



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**

<b>Code assigned:</b>	<b>2015.015a-aaD</b>	(to be completed by ICTV officers)
<b>Short title: Revision on the family <i>Polyomaviridae</i> (76 species, four genera)</b> (e.g. 6 new species in the genus <i>Zetavirus</i> )		
<b>Modules attached</b> (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 type="checkbox"/>	6 <input type="checkbox"/>
	7 <input checked="" type="checkbox"/>	8 <input checked="" type="checkbox"/>
	9 <input type="checkbox"/>	10 <input checked="" type="checkbox"/>

**Author(s):**

Polyomaviridae Study Group: Sébastien Calvignac-Spencer, Mariet Feltkamp, Matthew D. Daugherty, Ugo Moens, Torbjörn Ramqvist, Reimar Johnes, Bernhard Ehlers

**Corresponding author with e-mail address:**

Bernhard Ehlers; e-mail: ehlersb@rki.de

**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)

Polyomaviridae Study Group

**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):

October 22, 2015

**ICTV-EC comments and response of the proposer:**

**Overview**

The progressive identification of novel polyomavirus (PyV) genomic sequences in various mammals, birds and fish that are similar to those presently classified as members of the *Polyomaviridae* family induced a revision of the *Polyomaviridae* family classification scheme. The current proposal represents an update of the taxonomy of the family *Polyomaviridae* by: 1) redefining the species demarcation criteria; 2) creating 68 novel species and assigning 73 species to 4 novel genera; 3) setting up genus demarcation criteria based on phylogenetic analysis and 4) creating 4 novel genera.

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	<b>2015.015aD</b>	(assigned by ICTV officers)
<b>To create 34 new species within:</b>		
Genus:	<b><i>Alphapolyomavirus</i> (new)</b>	
Subfamily:		
Family:	<b><i>Polyomaviridae</i></b>	
Order:		
<p>Fill in all that apply.</p> <ul style="list-style-type: none"> <li>• If the higher taxon has yet to be created (in a later module, below) write “(new)” after its proposed name.</li> <li>• If no genus is specified, enter “unassigned” in the genus box.</li> </ul>		
Name of new species:	Representative isolate: (only 1 per species please)	GenBank sequence accession number(s)
<i>Acerodon celebensis polyomavirus 1</i>	BatPyV5b-2	AB972940
<i>Artibeus planirostris polyomavirus 2</i>	BatPyV-3a	JQ958886
<i>Artibeus planirostris polyomavirus 3</i>	BatPyV-4a	JQ958887
<i>Ateles paniscus polyomavirus 1</i>	ApanPyV1 isolate #1961	JX159987
<i>Cardioderma cor polyomavirus 1</i>	CardiodermaPyV-KY336	JX520659
<i>Carollia perspicillata polyomavirus 1</i>	BatPyV-4b	JQ958889
<i>Chlorocebus pygerythrus polyomavirus 1</i>	VmPyV1	AB767298
<i>Chlorocebus pygerythrus polyomavirus 3</i>	VmPyV3	AB767297
<i>Dobsonia moluccensis polyomavirus 1</i>	BatPyV5a	AB972945
<i>Eidolon helvum polyomavirus 1</i>	EidolonPyV-KY270	JX520660
<i>Gorilla gorilla polyomavirus 1</i>	GgorgPyV1 isolate #5766	HQ385752
<i>Human polyomavirus 5</i>	MCPyV isolate R17b	HM011556
<i>Human polyomavirus 8</i>	TSPyV	GU989205
<i>Human polyomavirus 9</i>	HPyV9 isolate #hu2540	HQ696595
<i>Human polyomavirus 12</i>	HPyV12 isolate #hu1403	JX308829
<i>Human polyomavirus 13</i>	NJPyV isolate NJ-PyV-2013	KF954417
<i>Macaca fascicularis polyomavirus 1</i>	MfasPyV1 isolate #2085	JX159986
<i>Molossus molossus polyomavirus 1</i>	BatPyV-3b	JQ958893
<i>Otomops martiensseni polyomavirus 1</i>	OtomopsPyV-KY156	JX520658
<i>Otomops martiensseni polyomavirus 2</i>	OtomopsPyV-KY157	JX520664
<i>Pan troglodytes polyomavirus 1</i>	ChPyV-Bob	FR692334
<i>Pan troglodytes polyomavirus 2</i>	PtroyPyV1a isolate #6444	HQ385746
<i>Pan troglodytes polyomavirus 3</i>	PtroyPyV2a isolate #6512	HQ385748
<i>Pan troglodytes polyomavirus 4</i>	PtroyPyV3 isolate #3161	JX159980
<i>Pan troglodytes polyomavirus 5</i>	PtroyPyV4 isolate #3147	JX159981
<i>Pan troglodytes polyomavirus 6</i>	PtroyPyV5 isolate #5743	JX159982
<i>Pan troglodytes polyomavirus 7</i>	PtrosPyV2 isolate #6350	JX159983
<i>Papio cynocephalus polyomavirus 1</i>	YbPyV1	AB767294
<i>Ptilocolobus rufomitratu polyomavirus 1</i>	PrufPyV1 isolate #4601	JX159984
<i>Pongo abelii polyomavirus 1</i>	OraPyV-Pi	FN356901
<i>Pongo pygmaeus polyomavirus 1</i>	OraPyV-Bo	FN356900
<i>Procyon lotor polyomavirus 1</i>	RacPyV	JQ178241
<i>Pteropus vampyrus polyomavirus 1</i>	BatPyV5b-1	AB972944
<i>Sturnira lilium polyomavirus 1</i>	BatPyV-B0454	JQ958888

**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

**Criteria for species demarcation:**

**1. Public availability of the complete genome sequence and publication in a peer-reviewed journal**

**2. A typical PyV genome organization, i.e., the early and late region encoding the T antigens and the structural viral proteins, respectively, separated by a noncoding control region**

**3. Sufficient information on the natural host is available.**

Note: In cases where the host species cannot be firmly identified by host morphology, molecular methods (e.g. cytochrome B gene CDS analysis) shall be used.

**4. Observed genetic distance to a member of the most closely related species is >15% for large T antigen (LTA<sub>g</sub>) coding sequence.**

Note: this 15% criterion accommodates the current SV40, BKPyV, JCPyV, MCPyV, HPyV6, HPyV7, MWPyV, KIPyV and WUPyV isolates as single species, respectively (Figure 1).

**5. When two PyVs exhibit <15% observed genetic distance, biological properties may be of additional critical importance (e.g. host specificity, disease association, tissue tropism etc.)**

Note:

Species were named by a combination of the Latin host species name plus “*polyomavirus*”, followed by a consecutive number.

Exceptions from the proposed scheme are:

Species: *Aves polyomavirus 1*. Species member: Budgerigar fledgling disease polyomavirus (an avian polyomavirus). The PyV that was first detected in budgerigars but was found to epizootically infect several bird species.

All species accommodating human PyVs. They are named *Human polyomavirus* (instead of “*Homo sapiens polyomavirus*”), followed by a consecutive number.

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	<b>2015.015bD</b>	(assigned by ICTV officers)
<b>To create 22 new species within:</b>		
Genus:	<b>Betapolyomavirus (new)</b>	
Subfamily:		
Family:	<b>Polyomaviridae</b>	
Order:		
Fill in all that apply.		
<ul style="list-style-type: none"> <li>• If the higher taxon has yet to be created (in a later module, below) write “(new)” after its proposed name.</li> <li>• If no genus is specified, enter “unassigned” in the genus box.</li> </ul>		
<b>Name of new species:</b>	<b>Representative isolate: (only 1 per species please)</b>	<b>GenBank sequence accession number(s)</b>
<i>Acerodon celebensis polyomavirus 2</i>	BatPyV6a	AB972941
<i>Artibeus planirostris polyomavirus 1</i>	BatPyV-2c	JQ958890
<i>Cebus albifrons polyomavirus 1</i>	CalbPyV1 isolate #2141	JX159988
<i>Cercopithecus erythrotis polyomavirus 1</i>	CeryPyV1 isolate #4077	JX159985
<i>Chlorocebus pygerythrus polyomavirus 2</i>	VmPyV2	AB767299
<i>Desmodus rotundus polyomavirus 1</i>	BatPyV2a	JQ958892
<i>Dobsonia moluccensis polyomavirus 2</i>	BatPyV6b	AB972947
<i>Dobsonia moluccensis polyomavirus 3</i>	BatPyV6c	AB972946
<i>Equus caballus polyomavirus 1</i>	EPyV isolate CU03	JQ412134
<i>Human polyomavirus 3</i>	KIPyV strain Stockholm 60	EF127906
<i>Human polyomavirus 4</i>	WUPyV	EF444549
<i>Loxodonta africana polyomavirus 1</i>	AelPyV1	KF147833
<i>Mastomys natalensis polyomavirus 1</i>	MasPyV	AB588640
<i>Meles meles polyomavirus 1</i>	MmelPyV1-FR	KP644238
<i>Miniopterus africanus polyomavirus 1</i>	MiniopterusPyV-KY369	JX520661
<i>Myotis lucifugus polyomavirus 1</i>	MyoPyV isolate VM2008_14	FJ188392
<i>Papio cynocephalus polyomavirus 2</i>	YbPyV2	AB767295
<i>Pteronotus davyi polyomavirus 1</i>	PteronotusPyV-GTM203	JX520662
<i>Pteronotus parnellii polyomavirus 1</i>	BatPyV-2b	JQ958891
<i>Saimiri boliviensis polyomavirus 1</i>	SqPyV isolate Squi0106	AM748741
<i>Saimiri sciureus polyomavirus 1</i>	SsciPyV1 isolate #2033	JX159989
<i>Zalophus californianus polyomavirus 1</i>	SLPyV, CSLPyV	GQ331138

**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

**Criteria for species demarcation:**

**1. As for members of the genus *Alphapolyomavirus***

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	<b>2015.015cD</b>	(assigned by ICTV officers)
<b>To create 6 new species within:</b>		
Genus:	<b><i>Gammapolyomavirus (new)</i></b>	Fill in all that apply. • If the higher taxon has yet to be created (in a later module, below) write “ <b>(new)</b> ” after its proposed name. • If no genus is specified, enter “ <b>unassigned</b> ” in the genus box.
Subfamily:		
Family:	<b><i>Polyomaviridae</i></b>	
Order:		
<b>Name of new species:</b>	<b>Representative isolate: (only 1 per species please)</b>	<b>GenBank sequence accession number(s)</b>
<i>Anser anser polyomavirus 1</i>	GHPyV	AY140894
<i>Corvus monedula polyomavirus 1</i>	CPyV	DQ192570
<i>Cracticus torquatus polyomavirus 1</i>	Butcherbird PyV	KF360862
<i>Pygoscelis adeliae polyomavirus 1</i>	AdPyV	KP033140
<i>Pyrrhula pyrrhula polyomavirus 1</i>	FPyV	DQ192571
<i>Serinus canaria polyomavirus 1</i>	CaPyV	GU345044

<p><b>Reasons to justify the creation and assignment of the new species:</b></p> <ul style="list-style-type: none"> <li>• Explain how the proposed species differ(s) from all existing species.           <ul style="list-style-type: none"> <li>○ If species demarcation criteria (see module 3) have previously been defined for the genus, <b>explain how the new species meet these criteria.</b></li> <li>○ 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.</li> </ul> </li> <li>• Further material in support of this proposal may be presented in the Appendix, Module 9</li> </ul>
<p><b>Criteria for species demarcation:</b></p> <p><b>1. As for members of the genus <i>Alphapolyomavirus</i></b></p>

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	<b>2015.015dD</b>	(assigned by ICTV officers)
<b>To create 4 new species within:</b>		
Genus:	<b><i>Deltapolyomavirus (new)</i></b>	Fill in all that apply. • If the higher taxon has yet to be created (in a later module, below) write “ <b>(new)</b> ” after its proposed name. • If no genus is specified, enter “ <b>unassigned</b> ” in the genus box.
Subfamily:		
Family:	<b><i>Polyomaviridae</i></b>	
Order:		
<b>Name of new species:</b>	<b>Representative isolate: (only 1 per species please)</b>	<b>GenBank sequence accession number(s)</b>
<i>Human polyomavirus 6</i>	HPyV6 strain 607a	HM011560
<i>Human polyomavirus 7</i>	HPyV7 strain 713a	HM011566
<i>Human polyomavirus 10</i>	MWPyV strain MA095	JQ898291
<i>Human polyomavirus 11</i>	StLPyV strain MA138	JX463183

<p><b>Reasons to justify the creation and assignment of the new species:</b></p> <ul style="list-style-type: none"> <li>• Explain how the proposed species differ(s) from all existing species.           <ul style="list-style-type: none"> <li>○ If species demarcation criteria (see module 3) have previously been defined for the genus, <b>explain how the new species meet these criteria.</b></li> <li>○ 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.</li> </ul> </li> <li>• Further material in support of this proposal may be presented in the Appendix, Module 9</li> </ul>
<p><b>Criteria for species demarcation:</b></p> <p><b>1. As for members of the genus <i>Alphapolyomavirus</i></b></p>

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	<b>2015.015dD</b>	(assigned by ICTV officers)	
<b>To create 2 new species within:</b>			
Genus:	<i>unassigned</i>	Fill in all that apply. • If the higher taxon has yet to be created (in a later module, below) write “ <b>(new)</b> ” after its proposed name. • If no genus is specified, enter “ <b>unassigned</b> ” in the genus box.	
Subfamily:			
Family:	<b><i>Polyomaviridae</i></b>		
Order:			
<b>Name of new species:</b>	<b>Representative isolate: (only 1 per species please)</b>	<b>GenBank sequence accession number(s)</b>	
<i>Delphinus delphis polyomavirus 1</i> <i>Centropristis striata polyomavirus 1</i>	Delphinus delphis polyomavirus 1 Black sea bass polyomavirus 1	KC594077 KP071318	

<p><b>Reasons to justify the creation and assignment of the new species:</b></p> <ul style="list-style-type: none"> <li>• Explain how the proposed species differ(s) from all existing species.                     <ul style="list-style-type: none"> <li>○ If species demarcation criteria (see module 3) have previously been defined for the genus, <b>explain how the new species meet these criteria.</b></li> <li>○ 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.</li> </ul> </li> <li>• Further material in support of this proposal may be presented in the Appendix, Module 9</li> </ul>
<p><b>Criteria for species demarcation:</b></p> <p><b>1. As for members of the genus <i>Alphapolyomavirus</i></b></p>

MODULE 3: **NEW GENUS**

creating a new genus

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

Code	<b>2015.015eD</b>	(assigned by ICTV officers)
<b>To create a new genus within:</b>		
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:	<b><i>Polyomaviridae</i></b>	
Order:		

naming a new genus

Code	<b>2015.015fD</b>	(assigned by ICTV officers)
<b>To name the new genus: <i>Alphapolyomavirus</i></b>		

Assigning the type species and other species to a new genus

Code	<b>2015.015gD</b>	(assigned by ICTV officers)
<b>To designate the following as the type species of the new genus</b>		
<b><i>Mus musculus polyomavirus 1</i></b>		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). <b>Please enter here the TOTAL number of species (including the type species) that the genus will contain:</b>		
<b>36</b>		

**Reasons to justify the creation of a new genus:**

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

The genus is based on statistically well supported phylogenetic tree topology calculated from large T antigen amino acid sequences (Figure 2; Appendix).

**Origin of the new genus name:**

It is derived from the greek alphabet in combination with the family name.

**Reasons to justify the choice of type species:**

First discovered member of the genus

**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.

As shown in module 2



MODULE 3: **NEW GENUS**

creating a new genus

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

Code	<b>2015.015hD</b>	(assigned by ICTV officers)
<b>To create a new genus within:</b>		
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:	<b><i>Polyomaviridae</i></b>	
Order:		

naming a new genus

Code	<b>2015.015iD</b>	(assigned by ICTV officers)
<b>To name the new genus: <i>Betapolyomavirus</i></b>		

Assigning the type species and other species to a new genus

Code	<b>2015.015jD</b>	(assigned by ICTV officers)
<b>To designate the following as the type species of the new genus</b>		
<b><i>Macaca mulatta polyomavirus 1</i></b>		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). <b>Please enter here the TOTAL number of species (including the type species) that the genus will contain:</b>		
<b>26</b>		

**Reasons to justify the creation of a new genus:**

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

The genus is based on statistically well supported phylogenetic tree topology calculated from large T antigen amino acid sequences (Figure 2; Appendix).

**Origin of the new genus name:**

It is derived from the greek alphabet in combination with the family name.

**Reasons to justify the choice of type species:**

Best studied member of the genus

**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.

As shown in module 2

MODULE 3: **NEW GENUS**

creating a new genus

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

Code	<b>2015.015kD</b>	(assigned by ICTV officers)
<b>To create a new genus within:</b>		
Subfamily:		Fill in all that apply. • If the higher taxon has yet to be created (in a later module, below) write “ <b>(new)</b> ” after its proposed name. • If no family is specified, enter “ <b>unassigned</b> ” in the family box
Family:	<b><i>Polyomaviridae</i></b>	
Order:		

naming a new genus

Code	<b>2015.015lD</b>	(assigned by ICTV officers)
<b>To name the new genus: <i>Gammampolyomavirus</i></b>		

Assigning the type species and other species to a new genus

Code	<b>2015.015mD</b>	(assigned by ICTV officers)
<b>To designate the following as the type species of the new genus</b>		
<b><i>Aves polyomavirus 1</i></b>		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). <b>Please enter here the TOTAL number of species (including the type species) that the genus will contain:</b>		
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

The genus is based on statistically well supported phylogenetic tree topology calculated from large T antigen amino acid sequences (Figure 2; Appendix).

**Origin of the new genus name:**

It is derived from the greek alphabet in combination with the family name.

**Reasons to justify the choice of type species:**

First discovered member of the genus

**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.

As shown in module 2

MODULE 3: **NEW GENUS**

creating a new genus

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

Code	<b>2015.015nD</b>	(assigned by ICTV officers)
<b>To create a new genus within:</b>		
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:	<b><i>Polyomaviridae</i></b>	
Order:		

naming a new genus

Code	<b>2015.015oD</b>	(assigned by ICTV officers)
<b>To name the new genus: <i>Deltapolyomavirus</i></b>		

Assigning the type species and other species to a new genus

Code	<b>2015.015pD</b>	(assigned by ICTV officers)
<b>To designate the following as the type species of the new genus</b>		
<b><i>Human polyomavirus 6</i></b>		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). <b>Please enter here the TOTAL number of species (including the type species) that the genus will contain:</b>		
<b>4</b>		

**Reasons to justify the creation of a new genus:**

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

The genus is based on statistically well supported phylogenetic tree topology calculated from large T antigen amino acid sequences (Figure 2; Appendix).

**Origin of the new genus name:**

It is derived from the greek alphabet in combination with the family name.

**Reasons to justify the choice of type species:**

First discovered member of the genus

**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.

As shown in module 2

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	<b>2015.015qD</b>	(assigned by ICTV officers)
<b>To remove the following taxon (or taxa) from their present position:</b>		
<b>Genus <i>Polyomavirus</i></b>		
<b>The present taxonomic position of these taxon/taxa:</b>		
Genus:		Fill in all that apply.
Subfamily:		
Family:	<i>Polyomaviridae</i>	
Order:		
If the taxon/taxa are to be abolished (i.e. not reassigned to another taxon) write "yes" in the box on the right		
<b>Reasons to justify the removal:</b>		
Explain why the taxon (or taxa) should be removed		
<b>The genus is replaced by 4 new genera (see modules 3)</b>		

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	<b>2015.015rD</b>	(assigned by ICTV officers)
<b>To remove the following taxon (or taxa) from their present position:</b>		
<p><b>Species <i>African green monkey polyomavirus</i></b>  <b>Species <i>Baboon polyomavirus 2</i></b>  <b>Species <i>Human polyomavirus</i></b>  <b>Species <i>Rabbit kidney vacuolating virus</i></b>  <b>Species <i>Simian virus 12</i></b></p>		
<b>The present taxonomic position of these taxon/taxa:</b>		
Genus:		Fill in all that apply.
Subfamily:		
Family:	<i>Polyomaviridae</i>	
Order:		
If the taxon/taxa are to be abolished (i.e. not reassigned to another taxon) write "yes" in the box on the right		<b>YES</b>

**Reasons to justify the removal:**

Explain why the taxon (or taxa) should be removed

**The 5 species were provisional and shall now be abolished from the *Polyomaviridae*, because of the following reasons:**

**African green monkey polyomavirus: host is uncertain**

**Baboon polyomavirus 2: no genome sequence available**

**Human polyomavirus: this provisional species name is vague and as such cannot be assigned to a specific virus**

**Rabbit kidney vacuolating virus: no genome sequence available**

**Simian virus 12: host is uncertain**

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	<b>2015.015sD</b>	(assigned by ICTV officers)
<b>To remove the following taxon (or taxa) from their present position:</b>		
Species <i>Murine polyomavirus</i> Species <i>Hamster polyomavirus</i>		
<b>The present taxonomic position of these taxon/taxa:</b>		
Genus:	<i>Polyomavirus (to be removed)</i>	Fill in all that apply.
Subfamily:		
Family:	<i>Polyomaviridae</i>	
Order:		
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:**

Explain why the taxon (or taxa) should be removed

**The genus *Polyomavirus* shall be removed and be replaced by 4 novel genera.**

**Part (b)** re-assign to a higher taxon

Code	<b>2015.015tD</b>	(assigned by ICTV officers)
<b>To re-assign the taxon (or taxa) listed in Part (a) as follows:</b>		
Genus:	<i>Alphapolyomavirus (new)</i>	Fill in all that apply. • If the higher taxon has yet to be created write " <b>(new)</b> " after its proposed name and complete relevant module to create it. If no genus is specified, enter " <b>unassigned</b> " in the genus box.
Subfamily:		
Family:	<i>Polyomaviridae</i>	
Order:		

**Reasons to justify the re-assignment:**

- If it is proposed to re-assign species to an existing genus, please 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 accession numbers for genomic sequences
- Further material in support of this proposal may be presented in the Appendix, Module 9

**The species are part of the phylogenetic clade that constitutes the new genus *Alphapolyomavirus*.**

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	<b>2015.015uD</b>	(assigned by ICTV officers)
<b>To remove the following taxon (or taxa) from their present position:</b>		
<p><b>Species <i>BK polyomavirus</i></b>  <b>Species <i>JC polyomavirus</i></b>  <b>Species <i>Murine pneumotropic virus</i></b>  <b>Species <i>Simian virus 40</i></b></p>		
<b>The present taxonomic position of these taxon/taxa:</b>		
Genus:	<i>Polyomavirus (to be removed)</i>	Fill in all that apply.
Subfamily:		
Family:	<i>Polyomaviridae</i>	
Order:		
<p>If the taxon/taxa are to be abolished (i.e. not reassigned to another taxon) write "yes" in the box on the right</p>		

**Reasons to justify the removal:**

Explain why the taxon (or taxa) should be removed

**The genus *Polyomavirus* shall be removed and be replaced by 4 novel genera.**

**Part (b)** re-assign to a higher taxon

Code	<b>2015.015vD</b>	(assigned by ICTV officers)
<b>To re-assign the taxon (or taxa) listed in Part (a) as follows:</b>		
Genus:	<i>Betapolyomavirus (new)</i>	<p>Fill in all that apply.</p> <ul style="list-style-type: none"> <li>• If the higher taxon has yet to be created write "<b>(new)</b>" after its proposed name and complete relevant module to create it.</li> </ul> <p>If no genus is specified, enter "<b>unassigned</b>" in the genus box.</p>
Subfamily:		
Family:	<i>Polyomaviridae</i>	
Order:		

**Reasons to justify the re-assignment:**

- If it is proposed to re-assign species to an existing genus, please 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 accession numbers for genomic sequences
- Further material in support of this proposal may be presented in the Appendix, Module 9

**The species are members of the phylogenetic clade that constitutes the new genus *Betapolyomavirus*.**



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	<b>2015.015wD</b>	(assigned by ICTV officers)
<b>To remove the following taxon (or taxa) from their present position:</b>		
<b>Species <i>Budgerigar fledgling disease polyomavirus</i></b>		
<b>The present taxonomic position of these taxon/taxa:</b>		
Genus:	<i>Polyomavirus (to be removed)</i>	Fill in all that apply.
Subfamily:		
Family:	<i>Polyomaviridae</i>	
Order:		
If the taxon/taxa are to be abolished (i.e. not reassigned to another taxon) write "yes" in the box on the right		
<b>Reasons to justify the removal:</b>		
Explain why the taxon (or taxa) should be removed		
<b>The genus <i>Polyomavirus</i> shall be removed and be replaced by 4 novel genera.</b>		

**Part (b)** re-assign to a higher taxon

Code	<b>2015.015xD</b>	(assigned by ICTV officers)
<b>To re-assign the taxon (or taxa) listed in Part (a) as follows:</b>		
Genus:	<i>Gammapolyomavirus (new)</i>	Fill in all that apply. <ul style="list-style-type: none"> <li>• If the higher taxon has yet to be created write "<b>(new)</b>" after its proposed name and complete relevant module to create it.</li> <li>If no genus is specified, enter "<b>unassigned</b>" in the genus box.</li> </ul>
Subfamily:		
Family:	<i>Polyomaviridae</i>	
Order:		

**Reasons to justify the re-assignment:**

- If it is proposed to re-assign species to an existing genus, please 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 accession numbers for genomic sequences
- Further material in support of this proposal may be presented in the Appendix, Module 9

**The species is part of the phylogenetic clade that constitutes the new genus *Gammapolyomavirus*.**

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	<b>2015.015yD</b>	(assigned by ICTV officers)
<b>To remove the following taxon (or taxa) from their present position:</b>		
<b>Species <i>Bovine polyomavirus</i></b>		
<b>The present taxonomic position of these taxon/taxa:</b>		
Genus:	<i>Polyomavirus</i> (to be removed)	Fill in all that apply.
Subfamily:		
Family:	<i>Polyomaviridae</i>	
Order:		
If the taxon/taxa are to be abolished (i.e. not reassigned to another taxon) write "yes" in the box on the right		
<b>Reasons to justify the removal:</b> Explain why the taxon (or taxa) should be removed		
<b>The genus <i>Polyomavirus</i> shall be removed.</b>		

**Part (b)** re-assign to a higher taxon

Code	<b>2015.015zD</b>	(assigned by ICTV officers)
<b>To re-assign the taxon (or taxa) listed in Part (a) as follows:</b>		
Genus:	<i>unassigned</i>	Fill in all that apply. <ul style="list-style-type: none"> <li>• If the higher taxon has yet to be created write "<b>(new)</b>" after its proposed name and complete relevant module to create it.</li> <li>If no genus is specified, enter "<b>unassigned</b>" in the genus box.</li> </ul>
Subfamily:		
Family:	<i>Polyomaviridae</i>	
Order:		

**Reasons to justify the re-assignment:**

- If it is proposed to re-assign species to an existing genus, please 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 accession numbers for genomic sequences
- Further material in support of this proposal may be presented in the Appendix, Module 9

**The species is not member of any of the 4 phylogenetic clades that constitute the 4 new genera.**

MODULE 8: **RENAME**

Use this module to change the name of one or more existing taxa (but note that stability of nomenclature is encouraged wherever possible). Insert extra lines in the table if needed.

Renaming one or more taxa

Code	<b>2015.015aaD</b>	(assigned by ICTV officers)
<b>To rename the following taxon (or taxa):</b>		
<b>Current name</b>	<b>Proposed name</b>	
<i>BK polyomavirus</i>	<i>Human polyomavirus 1</i>	
<i>Bovine polyomavirus</i>	<i>Bos taurus polyomavirus 1</i>	
<i>Budgerigar fledgling disease polyomavirus</i>	<i>Aves polyomavirus 1</i>	
<i>Hamster polyomavirus</i>	<i>Mesocricetus auratus polyomavirus 1</i>	
<i>JC polyomavirus</i>	<i>Human polyomavirus 2</i>	
<i>Murine polyomavirus</i>	<i>Mus musculus polyomavirus 1</i>	
<i>Murine pneumotropic virus</i>	<i>Mus musculus polyomavirus 2</i>	
<i>Simian virus 40</i>	<i>Macaca mulatta polyomavirus 1</i>	
<b>Reasons to justify the renaming:</b>		
Explain why the taxon (or taxa) should be renamed		
Renaming is necessary in order to follow the proposed new naming rule (Latin host species name plus “ <i>polyomavirus</i> ”, followed by a consecutive number).		

## Genus delineation

The accelerated pace of polyomavirus (PyV) discovery has resulted in the identification of as many as >100 viral species candidates over the last decade (as per the new species demarcation criterion; see document attached). The Polyomaviridae Study Group (SG) therefore considered an urgent issue to officially propose novel genera. The proposal of the last SG, although published, had not been formally approved by the ICTV [1], with the result that the committee currently recognizes a single genus, *Polyomavirus*, within the family.

Most novel PyVs have not yet been isolated. The extent of biological information we can get about them is essentially restricted to their host, genomic organization and evolutionary relationships.

PyVs appear to be very host specific. Despite the use of broad-ranging and flexible detection methods, there is no report about any PyV first discovered in an organism and later detected in another (with the exception of SV40 and budgerigar fledgling disease polyomavirus). Across family level phylogenies there is little evidence for pronounced co-divergence with their hosts [2], but when it comes to the very deep nodes they mostly support the separation of PyVs infecting birds and mammals. Although the lack of observed co-divergence may reflect a mere sampling artifact (and be corrected in the future), at the moment there is no real possibility to use hosts as a major factor (or virus trait) to build a taxonomy upon.

The genomic organization of PyVs is very stable. Although a number of accessory open reading frames have been described, a single one could be ascribed as a landmark characterizing a monophyletic group of PyVs (ALTO; [3]). Altogether it therefore seems that genomic organization cannot really be considered as a driving element for genus-level delineation.

This paucity of information leaves the SG with the unique option to use reconstructed evolutionary relationships for the delineation of genera. Although the SG acknowledges that full-genome analyses would in principle be the ideal tool box [4], the recent realization that recombination events can significantly reshuffle sometimes long-diverged genomes call for precaution [2, 5]. The SG therefore recommends that a single of the three major coding sequences be used for the delineation of genera. To the best of the SG knowledge, there has been no report thus far of meaningful recombination events within these three coding sequences. The SG proposes that evolutionary relationships derived from analyses of the large T antigen (LT) sequences be used for this purpose. Our estimate of amino acid rate variation based on relaxed molecular clock models run with BEAST v1.8.2 was lower for LT than for VP1 and VP2 (Figure A1), which facilitates phylogenetic analyses. In addition, more internal branches appear as relatively well supported with this same fragment, as notably revealed by overlaying posterior sets of trees generated with BEAST v1.8.2 with DensiTree v2.01 (Figure A2).

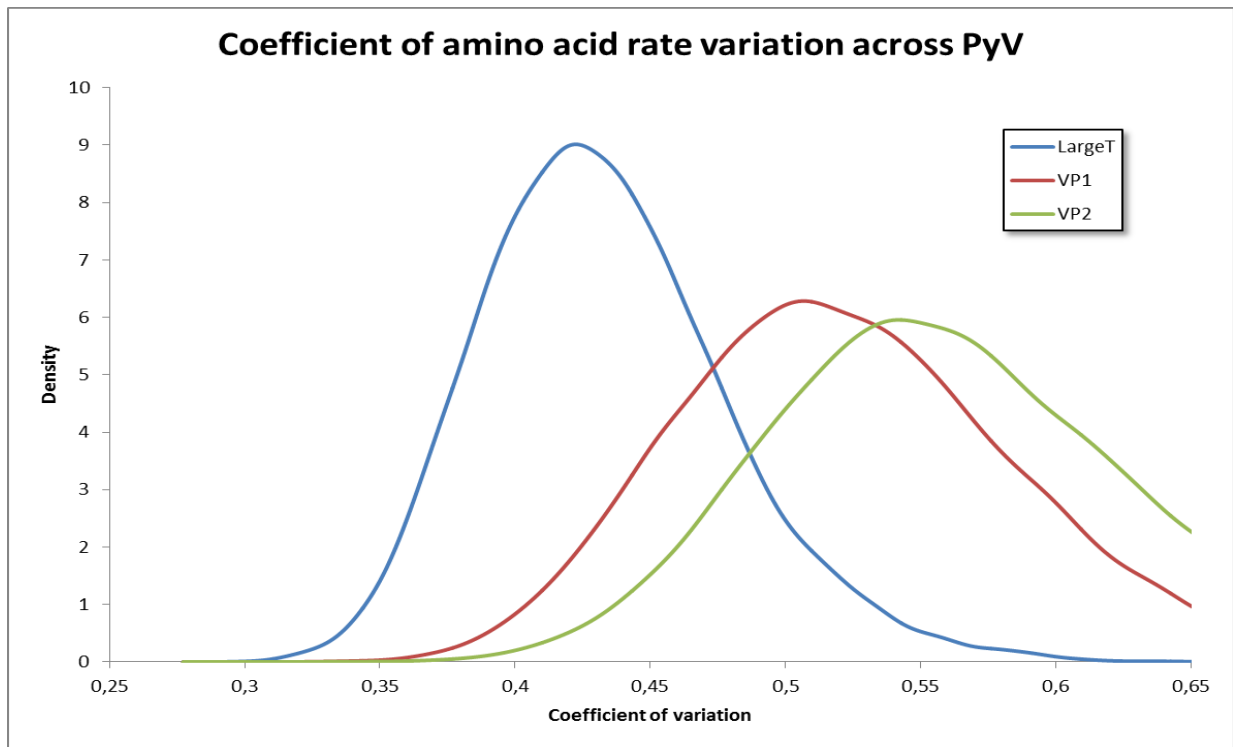
Figure A3 represents a chronogram derived from an alignment of conserved amino acid blocks (selected with Gblocks v0.1) and reconstructed with BEAST v1.8.2 under the best model of amino acid substitution (LG+F+I+G; as determined with ProtTest v3.2), a relaxed clock (lognormal) and a birth-death model of speciation. As far as the SG is aware, it comprises sequences representative of most lineages described to date; only unique sequences with >5%

amino acid divergence were retained here. Tips display species names (black), vernacular names followed by accession numbers (grey) or, in the case of viruses other than polyomaviruses comprising a LT sequence, abbreviations followed by accession numbers. Note that not all newly created species appear in this tree, which was meant to help with genus delineation only. Branch thickness is proportional to their posterior probability support (thin branches are less and less supported). A similar topology was supported by an analysis with PhyML v3 using the BEST tree search algorithm. SH-aLRT/posterior probability support values are reported above branches.

It should be noted that frequency plots of observed or patristic distances did not allow for the identification of any clear taxonomic gap, whether with LT, VP1 or VP2 (data not shown). Based on this, the SG recommends the creation of four genera. These four genera stand for four relatively large radiations of PyV that altogether collect most of the species created by the SG. The only exceptions are *Centropristis striata polyomavirus 1*, *Bos taurus polyomavirus 1* and *Delphinus delphis polyomavirus 1*, which are not assigned to any genus. The virus populating the species *Centropristis striata polyomavirus 1* is the only published PyV infecting fish (other fish PyVs are available in GenBank but are not published) while the phylogenetic placement of the PyVs populating the species *Bos taurus polyomavirus 1* and *Delphinus delphis polyomavirus 1* comes with some ambiguity (analyses restricted to mammalian PyV weakly support their sistership, in disagreement with Figure A3; data not shown).

The genus *Gammampolyomavirus* [1] gathers all PyV known to infect birds; its type species is *Aves polyomavirus 1*. The three other genera are only known to infect mammals; their most recent common ancestors (MRCA) approximately emerged in the same timeframe as the MRCA of the genus *Gammampolyomavirus*. The type species of the genus *Alphapolyomavirus* is *Mus musculus polyomavirus 1* (common name: murine polyomavirus; the first PyV discovered). The type species of the genus *Betapolyomavirus* is *Macaca mulatta polyomavirus 1* (common name: SV40; the first discovered PyV in this genus). The type species of the genus *Deltapolyomavirus* is *Human polyomavirus 6* (common name: human polyomavirus 6; the first discovered PyV in this genus). All (but the three abovementioned) PyV species recognized by the SG have been assigned to a genus.

The assignment of novel PyV to any genus will rely on their unambiguous phylogenetic placement within the according clade, as demonstrated by sound phylogenetic analyses.

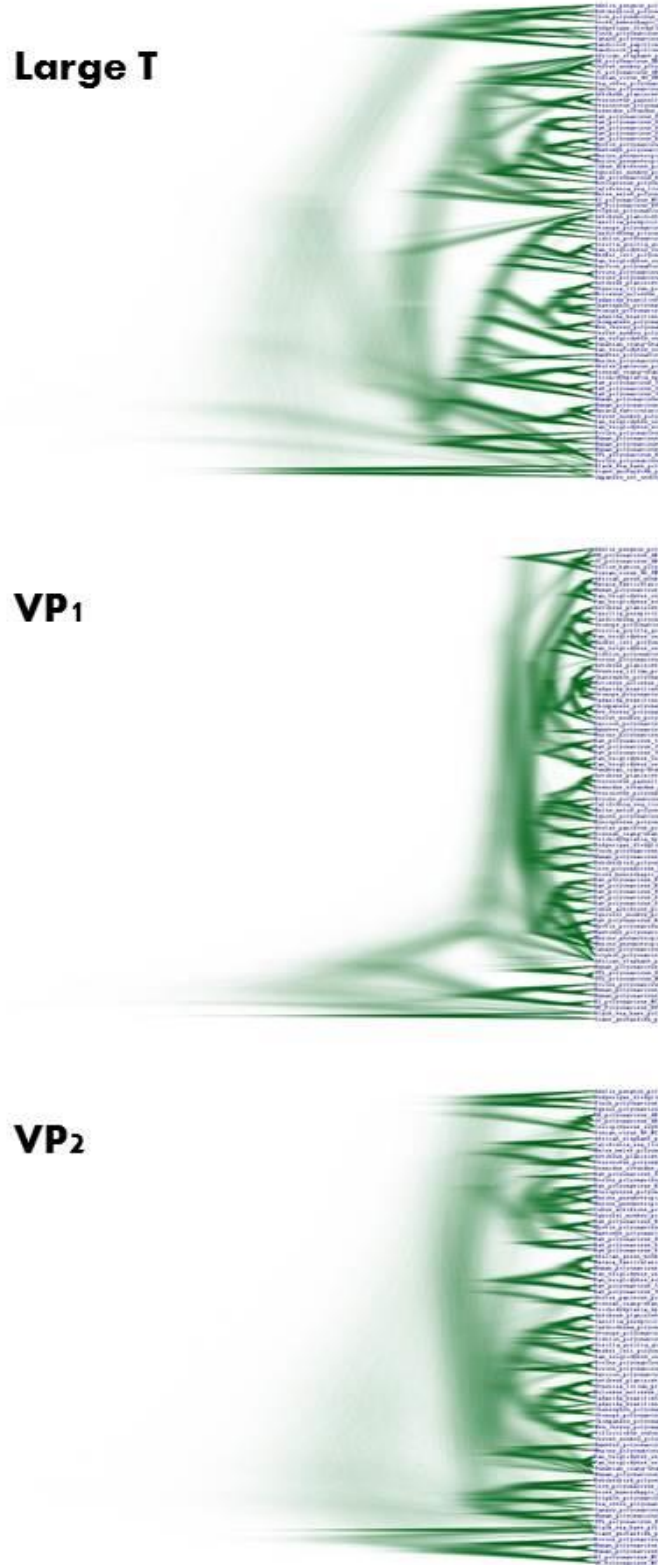


**Figure A1. Bayesian estimates of the coefficient of variation of the amino acid substitution rate (across lineages).**

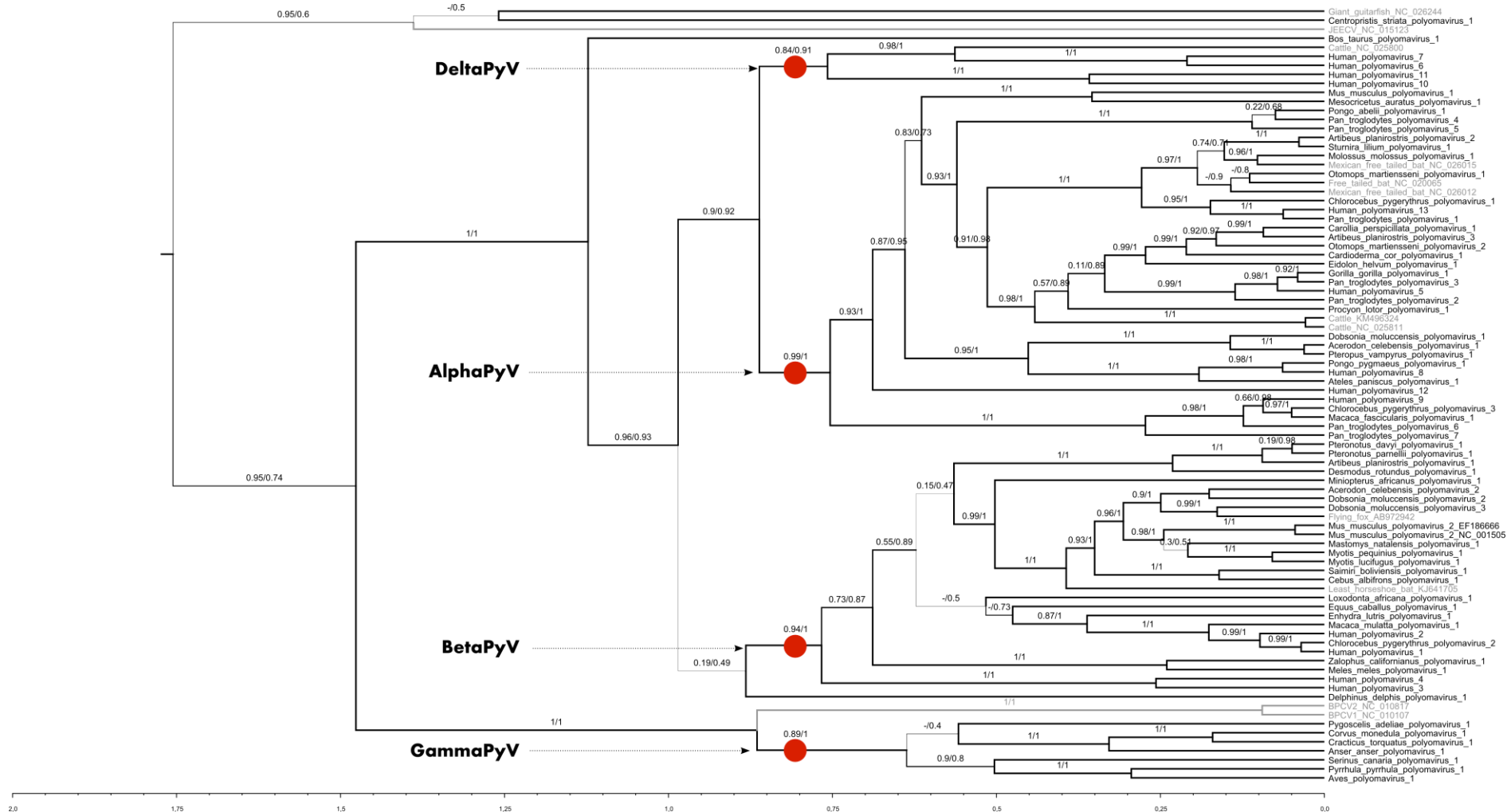
**Large T**

**VP<sub>1</sub>**

**VP<sub>2</sub>**



**Figure A2. Superposition of sets of posterior trees.** In all cases, 9000 posterior trees were overlaid using DensiTree v2.01. Fuzziness and branch intersections indicate branch length and topological uncertainty.



**Figure A3.** LT-derived Bayesian chronogram of the family *Polyomaviridae*. The branches supporting the existence of the four genera whose creation is recommended by the SG are highlighted with a red circle. Branch supports are reported above branches (SH-aLRT/posterior probability). Detailed methods are described in the text. PyV: polyomavirus.



## References:

1. Johnes R, Buck CB, Allander T, Atwood WJ, Garcea RL, Imperiale MJ, Major EO, Ramqvist T, Norkin LC: **Taxonomical developments in the family Polyomaviridae.** *Arch Virol* 2011, **156**:1627-1634.
  2. Tao Y, Shi M, Conrardy C, Kuzmin IV, Recuenco S, Agwanda B, Alvarez DA, Ellison JA, Gilbert AT, Moran D, et al: **Discovery of diverse polyomaviruses in bats and the evolutionary history of the Polyomaviridae.** *J Gen Virol* 2013, **94**:738-748.
  3. Carter JJ, Daugherty MD, Qi X, Bheda-Malge A, Wipf GC, Robinson K, Roman A, Malik HS, Galloway DA: **Identification of an overprinting gene in Merkel cell polyomavirus provides evolutionary insight into the birth of viral genes.** *Proc Natl Acad Sci U S A* 2013, **110**:12744-12749.
  4. Lauber C, Gorbalenya AE: **Partitioning the genetic diversity of a virus family: approach and evaluation through a case study of picornaviruses.** *J Virol* 2012, **86**:3890-3904.
  5. Lim ES, Reyes A, Antonio M, Saha D, Ikumapayi UN, Adeyemi M, Stine OC, Skelton R, Brennan DC, Mkakosya RS, et al: **Discovery of STL polyomavirus, a polyomavirus of ancestral recombinant origin that encodes a unique T antigen by alternative splicing.** *Virology* 2013, **436**:295-303.
-