material in support of this proposal

References:

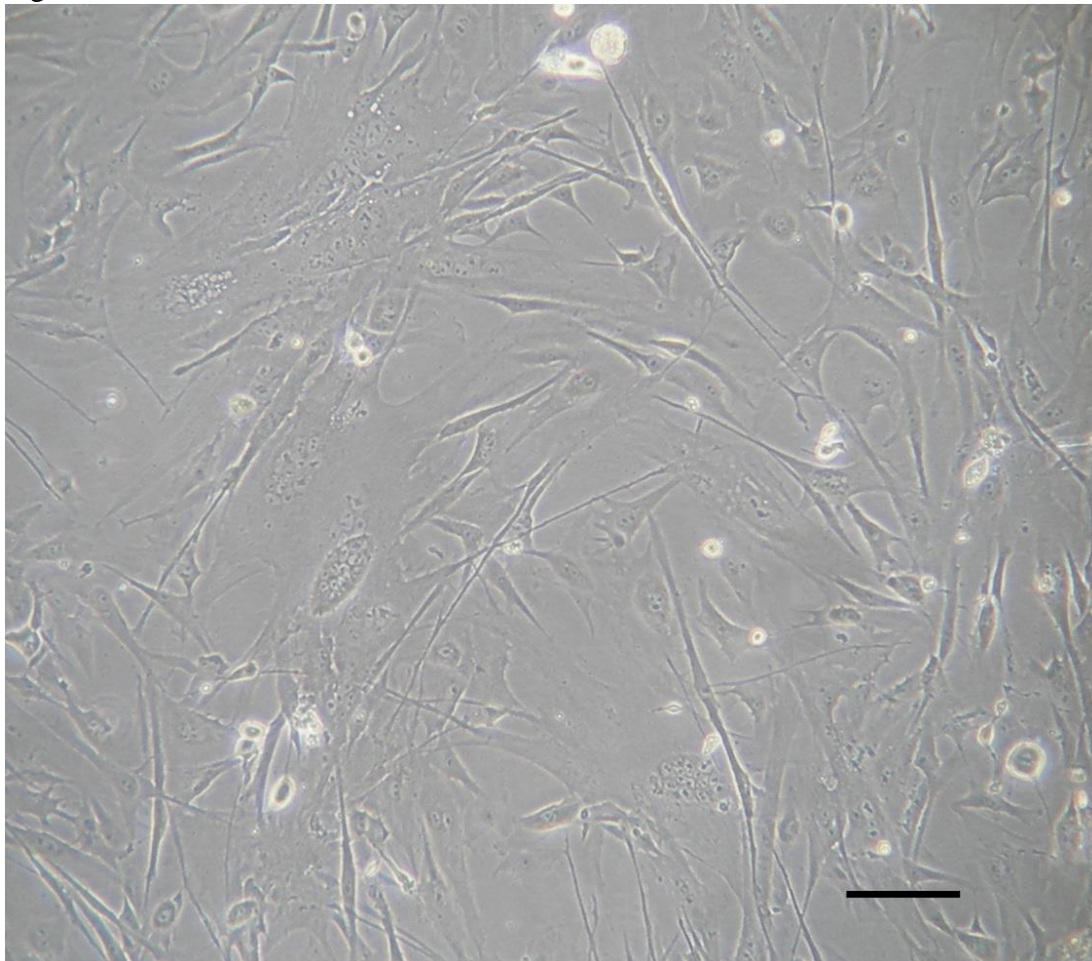
Hyndman TH, Marschang RE, Wellehan JFX Jr., Nicholls PK. 2012. Isolation and molecular identification of Sunshine virus: a novel paramyxovirus found in Australian snakes. *Infection, Genetics, and Evolution* 12:1436-1446.

Hyndman TH, Shilton CM, Doneley RJT, Nicholls PK. 2012. Sunshine virus in Australian pythons. *Veterinary Microbiology* 161:77-87.

Annex:

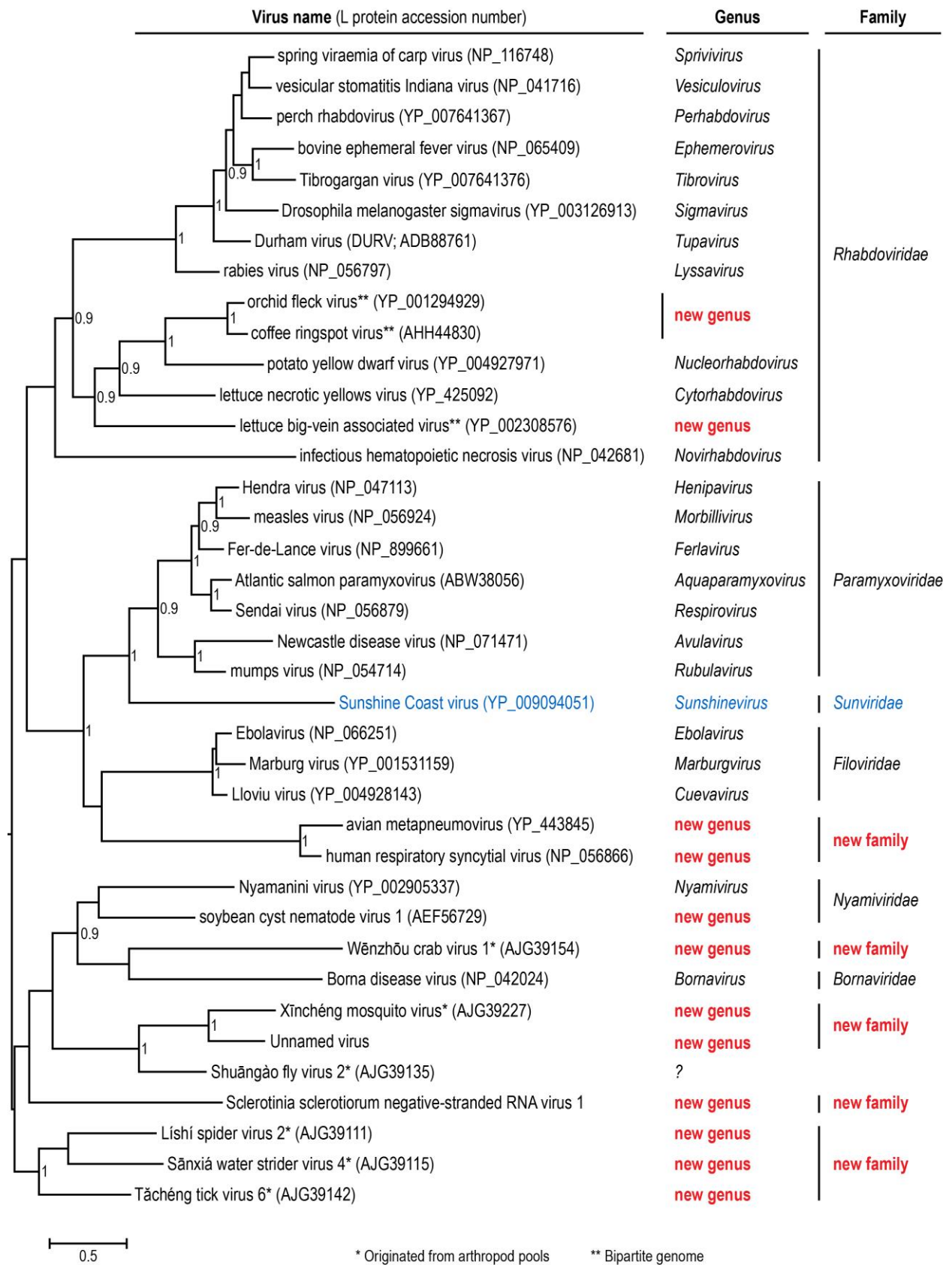
Include as much information as necessary to support the proposal, including diagrams comparing the old and new taxonomic orders. The use of Figures and Tables is strongly recommended but direct pasting of content from publications will require permission from the copyright holder together with appropriate 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.

Figure 1:



Viper heart (VH2) cells infected with *Melanocephalus sunshine coast* virus. Widespread syncytial cell formation can be seen. Scale bar = 100 μ m.

Figure 2.



Phylogenetic relationships of selected mononegaviruses. A maximum-likelihood tree was constructed using PhyML 3.0 (<http://www.atgc-montpellier.fr/phyml/>) based on a multiple amino acid sequence

alignment of the entire L polymerase. Ambiguously aligned regions were removed using Gblocks 0.91b (http://molevol.cmima.csic.es/castresana/Gblocks_server.html) with the all options of less stringent selection. The best-fit model LG+I +G+F was selected using ProtTest ver. 2.4 (http://darwin.uvigo.es/software/prottest2_server.html). Virus names (the member of type species or others) and GenBank/Refseq accession numbers are shown. The names of proposed genus and family are highlighted in blue. Numbers at the nodes represent aLRT values derived using an SH like calculation (only values greater than 0.9 are shown).

Figure 3. Genome map of Sunshine Coast virus from Hyndman et al., 2012. Note novel ORF between the N and putative P genes. This ORF has no significant homology with current sequences in GenBank.

