

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:	2016.001a-agF			(to be completed by ICTV officers)		
Short title: Establishing eight in Genomoviridae (e.g. 6 new species in the genus 2 Modules attached (modules 1 and 11 are required)	_	1 🖂 6 🗌 11 🖂	hree spec	ies in the 3 ⊠ 8 □	family 4	5
Author(s):						
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mart.krupovic@pasteur.fr; avar	rsani@gmail.c	<u>om</u>				
List the ICTV study group(s)	that have see	n this pro	posal:			
A list of study groups and contacts http://www.ictvonline.org/subcommin doubt, contact the appropriate schair (fungal, invertebrate, plant, pvertebrate viruses)	mittees.asp . If subcommittee					
ICTV Study Group comment	s (if any) and	response	of the pro	poser:		
Date first submitted to ICTV: Date of this revision (if differen	nt to above):		July 2	2016		
ICTV-EC comments and response of the proposer:						

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.

Genus: Gemycircularvirus  Subfamily: Genomoviridae Order: Family: Genomoviridae Order: Genomo	Code	201	6.001aF		(assigned by IC	TV office	rs)	
Subfamily:   Genomoviridae   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.   Name of new species:   Representative isolate: (only 1 per species please)   RF371641	To crea	ite 42 r	new species within	:				
Subfamily:   Genomoviridae   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.   Name of new species:   Representative isolate: (only 1 per species please)   RF371641						Fill in	all that apply.	
Subfamily: Genomoviridae Order: Ramily: Genomoviridae Order: Representative isolate: ('new)' after its proposed name.  *If no genus is specified, enter "unassigned" in the genus box.  *Representative isolate: (only 1 per species please)  Blackbird associated gemycircularvirus 1  Bovine associated gemycircularvirus 1  Bovine associated gemycircularvirus 1  Bovine associated gemycircularvirus 1  Chickaele associated gemycircularvirus 1  Chickaele associated gemycircularvirus 1  Chickaele associated gemycircularvirus 1  Chickael associated gemycircularvirus 1  Chickael associated gemycircularvirus 1  Chickaele associated gemycircularvirus 1  Fuz-5x-2010  JX185429  Equina associated gemycircularvirus 1  Fuz-seal associated gemycircularvirus 1  Gerygone associated gemycircularvirus 1  Gerygone associated gemycircularvirus 1  Gerygone associated gemycircularvirus 3  Hypericum associated gemycircularvirus 3  P24a  Kr371637  Gerygone associated gemycircularvirus 3  Hypericum associated gemycircularvirus 1  Mallard associated gemycircularvirus 1  Mallard associated gemycircularvirus 1  Mongoose associated gemycircularvirus 1  Porcine associated gemycircularvirus 2  Porcine associated gemycircularvirus 3  Porcine associated gemycircularvirus 3  Porcine associated gemycircularvirus 3  Porcine associated gemycircularvirus 3  Porcine associated gemycircularvirus 4  Porcine associated gemycircularvirus 5  Total 103791  Fireropus associated gemycircularvirus 7	(	denus:	Gemycircularviru	2.5				
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Sewage derived gemycircularvirus 1 BS3917 KJ547638							KJ547638	

Sewage derived gemycircularvirus 2	BS4117	KJ547641
Sewage derived gemycircularvirus 3	BS4014	KJ547636
Sewage derived gemycircularvirus 4	BS3972	KJ547640
Sewage derived gemycircularvirus 5	BS3970	KJ547639
Sheep associated gemycircularvirus 1	47 Fec80064 sheep	KT862249
Soybean associated gemycircularvirus 1	SlaGemV1-1	KT598248

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

- Explain how the proposed species differ(s) from all existing species.
  - o If species demarcation criteria (see module 3) have previously been defined for the genus, **explain how the new species meet these criteria**.
  - o 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 11

Currently the genus *Gemycircularvirus* contains a single species, *Sclerotinia gemycircularvirus I*, encompassing a single isolate, Sclerotinia sclerotiorum hypovirulence-associated DNA virus 1 (SsHADV-1) (Krupovic et al., 2016). However, 120 viral genomes with varying degree of similarity — from rather divergent to nearly identical — to that of SsHADV-1 have been sequenced from various samples. Although initially detected by high-throughput sequencing the vast majority (~90%) of these genomes were subsequently PCR amplified from the original samples, cloned and sequenced using Sanger method to ensure high quality of the genomic data. A proper taxonomic framework and demarcation criteria are necessary to accommodate these viruses within the family *Genomoviridae*. The purpose of this proposal is to establish such demarcation criteria.

Maximum likelihood phylogenetic analyses based on the rolling circle replication initiation protein (RC-Rep) of 121 genomoviruses revealed several well-supported clades that could be considered as genera within the family (Figure 1). Genomoviruses form a sister group to geminiviruses in the RC-Rep-based phylogenetic analyses (Krupovic et al., 2016). Thus, to assess the taxonomic structure of the *Genomoviridae*, we used geminiviral sequences as a guide. Five clades and 4 additional singletons within the *Genomoviridae* branch display equivalent intra-family divergence as the established genera within the family *Geminiviridae* in both nucleotide and protein sequence inferred phylogenies (Figure 2).

Consequently, in module 3 we propose to establish 8 new genera (in addition to the existing genus *Gemycircularvirus*) within the family *Genomoviridae* (see below). We note that the clades obtained in the RC-Rep based phylogeny are not fully consistent with those obtained in the phylogenetic analysis of the full genome or the highly diverse capsid protein (CP) sequences (Figure 3, 4, 5). The reason for this mismatch is likely to be intra-familial recombination between different genomovirus genomes resulting in chimeric entities encoding RC-Rep and CP with different evolutionary histories. Given that CP sequences of genomoviruses are considerably more divergent that the RC-Rep sequences (Figure 5), it appears reasonable to establish the taxonomic framework using the RC-Rep (Figure 4). The latter protein is also conserved in other eukaryotic ssDNA viruses (which is not the case for the capsid proteins) and can thus be used to assess the place of genomoviruses within the larger community of ssDNA viruses.

To determine the optimal species demarcation criteria within the tentative genera, we analyzed the distribution of genome-wide pairwise identities (one minus Hamming distances of pairwise aligned sequences with pairwise deletion of gaps) across all 121 genomes that fall into the *Genomoviridae* family (Figure 2, 6). The analysis has shown that 78% pairwise identity might

be a conservative value for species demarcation.

All of the proposed species (n=43; 73 isolates) within the genus *Gemycircularvirus* share between 56% and 77% genome-wide sequence similarity with other isolates within the same genus. Isolates within the 43 species cluster with 99% and 96% branch support within phylogenetic trees constructed from either RC-Rep or full genome sequences respectively (Figure 3-4).

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	201	6.001bF	(assigned by IC	(assigned by ICTV officers)			
To crea	ate 16 1	new species within	ı:				
					all that apply.		
	Genus:	Gemykibivirus (n	iew)		ne higher taxon has yet to be		
Subf	amily:				ated (in a later module, below) write <b>ew)</b> " after its proposed name.		
Fa	amily:	Genomoviridae		If no genus is specified, enter			
	Order:				assigned" in the genus box.		
Name (	of new	species:	Representative iso	late:	GenBank sequence accession		

Name of new species:	Representative isolate: (only 1 per species please)	GenBank sequence accession number(s)
Badger associated gemykibivirus 1	588t	KP263543
Black robin associated gemykibivirus 1	P21	KF371634
Blackbird associated gemykibivirus 1	P22	KF371633
Bovine associated gemykibivirus 1	HCBI8.215	LK931483
Dragonfly associated gemykibivirus 1	FL1-2X-2010	JX185430
Human associated gemykibivirus 1	MSSI2.225	LK931485
Human associated gemykibivirus 2	SL1	KP133075
Human associated gemykibivirus 3	GemyC1c	KP987887
Human associated gemykibivirus 4	GeTz1	KT363839
Human associated gemykibivirus 5	HV-GcV2	KU343137
Mongoose associated gemykibivirus 1	160b	KP263545
Pteropus associated gemykibivirus 1	Tbat A 64418	KT732813
Rhinolophus associated gemykibivirus 1	BtRh-CV-6/Tibet2013	KJ641737
Rhinolophus associated gemykibivirus 2	BtRf-CV-8/NM2013	KJ641726
Sewage derived gemykibivirus 1	BS4149	KJ547643
Sewage derived gemykibivirus 2	BS3911	KJ547642

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

- Explain how the proposed species differ(s) from all existing species.
  - o If species demarcation criteria (see module 3) have previously been defined for the genus, **explain how the new species meet these criteria**.
  - o 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 11

Maximum likelihood phylogenetic analyses based on the rolling circle replication initiation protein (RC-Rep) of 121 genomoviruses revealed several well-supported clades that could be considered as genera within the family (Figure 1). Genomoviruses form a sister group to geminiviruses in the RC-Rep-based phylogenetic analyses (Krupovic et al., 2016). Thus, to assess the taxonomic structure of the *Genomoviridae*, we used geminiviral sequences as a guide. Five clades and 4 additional singletons within the *Genomoviridae* branch display equivalent intra-family divergence as the established genera within the family *Geminiviridae* in both nucleotide and protein sequence inferred phylogenies (Figure 2).

Consequently, in module 3 we propose to establish 8 new genera (in addition to the existing genus *Gemycircularvirus*) within the family *Genomoviridae* (see below). We note that the clades obtained in the RC-Rep based phylogeny are not fully consistent with those obtained in the phylogenetic analysis of the full genome or the highly diverse capsid protein (CP) sequences (Figure 3, 4, 5). The reason for this mismatch is likely to be intra-familial recombination between different genomovirus genomes resulting in chimeric entities encoding RC-Rep and CP with different evolutionary histories. Given that CP sequences of genomoviruses are considerably more divergent that the RC-Rep sequences (Figure 5), it appears reasonable to establish the taxonomic framework using the RC-Rep (Figure 4). The latter protein is also conserved in other eukaryotic ssDNA viruses (which is not the case for the capsid proteins) and can thus be used to assess the place of genomoviruses within the larger community of ssDNA viruses.

To determine the optimal species demarcation criteria within the tentative genera, we analyzed the distribution of genome-wide pairwise identities (one minus Hamming distances of pairwise aligned sequences with pairwise deletion of gaps) across all 121 genomes that fall into the *Genomoviridae* family (Figure 2, 6). The analysis has shown that 78% pairwise identity might be a conservative value for species demarcation.

All of the proposed species (n=16; 29 isolates) within the genus *Gemykibivirus* share between 57% and 77% genome-wide sequence similarity with other isolates within the same genus. Isolates within the 15 species cluster with 99% branch support within phylogenetic trees constructed from RC-Rep and two well supported clades (100 and 96%) from full genome sequences (Figure 3-4).

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	Code $2016.001cF$ (assigned by IC			TV office	rs)		
To crea	te 5 no	ew species within:					
						all that apply.	
G	enus:	Gemygorvirus (no	ew)			e higher taxon has yet to be	
Subfa	mily:					ated (in a later module, below) write ew)" after its proposed name.	
Fa	mily:	Genomoviridae			<ul> <li>If no genus is specified, enter</li> </ul>		
(	Order:	er:			"unassigned" in the genus box.		
Name of new species:		_	epresentative isolate: nly 1 per species please)		GenBank sequence accession number(s)		
Canine as	sociated	gemygorvirus 1	53 Fe	c7 dog		KT862254	
Mallard associated gemygorvirus 1 4 Fec7		7 duck		KT862238			
Pteropus associated gemygorvirus 1 Tbat		Tbat A	\ 103952		KT732790		
Sewage derived gemygorvirus 1 BS396		63		KJ547635			
Starling associated gemygorvirus 1 P14				KF371632			

## 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.
  - o 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 11

Maximum likelihood phylogenetic analyses based on the rolling circle replication initiation protein (RC-Rep) of 121 genomoviruses revealed several well-supported clades that could be considered as genera within the family (Figure 1). Genomoviruses form a sister group to geminiviruses in the RC-Rep-based phylogenetic analyses (Krupovic et al., 2016). Thus, to assess the taxonomic structure of the *Genomoviridae*, we used geminiviral sequences as a guide. Five clades and 4 additional singletons within the *Genomoviridae* branch display equivalent intra-family divergence as the established genera within the family *Geminiviridae* in both nucleotide and protein sequence inferred phylogenies (Figure 2).

Consequently, in module 3 we propose to establish 8 new genera (in addition to the existing genus *Gemycircularvirus*) within the family *Genomoviridae* (see below). We note that the clades obtained in the RC-Rep based phylogeny are not fully consistent with those obtained in the phylogenetic analysis of the full genome or the highly diverse capsid protein (CP) sequences (Figure 3, 4, 5). The reason for this mismatch is likely to be intra-familial recombination between different genomovirus genomes resulting in chimeric entities encoding RC-Rep and CP with different evolutionary histories. Given that CP sequences of genomoviruses are considerably more divergent that the RC-Rep sequences (Figure 5), it appears reasonable to establish the taxonomic framework using the RC-Rep (Figure 4). The latter protein is also conserved in other eukaryotic ssDNA viruses (which is not the case for the capsid proteins) and can thus be used to assess the place of genomoviruses within the larger community of ssDNA viruses.

To determine the optimal species demarcation criteria within the tentative genera, we analyzed the distribution of genome-wide pairwise identities (one minus Hamming distances of pairwise aligned sequences with pairwise deletion of gaps) across all 121 genomes that fall into the *Genomoviridae* family (Figure 2, 6). The analysis has shown that 78% pairwise identity might be a conservative value for species demarcation.

All of the proposed species (n=5; 9 isolates) within the genus *Gemygorvirus* share between 61% and 77% genome-wide sequence similarity with other isolates within the same genus. Isolates within the 5 species cluster with 100% and 99% branch support within phylogenetic trees constructed from either RC-Rep or full genome sequences respectively (Figure 3-4).

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	<i>201</i>	6.001dF	(assigned by IC	CTV office	ers)
To crea	te 2 ne	ew species within:			
6	enus:	Gemykolovirus (n	10W)		all that apply. e higher taxon has yet to be
		Gemykolovirus (r	iew)		ated (in a later module, below) write
Subia	ımily:			"(ne	ew)" after its proposed name.
Fa	mily:	Genomoviridae		•	genus is specified, enter
(	Order:				assigned" in the genus box.
Name of new species:		Representative isolate: (only 1 per species please)		GenBank sequence accession number(s)	
Pteropus associated gemykolovirus 1 Tbat A		Tbat A 103779		KT732798	
Pteropus associated gemykolovirus 2 Tbat H 103921		Tbat H 103921		KT732800	

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

- Explain how the proposed species differ(s) from all existing species.
  - o If species demarcation criteria (see module 3) have previously been defined for the genus, **explain how the new species meet these criteria**.
  - o 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 11

Maximum likelihood phylogenetic analyses based on the rolling circle replication initiation protein (RC-Rep) of 121 genomoviruses revealed several well-supported clades that could be considered as genera within the family (Figure 1). Genomoviruses form a sister group to geminiviruses in the RC-Rep-based phylogenetic analyses (Krupovic et al., 2016). Thus, to assess the taxonomic structure of the *Genomoviridae*, we used geminiviral sequences as a guide. Five clades and 4 additional singletons within the *Genomoviridae* branch display equivalent intra-family divergence as the established genera within the family *Geminiviridae* in both nucleotide and protein sequence inferred phylogenies (Figure 2).

Consequently, in module 3 we propose to establish 8 new genera (in addition to the existing genus *Gemycircularvirus*) within the family *Genomoviridae* (see below). We note that the clades obtained in the RC-Rep based phylogeny are not fully consistent with those obtained in the phylogenetic analysis of the full genome or the highly diverse capsid protein (CP) sequences (Figure 3, 4, 5). The reason for this mismatch is likely to be intra-familial recombination between different genomovirus genomes resulting in chimeric entities encoding RC-Rep and CP with different evolutionary histories. Given that CP sequences of genomoviruses are considerably more divergent that the RC-Rep sequences (Figure 5), it appears reasonable to establish the taxonomic framework using the RC-Rep (Figure 4). The latter protein is also conserved in other eukaryotic ssDNA viruses (which is not the case for the capsid proteins) and can thus be used to assess the place of genomoviruses within the larger community of ssDNA viruses.

To determine the optimal species demarcation criteria within the tentative genera, we analyzed the distribution of genome-wide pairwise identities (one minus Hamming distances of pairwise aligned sequences with pairwise deletion of gaps) across all 121 genomes that fall into the *Genomoviridae* family (Figure 2, 6). The analysis has shown that 78% pairwise identity might be a conservative value for species demarcation.

All of the proposed species (n=2; 3 isolates) within the genus *Gemykolovirus* share between 63% and 77% genome-wide sequence similarity with other isolates within the same genus. Isolates within the 2 species cluster with 100% and 89% branch support within phylogenetic trees constructed from either RC-Rep or full genome sequences respectively (Figure 3-4).

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	201	6.001eF	(assigned by IC	TV office	ers)	
To crea	ite 1 ne	ew species within:				
					all that apply.	
G	Genus:	Gemyvongvirus (	new)	If the higher taxon has yet to be		
Subfa	amily:			created (in a later module, below) write  "(new)" after its proposed name.  • If no genus is specified, enter		
Fe	amily:	nily: Genomoviridae				
	Order:			"unassigned" in the genus box.		
Name of new species:		Representative isolate: (only 1 per species please)		GenBank sequence accession number(s)		
Human associated gemyvongvirus 1 DE		DB1		KP974693		

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

- Explain how the proposed species differ(s) from all existing species.
  - o If species demarcation criteria (see module 3) have previously been defined for the genus, **explain how the new species meet these criteria**.
  - o 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 11

Maximum likelihood phylogenetic analyses based on the rolling circle replication initiation protein (RC-Rep) of 121 genomoviruses revealed several well-supported clades that could be considered as genera within the family (Figure 1). Genomoviruses form a sister group to geminiviruses in the RC-Rep-based phylogenetic analyses (Krupovic et al., 2016). Thus, to assess the taxonomic structure of the *Genomoviridae*, we used geminiviral sequences as a guide. Five clades and 4 additional singletons within the *Genomoviridae* branch display equivalent intra-family divergence as the established genera within the family *Geminiviridae* in both nucleotide and protein sequence inferred phylogenies (Figure 2).

Consequently, in module 3 we propose to establish 8 new genera (in addition to the existing genus *Gemycircularvirus*) within the family *Genomoviridae* (see below). We note that the clades obtained in the RC-Rep based phylogeny are not fully consistent with those obtained in the phylogenetic analysis of the full genome or the highly diverse capsid protein (CP) sequences (Figure 3, 4, 5). The reason for this mismatch is likely to be intra-familial recombination between different genomovirus genomes resulting in chimeric entities encoding RC-Rep and CP with different evolutionary histories. Given that CP sequences of genomoviruses are considerably more divergent that the RC-Rep sequences (Figure 5), it appears reasonable to establish the taxonomic framework using the RC-Rep (Figure 4). The latter protein is also conserved in other eukaryotic ssDNA viruses (which is not the case for the capsid proteins) and can thus be used to assess the place of genomoviruses within the larger community of ssDNA viruses.

The single species *Human associated gemyvongvirus 1* within the genus *Gemyvongvirus* shares

between 56% and 62% genome-wide sequence similarity with other isolates in other genera and is a divergent taxon in the phylogenetic trees constructed from either RC-Rep or full genome sequences (Figure 3-4).

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.

	1110 01 (0) 101 0110 1001011				
Code <b>20</b>	16.001fF	(assigned by IC	TV office	rs)	
To create 3	new species within	:			
				all that apply.	
Genus	: Gemykrogvirus	(new)		e higher taxon has yet to be	
Subfamily	·:		created (in a later module, below) write  "(new)" after its proposed name.  • If no genus is specified, enter		
Family	: Genomoviridae				
Order	••			assigned" in the genus box.	
Name of new species:		Representative isol (only 1 per species pl		GenBank sequence accession number(s)	
Bovine associated gemykrogvirus 1 HCB1		HCB19.212		LK931484	
		FaGmCV-13		KJ938717	
Sewage derived	rage derived gemykrogvirus 1 BS3913		KJ547634		

#### 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**.
  - o 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 11

Maximum likelihood phylogenetic analyses based on the rolling circle replication initiation protein (RC-Rep) of 121 genomoviruses revealed several well-supported clades that could be considered as genera within the family (Figure 1). Genomoviruses form a sister group to geminiviruses in the RC-Rep-based phylogenetic analyses (Krupovic et al., 2016). Thus, to assess the taxonomic structure of the *Genomoviridae*, we used geminiviral sequences as a guide. Five clades and 4 additional singletons within the *Genomoviridae* branch display equivalent intra-family divergence as the established genera within the family *Geminiviridae* in both nucleotide and protein sequence inferred phylogenies (Figure 2).

Consequently, in module 3 we propose to establish 8 new genera (in addition to the existing genus *Gemycircularvirus*) within the family *Genomoviridae* (see below). We note that the clades obtained in the RC-Rep based phylogeny are not fully consistent with those obtained in the phylogenetic analysis of the full genome or the highly diverse capsid protein (CP) sequences (Figure 3, 4, 5). The reason for this mismatch is likely to be intra-familial recombination between different genomovirus genomes resulting in chimeric entities encoding RC-Rep and CP with different evolutionary histories. Given that CP sequences of genomoviruses are considerably more divergent that the RC-Rep sequences (Figure 5), it appears reasonable to establish the taxonomic framework using the RC-Rep (Figure 4). The latter protein is also conserved in other eukaryotic ssDNA viruses (which is not the case for the capsid proteins) and can thus be used to assess the place of genomoviruses within the larger community of ssDNA viruses.

To determine the optimal species demarcation criteria within the tentative genera, we analyzed the distribution of genome-wide pairwise identities (one minus Hamming distances of pairwise aligned sequences with pairwise deletion of gaps) across all 121 genomes that fall into the *Genomoviridae* family (Figure 2, 6). The analysis has shown that 78% pairwise identity might be a conservative value for species demarcation.

All of the proposed species (n=3; 3 isolates) within the genus *Gemykrogvirus* share between 67% and 77% genome-wide sequence similarity with other isolates within the same genus. Isolates within the 3 species cluster with 99% and 100% branch support within phylogenetic trees constructed from either RC-Rep or full genome sequences respectively (Figure 3-4).

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>20</b>	16.001gF	(assigned by IC	TV office	ers)		
To create 1	new species within:					
				all that apply.		
Genus	: Gemytondvirus (	new)	If the higher taxon has yet to be			
Subfamily	:			created (in a later module, below) write "(new)" after its proposed name.		
Family	: Genomoviridae		If no genus is specified, enter			
Order	:		"unassigned" in the genus box.			
Name of new species:		Representative isol (only 1 per species p		GenBank sequence accession number(s)		
Ostrich associated gemytondvirus 1 as3		as3		KF371630		

### 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.
  - o 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 11

Maximum likelihood phylogenetic analyses based on the rolling circle replication initiation protein (RC-Rep) of 121 genomoviruses revealed several well-supported clades that could be considered as genera within the family (Figure 1). Genomoviruses form a sister group to geminiviruses in the RC-Rep-based phylogenetic analyses (Krupovic et al., 2016). Thus, to assess the taxonomic structure of the *Genomoviridae*, we used geminiviral sequences as a guide. Five clades and 4 additional singletons within the *Genomoviridae* branch display equivalent intra-family divergence as the established genera within the family *Geminiviridae* in both nucleotide and protein sequence inferred phylogenies (Figure 2).

Consequently, in module 3 we propose to establish 8 new genera (in addition to the existing genus *Gemycircularvirus*) within the family *Genomoviridae* (see below). We note that the clades obtained in the RC-Rep based phylogeny are not fully consistent with those obtained in the phylogenetic analysis of the full genome or the highly diverse capsid protein (CP) sequences (Figure 3, 4, 5). The reason for this mismatch is likely to be intra-familial recombination between different genomovirus genomes resulting in chimeric entities encoding RC-Rep and CP with different evolutionary histories. Given that CP sequences of genomoviruses are considerably more divergent that the RC-Rep sequences (Figure 5), it appears reasonable to establish the taxonomic framework using the RC-Rep (Figure 4). The latter protein is also conserved in other eukaryotic ssDNA viruses (which is not the case for the capsid proteins) and can thus be used to assess the place of genomoviruses within the larger community of ssDNA viruses.

The single species Ostrich associated gemytondvirus 1 within the genus Gemytondvirus shares

between 53% and 61% genome-wide sequence similarity with other isolates in other genera and is a divergent taxon in the phylogenetic trees constructed from either RC-Rep or full genome sequences (Figure 3-4).

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>2</b> 6	01	016.001 hF (assigned by IC			ers)		
To create	1 ne	w species within:					
					all that apply.		
Gent	us:	us: Gemykroznavirus (new)			If the higher taxon has yet to be		
Subfami	ly:			created (in a later module, below) write "(new)" after its proposed name.			
Fami	lly:	Genomoviridae		If no genus is specified, enter			
Ord	er:				assigned" in the genus box.		
Name of new species:		Representative isolate: (only 1 per species please)		GenBank sequence accession number(s)			
Rabbit associated gemykroznavirus 1 as3:		as35		KF371631			

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

- Explain how the proposed species differ(s) from all existing species.
  - o If species demarcation criteria (see module 3) have previously been defined for the genus, **explain how the new species meet these criteria**.
  - o 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 11

Maximum likelihood phylogenetic analyses based on the rolling circle replication initiation protein (RC-Rep) of 121 genomoviruses revealed several well-supported clades that could be considered as genera within the family (Figure 1). Genomoviruses form a sister group to geminiviruses in the RC-Rep-based phylogenetic analyses (Krupovic et al., 2016). Thus, to assess the taxonomic structure of the *Genomoviridae*, we used geminiviral sequences as a guide. Five clades and 4 additional singletons within the *Genomoviridae* branch display equivalent intra-family divergence as the established genera within the family *Geminiviridae* in both nucleotide and protein sequence inferred phylogenies (Figure 2).

Consequently, in module 3 we propose to establish 8 new genera (in addition to the existing genus *Gemycircularvirus*) within the family *Genomoviridae* (see below). We note that the clades obtained in the RC-Rep based phylogeny are not fully consistent with those obtained in the phylogenetic analysis of the full genome or the highly diverse capsid protein (CP) sequences (Figure 3, 4, 5). The reason for this mismatch is likely to be intra-familial recombination between different genomovirus genomes resulting in chimeric entities encoding RC-Rep and CP with different evolutionary histories. Given that CP sequences of genomoviruses are considerably more divergent that the RC-Rep sequences (Figure 5), it appears reasonable to establish the taxonomic framework using the RC-Rep (Figure 4). The latter protein is also conserved in other eukaryotic ssDNA viruses (which is not the case for the capsid proteins) and can thus be used to assess the place of genomoviruses within the larger community of ssDNA viruses.

The single species Rabbit associated gemykroznavirus 1 within the genus Gemykroznavirus

shares between 56% and 61% genome-wide sequence similarity with other isolates in other genera and is a divergent taxon in the phylogenetic trees constructed from either RC-Rep or full genome sequences (Figure 3-4).

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>20</b> .	16.001iF	(assigned by IC	TV office	ers)	
To create 1	new species within:				
				all that apply.	
Genus	Gemyduguivirus	(new)	If the higher taxon has yet to be		
Subfamily			created (in a later module, below) write "(new)" after its proposed name.		
Family	Genomoviridae		If no genus is specified, enter		
Order			"unassigned" in the genus box.		
Name of new species:		Representative isol (only 1 per species p		GenBank sequence accession number(s)	
Dragonfly associated gemyduguivirus 1 TO-I		TO-DFS3B2-2010		JX185428	

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

- Explain how the proposed species differ(s) from all existing species.
  - o If species demarcation criteria (see module 3) have previously been defined for the genus, **explain how the new species meet these criteria**.
  - o 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 11

Maximum likelihood phylogenetic analyses based on the rolling circle replication initiation protein (RC-Rep) of 121 genomoviruses revealed several well-supported clades that could be considered as genera within the family (Figure 1). Genomoviruses form a sister group to geminiviruses in the RC-Rep-based phylogenetic analyses (Krupovic et al., 2016). Thus, to assess the taxonomic structure of the *Genomoviridae*, we used geminiviral sequences as a guide. Five clades and 4 additional singletons within the *Genomoviridae* branch display equivalent intra-family divergence as the established genera within the family *Geminiviridae* in both nucleotide and protein sequence inferred phylogenies (Figure 2).

Consequently, in module 3 we propose to establish 8 new genera (in addition to the existing genus *Gemycircularvirus*) within the family *Genomoviridae* (see below). We note that the clades obtained in the RC-Rep based phylogeny are not fully consistent with those obtained in the phylogenetic analysis of the full genome or the highly diverse capsid protein (CP) sequences (Figure 3, 4, 5). The reason for this mismatch is likely to be intra-familial recombination between different genomovirus genomes resulting in chimeric entities encoding RC-Rep and CP with different evolutionary histories. Given that CP sequences of genomoviruses are considerably more divergent that the RC-Rep sequences (Figure 5), it appears reasonable to establish the taxonomic framework using the RC-Rep (Figure 4). The latter protein is also conserved in other eukaryotic ssDNA viruses (which is not the case for the capsid proteins) and can thus be used to assess the place of genomoviruses within the larger community of ssDNA viruses.

The single species Dragonfly associated gemyduguivirus 1 within the genus Gemyduguivirus

shares between 57% and 62% genome-wide sequence similarity with other isolates in other genera and is a divergent taxon in the phylogenetic trees constructed from either RC-Rep or full genome sequences (Figure 3-4).

creating a new genus

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

Code	201	6.001jF	(assigned by I	CTV officers)
To create a new genus within:				Fill in all that apply.
Subfa	mily:			If the higher taxon has yet to be created
Family: Genomoviridae			(in a later module, below) write "(new)" after its proposed name.	
C	rder:			<ul> <li>If no family is specified, enter</li> <li>"unassigned" in the family box</li> </ul>

naming a new genus

Code	2016.001kF	(assigned by ICTV officers)
To name the new genus: Gemykibivirus		

Assigning the type species and other species to a new genus

Code 2016.0011F (assigned by ICTV officers)

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

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:

16

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

Additional material in support of this proposal may be presented in the Appendix, Module 11

Phylogenetic analyses based on the nucleotide and amino acid sequences of the RC-Rep show that viruses included within the proposed genus *Gemykibivirus* form a monophyletic group sufficiently distinct from other genera within the *Genomoviridae*.

## Origin of the new genus name:

Gemini- and myco-like kibi virus: kibi means circular in Amharic

## Reasons to justify the choice of type species:

First genome to be identified in this 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.

We propose a 78% genome-wide pairwise identity as a species cut-off. That is, isolates whose genomes share < 78% genome-wide pairwise identity should be considered as putative new species. (Figures 2-7)

creating a new genus

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

Code	2016.001mF	(assigned by ICTV officers)
To create a new genus within:		Fill in all that apply.
Subfa	mily:	If the higher taxon has yet to be created
Fa	mily: Genomoviridae	(in a later module, below) write "(new)" after its proposed name.
C	order:	<ul> <li>If no family is specified, enter "unassigned" in the family box</li> </ul>

naming a new genus

Code	2016.001nF	(assigned by ICTV officers)
To name the new genus: Gemygorvirus		

Assigning the type species and other species to a new genus

Code 2016.001oF (assigned by ICTV officers)

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

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:

5

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

Additional material in support of this proposal may be presented in the Appendix, Module 11

Phylogenetic analyses based on the nucleotide and amino acid sequences of the RC-Rep show that viruses included within the proposed genus *Gemygorvirus* form a monophyletic group sufficiently distinct from other genera within the *Genomoviridae*.

## Origin of the new genus name:

Gemini- and myco-like gor virus: gor means round in Hindi

## Reasons to justify the choice of type species:

First genome to be identified in this 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.

We propose a 78% genome-wide pairwise identity as a species cut-off. That is, isolates whose

genomes share < 78% genome-wide pairwise identity should be considered as putative new species. (Figures 2-7)

creating a new genus

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

Code	2016.001pF	(assigned by ICTV officers)
To create	a new genus within:	Fill in all that apply.
Subfa	mily:	If the higher taxon has yet to be created  ("""""""""""""""""""""""""""""""""""
Fa	mily: Genomoviridae	(in a later module, below) write "(new)" after its proposed name.
	Order:	If no family is specified, enter     "unassigned" in the family box

naming a new genus

Code	2016.001qF	(assigned by ICTV officers)
To name the new genus: Gemykolovirus		

Assigning the type species and other species to a new genus

Code 2016.001rF (assigned by ICTV officers)

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

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:

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

Additional material in support of this proposal may be presented in the Appendix, Module 11

Phylogenetic analyses based on the nucleotide and amino acid sequences of the RC-Rep show that viruses included within the proposed genus *Gemykolovirus* form a monophyletic group sufficiently distinct from other genera within the *Genomoviridae*.

## Origin of the new genus name:

Gemini- and myco-like kolo virus: Kolo means round in Czech

## Reasons to justify the choice of type species:

First genome to be identified in this 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.

We propose a 78% genome-wide pairwise identity as a species cut-off. That is, isolates whose

genomes share < 78% genome-wide pairwise identity should be considered as putative new species. (Figures 2-7)

creating a new genus

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

Code	2016.001sF	(assigned by ICTV officers)
To create a new genus within:		
		Fill in all that apply.
Subfamily:		If the higher taxon has yet to be created  (in a later was disk, halous) write "(a ana)"
Family: <i>Genomoviridae</i>		(in a later module, below) write "(new)" after its proposed name.
C	Order:	<ul> <li>If no family is specified, enter</li> </ul>
		"unassigned" in the family box

naming a new genus

Code	2016.001tF	(assigned by ICTV officers)
To name th	To name the new genus: Gemyvongvirus	

Assigning the type species and other species to a new genus

Code 2016.001uF (assigned by ICTV officers)

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

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:

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

Additional material in support of this proposal may be presented in the Appendix, Module 11

Phylogenetic analyses based on the nucleotide and amino acid sequences of the RC-Rep show that *Human associated gemyvongvirus I* included within the proposed genus *Gemyvongvirus* is sufficiently distinct from other genera within the *Genomoviridae*.

## Origin of the new genus name:

Gemini- and myco-like vong virus: vong means circular in Lao

## Reasons to justify the choice of type species:

First genome to be identified in this 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.

creating a new genus

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

Code	2016.001vF	(assigned by ICTV officers)
To create	a new genus within:	
		Fill in all that apply.
Subfa	mily:	• If the higher taxon has yet to be created
Fa	mily: <i>Genomoviridae</i>	(in a later module, below) write "(new)" after its proposed name.
	Order:	<ul> <li>If no family is specified, enter</li> </ul>
		"unassigned" in the family box

naming a new genus

Code	2016.001wF	(assigned by ICTV officers)
To name the new genus: Gemykrogvirus		

Assigning the type species and other species to a new genus

Assigning the type species and other species to a new genus					
Code <b>2016.001xF</b>	(assigned by ICTV officers)				
To designate the following as the type sp	To designate the following as the type species of the new genus				
Bovine associated gemykrogvirus 1	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:  3					

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

Additional material in support of this proposal may be presented in the Appendix, Module 11

Phylogenetic analyses based on the nucleotide and amino acid sequences of the RC-Rep show that viruses included within the proposed genus *Gemykrogvirus* form a monophyletic group sufficiently distinct from other genera within the *Genomoviridae*.

## Origin of the new genus name:

Gemini- and myco-like korg virus: korg means round in Slovenian

## Reasons to justify the choice of type species:

First genome to be identified in this 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.

We propose a 78% genome-wide pairwise identity as a species cut-off. That is, isolates whose

genomes share < 78% genome-wide pairwise identity should be considered as putative new species (Figures 2-7).

creating a new genus

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

Code	2016.001yF	(assigned by ICTV officers)	
To create	To create a new genus within:		
		Fill in all that apply.	
Subfa	mily:	If the higher taxon has yet to be created  (in a later module, helps) write "(nam)"	
Fai	mily: Genomoviridae	(in a later module, below) write "(new)" after its proposed name.	
0	order:	If no family is specified, enter     "unassigned" in the family box	

naming a new genus

Code	2016.001zF	(assigned by ICTV officers)
To name th	he new genus: Gemytondvirus	

Assigning the type species and other species to a new genus

7 13315111115	Assigning the type species and other species to a new genus							
Code	2016.001aaF	(assigned by ICTV officers)						
To designate the following as the type species of the new genus								
Ostrich associated gemytondvirus 1  Every genus must have a type species. This should be a well characterized species although not necessarily the first to be discovered								
are being m	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 11

Phylogenetic analyses based on the nucleotide and amino acid sequences of the RC-Rep show that *Ostrich associated gemytondvirus 1* included within the proposed genus *Gemytondvirus* is sufficiently distinct from other genera within the *Genomoviridae*.

## Origin of the new genus name:

Gemini- and myco-like tond virus: tond means round in Maltese

## Reasons to justify the choice of type species:

First genome to be identified in this 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.

creating a new genus

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

001abF (as:	(assigned by ICTV officers)							
To create a new genus within:								
	Fill in all that apply.							
	If the higher taxon has yet to be created  """  """  """  """  """  """  """							
nomoviridae	(in a later module, below) write "(new)" after its proposed name.							
	If no family is specified, enter     "unassigned" in the family box							
	nus within:							

naming a new genus

Code	2016.001acF	(assigned by ICTV officers)				
To name th	To name the new genus: Gemykroznavirus					

Assigning the type species and other species to a new genus

71551511115	the type species and other specie	55 to a new genus			
Code	2016.001adF	(assigned by ICTV officers)			
To design:	ate the following as the type sp	oecies of the new genus			
Rabbit associated gemykroznavirus 1  Every genus must have a type species. This shows be a well characterized species although not necessarily the first to be discovered					
are being m	•	Please enter here the TOTAL number of species us will contain:			

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

Additional material in support of this proposal may be presented in the Appendix, Module 11

Phylogenetic analyses based on the nucleotide and amino acid sequences of the RC-Rep show that *Rabbit associated gemykroznavirus 1* included within the proposed genus *Gemykroznavirus* is sufficiently distinct from other genera within the *Genomoviridae*.

## Origin of the new genus name:

Gemini- and myco-like krozna virus: krozna means circular in Slovenian

## Reasons to justify the choice of type species:

First genome to be identified in this 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.

creating a new genus

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

Code	201	6.001aeF	(assigned by ICTV officers)					
To create	a new	genus within:		Fill in all that apply.				
Subfa	mily:			• If the higher taxon has yet to be created				
Fai	mily:	Genomoviridae		(in a later module, below) write "(new)" after its proposed name.				
0	rder:			If no family is specified, enter     "unassigned" in the family box				

naming a new genus

Code	2016.001afF	(assigned by ICTV officers)
To name th	he new genus: Gemduguivirus	

Assigning the type species and other species to a new genus

Code 2016.001agF (assigned by ICTV officers)

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

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:

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

Additional material in support of this proposal may be presented in the Appendix, Module 11

Phylogenetic analyses based on the nucleotide and amino acid sequences of the RC-Rep show that *Dragonfly associated gemyduguivirus 1* included within the proposed genus *Gemduguivirus* is sufficiently distinct from other genera within the *Genomoviridae*.

## Origin of the new genus name:

Gemini- and myco-like dugui virus: dugui means circular in Mongolian

## Reasons to justify the choice of type species:

First genome to be identified in this 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.

additional material in support of this proposal

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#### 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.

**Table 1:** Details of all isolates within the genus *Gemycircularvirus* 

Species	Accession	Isolate	Isolation source	Common Name	Sample type	Country	Reference
Blackbird associated gemycircularvirus 1	KF371641	P9	Turdus merula	Blackbird	Faeces	New Zealand	Sikorski et al., 2013
Blackbird associated gemycircularvirus 1 Blackbird associated	KF371642	P22	Turdus merula	Blackbird	Faeces	New Zealand	Sikorski et al., 2013 Sikorski et
gemycircularvirus 1	KF371643	as41	Ovis aries	Sheep	Faeces	New Zealand	al., 2013
Bovine associated gemycircularvirus 1	KT862253	52 Fec78023 cow	Bos taurus	Cow	Faeces	New Zealand	Steel et al., 2016
Bromus associated gemycircularyirus 1	KM510192	BasCV-3 NZ- NZG01 Sef-2012	Bromus hordeaceus	Soft brome / Bull grass	Leaf	New Zealand	Kraberger et al., 2015b
Cassava associated gemycircularvirus 1	JQ412056	G14	Manihot esculenta	Cassava	Leaf	Ghana	Dayaram et al., 2012
Cassava associated gemycircularvirus 1	JQ412057	G5	Manihot esculenta	Cassava	Leaf	Ghana	Dayaram et al., 2012
Chickadee associated gemycircularvirus 1	KT309029	254065908	Saccharum hybrid	Sugarcane	Leaf	Tonga	Male et al., 2015
Chicken associated gemycircularvirus 1 Chicken associated	KT862243	27 Fec79971 chicken	Gallus gallus domesticus	Chicken	Faeces	New Zealand	Steel et al., 2016 Steel et al.,
gemycircularvirus 1 Chicken associated	KT862244	29 Fec79971 Ilama	Lama glama	Llama	Faeces	New Zealand	2016 Steel et al.,
gemycircularvirus 1	KT862246	30 Fec79971 horse	Equus ferus caballus	Horse	Faeces	New Zealand	2016
Chicken associated gemycircularvirus 2	KT862242	27 Fec16497 chicken	Gallus gallus domesticus	Chicken	Faeces	New Zealand	Steel et al., 2016
Dragonfly associated gemycircularvirus 1	JX185429	FL2-5X-2010	Erythemis simplicicollis	Dragonfly	Abdome n	USA	Rosario et al., 2012
Equine associated gemycircularvirus 1 Fur seal associated	KT862248	30 Fec80061 horse	Equus ferus caballus	Horse New Zealand	Faeces	New Zealand	Steel et al., 2016 Sikorski et
gemycircularvirus 1 Fur seal associated	KF371638	as50	Arctocephalus forsteri	fur seal	Faeces	New Zealand	al., 2013 Steel et al.,
gemycircularvirus 1	KT862241	27 Fec1 chicken	Gallus gallus domesticus	Chicken Chatham	Faeces	New Zealand	2016
Gerygone associated gemycircularvirus 1	KF371636	P24a	Gerygone albofrontata	Island warbler	Faeces	New Zealand	Sikorski et al., 2013
Gerygone associated				Chatham Island			Sikorski et
gemycircularvirus 2	KF371637	P24b	Gerygone albofrontata	warbler Chatham	Faeces	New Zealand	al., 2013
Gerygone associated gemycircularvirus 3	KF371639	P24c	Gerygone albofrontata	Island warbler	Faeces	New Zealand	Sikorski et al., 2013
Hypericum associated gemycircularvirus 1	KF413620	VNHJ1W	Hypericum japonicum	Hypericum	Leaf	Vietnam	Du et al., 2014
Lama associated gemycircularvirus 1 Lama associated	KT862245	29 Fec80018 llama	Lama glama	Llama	Faeces	New Zealand	Steel et al., 2016 Steel et al.,
gemycircularvirus 1	KT862247	30 Fec80018 horse	Equus ferus caballus	Horse	Faeces	New Zealand	2016
Mallard associated gemycircularvirus 1	KF371635	as24	Anas platyrhynchos	Mallard duck	Faeces	New Zealand	Sikorski et al., 2013
Miniopterus associated	141044=40	BtMf-CV-			Pharyng eal & rectal	01.1	Wu et al.,
gemycircularvirus 1  Mongoose associated	KJ641719	23/GD2012	Miniopterus fuliginosus	Bat Egyptian	swabs	China	2015 Conceicao- Neto et al.,
gemycircularvirus 1  Mosquito associated	KP263547	478d	Herpestes ichneumon	mongoose	Faeces Mosquit o	Portugal	2015 Ng et al.,
gemycircularvirus 1	HQ335086	SDBVL G	Culex erythrothorax	Mosquito	samples	USA	2011

		01.0.1/4.110					_
Odonata associated	NNEO030E	OdaGmV-1-US-	laabaura naaita	Damaalfly	Abdome	USA	Dayaram e
gemycircularvirus 1	KM598385	260BC-12	Ischnura posita	Damselfly	n	USA	al., 2015
Odonata associated		OdaGmV-1-US-			Abdome		Dayaram e
gemycircularvirus 1	KM598386	260SR1-12	Pantala hymenaea	Dragonfly	n	USA	al., 2015
Odonata associated		OdaGmV-2-US-			Abdome		Dayaram e
gemycircularvirus 2	KM598387	1642KW-12	Aeshna multicolor	Dragonfly	n	USA	al., 2015
Odonata associated		OdaGmV-2-US-		• ,	Abdome		Dayaram e
gemycircularvirus 2	KM598388	1634LM2-12	Libellula saturata	Dragonfly	n	USA	al., 2015
Poaceae associated		PaGmV-1 TO					Li et al.,
gemycircularvirus 1	KT253577	STO14-29204 2014	Rattus norvegicus	Rat	Blood	China	2015
Poaceae associated	1(1200077	PaGmV-1 TO	Natius noivegicus	rat	Dioou	Offilia	Male et al.
	VT252570	STO15-29204 2014	Prophiaria daflava	Cianalarasa	Loof	Tongo	2015
gemycircularvirus 1	KT253578		Brachiaria deflexa	Signalgrass	Leaf	Tonga	
Poaceae associated	./=0=0==0	PaGmV-1 TO		0		_	Male et al.
gemycircularvirus 1	KT253579	STO18-29204 2014	Brachiaria deflexa	Signalgrass	Leaf	Tonga	2015
Porcine associated					_		Steel et al
gemycircularvirus 1	KT862250	49 Fec80061 pig	Sus scrofa domestica	Pig	Faeces	New Zealand	2016
Porcine associated							Sikorski et
gemycircularvirus 2	KF371640	as5	Sus scrofa	Domestic pig	Faeces	New Zealand	al., 2013
Pteropus associated				10			Male et al.
gemycircularvirus 1	KT732804	Tbat 45285	Pteropus tonganus	Bat	Faeces	Tonga	2016
Pteropus associated	111702004	1001 40200	r toropus toriganus	Dut	1 40000	Torigu	Male et al.
	VT72200E	That 47264	Dtoronuo tongonuo	Dot	Гасала	Tanga	
gemycircularvirus 1	KT732805	Tbat 47364	Pteropus tonganus	Bat	Faeces	Tonga	2016
Pteropus associated			<b>.</b>	5.	_	_	Male et al.
gemycircularvirus 2	KT732792	Tbat 103791	Pteropus tonganus	Bat	Faeces	Tonga	2016
Pteropus associated							Male et al
gemycircularvirus 2	KT732793	Tbat A 103791	Pteropus tonganus	Bat	Faeces	Tonga	2016
Pteropus associated							Male et al.
gemycircularvirus 3	KT732797	Tbat A 103852	Pteropus tonganus	Bat	Faeces	Tonga	2016
Pteropus associated	111102101	100002	7 toropus tongunus	Dut	1 40000	Toriga	Male et al.
	KT732814	Tbat H 103806	Dtoronuo tongonuo	Bat	Faccas	Tongo	2016
gemycircularvirus 4	K1732014	TDat H TUSOUG	Pteropus tonganus	Dal	Faeces	Tonga	
Pteropus associated					_	_	Male et al.
gemycircularvirus 5	KT732801	Tbat 12377	Pteropus tonganus	Bat	Faeces	Tonga	2016
Pteropus associated							Male et al
gemycircularvirus 5	KT732802	Tbat H 12377	Pteropus tonganus	Bat	Faeces	Tonga	2016
Pteropus associated					•	•	Male et al
gemycircularvirus 6	KT732803	Tbat 103951	Pteropus tonganus	Bat	Faeces	Tonga	2016
Pteropus associated			· · · · · · · · · · · · · · · · · · ·				Male et al
gemycircularvirus 6	KT732796	Tbat H 103639	Pteropus tonganus	Bat	Faeces	Tonga	2016
Pteropus associated	111702100	100000	r teropus torigurus	Dat	1 40003	Toriga	Male et al
	VT720007	That A 400740	Diamento de manero	Dat	Г	T	
gemycircularvirus 7	KT732807	Tbat A 103746	Pteropus tonganus	Bat	Faeces	Tonga	2016
Pteropus associated	./======	TI	5.	<b>5</b> .	_	_	Male et al
gemycircularvirus 7	KT732808	Tbat A 103909	Pteropus tonganus	Bat	Faeces	Tonga	2016
Pteropus associated							Male et al.
gemycircularvirus 7	KT732809	Tbat H 103746	Pteropus tonganus	Bat	Faeces	Tonga	2016
Pteropus associated							Male et al.
gemycircularvirus 7	KT732810	Tbat H 103909	Pteropus tonganus	Bat	Faeces	Tonga	2016
Pteropus associated		<del></del>	,			J -	Male et al
gemycircularvirus 7	KT732811	Tbat L 103746	Pteropus tonganus	Bat	Faeces	Tonga	2016
Pteropus associated	11.1.02011	1001 TU	, toropus torrgunus	Dut	1 40003	ı ongu	
,	VT720040	That I 402000	Dtoronus tongo:	Dot	Econor	Tonco	Male et al
gemycircularvirus 7	KT732812	Tbat L 103909	Pteropus tonganus	Bat	Faeces	Tonga	2016
Pteropus associated					_	_	Male et al.
gemycircularvirus 8	KT732806	Tbat 31579	Pteropus tonganus	Bat	Faeces	Tonga	2016
Pteropus associated							Male et al.
gemycircularvirus 9	KT732795	Tbat 21383	Pteropus tonganus	Bat	Faeces	Tonga	2016
Pteropus associated			· <b>·</b>			<del>-</del>	Male et al.
	KT732794	Tbat H 103958	Pteropus tonganus	Bat	Faeces	Tonga	2016
gemycircularvirus 10		1000000	. woopas wiigailus	Dut	. 40000	. Jugu	Uch et al.,
	TTT OZT OH						
Rat associated		Ch =irst C4	Hama conic	Llumar	Diagram	France	2015
Rat associated gemycircularvirus 1	KR912221	Ch-zjrat-01	Homo sapiens	Human	Plasma	France	2015
Rat associated gemycircularvirus 1 Sclerotinia	KR912221	•	•		Mycelial		Yu et al.,
Rat associated gemycircularvirus 1 Sclerotinia		Ch-zjrat-01 SsHADV-1 CN	Homo sapiens Sclerotinia sclerotiorum	Human Sclerotinia	Mycelial samples	France China	
Rat associated gemycircularvirus 1 Sclerotinia	KR912221	SsHADV-1 CN	•		Mycelial samples River		Yu et al., 2010
Rat associated gemycircularvirus 1 Sclerotinia	KR912221	•	•		Mycelial samples		Yu et al., 2010
Rat associated gemycircularvirus 1 Sclerotinia gemycircularvirus 1 Sclerotinia	KR912221	SsHADV-1 CN	•		Mycelial samples River		Yu et al., 2010
Rat associated gemycircularvirus 1 Sclerotinia gemycircularvirus 1 Sclerotinia	KR912221 GQ365709	SsHADV-1 CN SsHADV-1 NZ H6	Sclerotinia sclerotiorum		Mycelial samples River Sedime nts	China	Yu et al., 2010 Kraberger
Rat associated gemycircularvirus 1 Sclerotinia gemycircularvirus 1 Sclerotinia gemycircularvirus 1 gemycircularvirus 1	KR912221 GQ365709	SsHADV-1 CN SsHADV-1 NZ H6 2012	Sclerotinia sclerotiorum		Mycelial samples River Sedime nts River	China	Yu et al., 2010 Kraberger al., 2013
Rat associated gemycircularvirus 1 Sclerotinia gemycircularvirus 1 Sclerotinia gemycircularvirus 1 Sclerotinia gemycircularvirus 1 Sclerotinia	KR912221 GQ365709 KF268025	SsHADV-1 CN SsHADV-1 NZ H6 2012 SsHADV-1 NZ SR1	Sclerotinia sclerotiorum River Sediments		Mycelial samples River Sedime nts River Sedime	China New Zealand	Yu et al., 2010 Kraberger al., 2013 Kraberger
Rat associated gemycircularvirus 1 Sclerotinia gemycircularvirus 1 Sclerotinia gemycircularvirus 1 Sclerotinia gemycircularvirus 1 Sclerotinia	KR912221 GQ365709	SsHADV-1 CN SsHADV-1 NZ H6 2012	Sclerotinia sclerotiorum		Mycelial samples River Sedime nts River Sedime nts	China	Yu et al., 2010 Kraberger al., 2013
Rat associated gemycircularvirus 1 Sclerotinia gemycircularvirus 1 Sclerotinia gemycircularvirus 1 Sclerotinia gemycircularvirus 1 Sclerotinia gemycircularvirus 1	KR912221 GQ365709 KF268025	SsHADV-1 CN SsHADV-1 NZ H6 2012 SsHADV-1 NZ SR1 2012	Sclerotinia sclerotiorum River Sediments		Mycelial samples River Sedime nts River Sedime nts River	China New Zealand	Yu et al., 2010 Kraberger al., 2013 Kraberger al., 2013
Rat associated gemycircularvirus 1 Sclerotinia	KR912221 GQ365709 KF268025 KF268026	SsHADV-1 CN SsHADV-1 NZ H6 2012 SsHADV-1 NZ SR1 2012 SsHADV-1 NZ SR3	Sclerotinia sclerotiorum  River Sediments  River Sediments		Mycelial samples River Sedime nts River Sedime nts River Sedime	China  New Zealand  New Zealand	Yu et al., 2010 Kraberger al., 2013 Kraberger al., 2013 Kraberger
Rat associated gemycircularvirus 1 Sclerotinia	KR912221 GQ365709 KF268025	SsHADV-1 CN SsHADV-1 NZ H6 2012 SsHADV-1 NZ SR1 2012	Sclerotinia sclerotiorum River Sediments		Mycelial samples River Sedime nts River Sedime nts River Sedime nts	China New Zealand	Yu et al., 2010 Kraberger al., 2013 Kraberger al., 2013
Rat associated gemycircularvirus 1 Sclerotinia	KR912221 GQ365709 KF268025 KF268026	SsHADV-1 CN SsHADV-1 NZ H6 2012 SsHADV-1 NZ SR1 2012 SsHADV-1 NZ SR3	Sclerotinia sclerotiorum  River Sediments  River Sediments		Mycelial samples River Sedime nts River Sedime nts River Sedime	China  New Zealand  New Zealand	Yu et al., 2010 Kraberger al., 2013 Kraberger al., 2013 Kraberger
Rat associated gemycircularvirus 1 Sclerotinia	KR912221 GQ365709 KF268025 KF268026	SsHADV-1 CN SsHADV-1 NZ H6 2012 SsHADV-1 NZ SR1 2012 SsHADV-1 NZ SR3	Sclerotinia sclerotiorum  River Sediments  River Sediments		Mycelial samples River Sedime nts River Sedime nts River Sedime nts	China  New Zealand  New Zealand	Yu et al., 2010 Kraberger al., 2013 Kraberger al., 2013 Kraberger al., 2013
Rat associated gemycircularvirus 1 Sclerotinia	KR912221 GQ365709 KF268025 KF268026 KF268027	SsHADV-1 CN SsHADV-1 NZ H6 2012 SsHADV-1 NZ SR1 2012 SsHADV-1 NZ SR3 2012 SsHADV-1 NZ SR5	Sclerotinia sclerotiorum  River Sediments  River Sediments  River Sediments		Mycelial samples River Sedime nts River Sedime nts River Sedime nts River Sedime	China  New Zealand  New Zealand  New Zealand	Yu et al., 2010 Kraberger al., 2013 Kraberger al., 2013 Kraberger al., 2013
Sclerotinia gemycircularvirus 1 Sclerotinia	KR912221 GQ365709 KF268025 KF268026	SsHADV-1 CN SsHADV-1 NZ H6 2012 SsHADV-1 NZ SR1 2012 SsHADV-1 NZ SR3 2012 SsHADV-1 NZ SR5 2012	Sclerotinia sclerotiorum  River Sediments  River Sediments		Mycelial samples River Sedime nts	China  New Zealand  New Zealand	Yu et al., 2010 Kraberger al., 2013 Kraberger al., 2013 Kraberger al., 2013
Rat associated gemycircularvirus 1 Sclerotinia	KR912221 GQ365709 KF268025 KF268026 KF268027	SsHADV-1 CN SsHADV-1 NZ H6 2012 SsHADV-1 NZ SR1 2012 SsHADV-1 NZ SR3 2012 SsHADV-1 NZ SR5	Sclerotinia sclerotiorum  River Sediments  River Sediments  River Sediments		Mycelial samples River Sedime nts River Sedime nts River Sedime nts River Sedime	China  New Zealand  New Zealand  New Zealand	Yu et al., 2010 Kraberger al., 2013 Kraberger al., 2013 Kraberger al., 2013

Sclerotinia		SsHADV-1-US-			Abdome		Dayaram et
gemycircularvirus 1	KM598383	549DFS-12	Erythemis simplicicollis	Dragonfly	n	USA	al., 2015
Sclerotinia		SsHADV-1-US-			Abdome		Dayaram et
gemycircularvirus 1	KM598384	549SR-12	Pantala hymenaea	Dragonfly	n	USA	al., 2015
Sewage derived							Kraberger et
gemycircularvirus 1	KJ547638	BS3917	Sewage oxidation pond	-	Sewage	New Zealand	al., 2015a
Sewage derived		SaGmV-1 NZ-			_		Kraberger et
gemycircularvirus 1	KM821747	BS3970-2012	Sewage oxidation pond	-	Sewage	New Zealand	al., 2015a
Sewage derived							Kraberger et
gemycircularvirus 2	KJ547641	BS4117	Sewage oxidation pond	-	Sewage	New Zealand	al., 2015a
Sewage derived							Kraberger et
gemycircularvirus 3	KJ547636	BS4014	Sewage oxidation pond	-	Sewage	New Zealand	al., 2015a
Sewage derived							Kraberger et
gemycircularvirus 4	KJ547640	BS3972	Sewage oxidation pond	-	Sewage	New Zealand	al., 2015a
Sewage derived							Kraberger et
gemycircularvirus 4	KJ547637	BS3939	Sewage oxidation pond	-	Sewage	New Zealand	al., 2015a
Sewage derived							Kraberger et
gemycircularvirus 5	KJ547639	BS3970	Sewage oxidation pond	-	Sewage	New Zealand	al., 2015a
Sheep associated							Steel et al.,
gemycircularvirus 1	KT862249	47 Fec80064 sheep	Ovis aries	Sheep	Faeces	New Zealand	2016
Sheep associated							Steel et al.,
gemycircularvirus 1	KT862251	51 Fec80064 sheep	Ovis aries	Sheep	Faeces	New Zealand	2016
							Marzano &
Soybean associated							Domier,
gemycircularvirus 1	KT598248	SlaGemV1-1	Glycine max	Soybean	Leaf	USA	2015

Table 2: Details of all isolates within the genus Gemykibivirus

			<u> </u>	Common	Sample		
Species	Accession	Isolate	Isolation source	Name	type	Country	Reference
							Conceicao-
Badger associated				European			Neto et al.,
gemykibivirus 1	KP263543	588t	Meles meles	badger	Faeces	Portugal	2015
				Chatham			
Black robin associated				Island black	_		Sikorski et
gemykibivirus 1	KF371634	P21	Petroica traversi	robin	Faeces	New Zealand	al., 2013
Blackbird associated					_		Sikorski et
gemykibivirus 1	KF371633	P22	Turdus merula	Blackbird	Faeces	New Zealand	al., 2013
Bovine associated				_	_	_	Lamberto et
gemykibivirus 1	LK931483	HCBI8.215	Bos taurus	Cow	Serum	Germany	al., 2014
Dragonfly associated					Abdome		Rosario et
gemykibivirus 1	JX185430	FL1-2X-2010	Miathyria marcella	Dragonfly	n	USA	al., 2012
Human associated					_		Kraberger et
gemykibivirus 1	KJ547644	BS3980	Sewage oxidation pond	-	Sewage	New Zealand	al., 2015a
Human associated					_		Kraberger et
gemykibivirus 1	KJ547645	BS3849	Sewage oxidation pond	-	Sewage	New Zealand	al., 2015a
Human associated	1/0074004	DD0			DI.	•	
gemykibivirus 1	KP974694	DB2	Homo sapiens	Human	Plasma	Germany	unpublished
Human associated	11/004405	M0010 005	Hansa andana	Harris	Disast	0	Lamberto et
gemykibivirus 1	LK931485	MSSI2.225	Homo sapiens	Human	Blood	Germany	al., 2014
11					Cerebro		Dhan at al
Human associated	VD40075	01.4	Hanna and an	Harris	spinal	0.411	Phan et al.,
gemykibivirus 2	KP133075	SL1	Homo sapiens	Human	fluid	Sri Lanka	2015
Lluman accasiated					Cerebro		Dhan et al
Human associated gemykibivirus 2	KP133076	SL2	Homo sapiens	Human	spinal fluid	Sri Lanka	Phan et al., 2015
gerriykibivirus z	KF 133070	SLZ	Homo sapiens	Tiulliali	Cerebro	SII Lailka	2013
Human associated					spinal		Phan et al.,
gemykibivirus 2	KP133077	SL3	Homo sapiens	Human	fluid	Sri Lanka	2015
Human associated	KI 133077	OLO	Homo sapiens	Human	ilulu	OII Lairea	Phan et al.,
gemykibivirus 2	KP133078	BZ1	Homo sapiens	Human	Faeces	Brazil	2015
Human associated	11 100070	DZI	пото заріств	Haman	1 40003	Diazii	Phan et al.,
gemykibivirus 2	KP133079	BZ2	Homo sapiens	Human	Faeces	Brazil	2015
Human associated	141 100070	522	riome adpiene	riaman	1 40000	Diuzii	Phan et al.,
gemykibivirus 2	KP133080	NP	Untreated sewage	_	Sewage	Nepal	2015
Human associated	14. 100000		3111.04.04.05.14.90		20.1.490		
gemykibivirus 3	KP987887	GemyC1c	Homo sapiens	Human	Plasma	France	unpublished
gomynaannaa		oo, o . o	Treme captone				Conceicao-
Human associated				Egyptian			Neto et al.,
gemykibivirus 3	KP263546	541c	Herpestes ichneumon	mongoose	Faeces	Portugal	2015
<u> </u>			- p	- 3	Buccal	J <del></del>	
				Black-	and		
Human associated				capped	cloacal		Hanna et al.,
gemykibivirus 4	KT363839	GeTz1	Poecile atricapillus	chickadee	swab	USA	2015
gennykibivirus 4	K1303039	GEIZI	roeciie atricapiiius	chickadee	Swap	USA	2010

Human associated					Pericard		
gemykibivirus 5	KU343137	HV-GcV2	Homo sapiens	Human	ial fluid	France	unpublished
Mongoose associated gemykibivirus 1	KP263545	160b	Herpestes ichneumon	Egyptian mongoose	Faeces	Portugal	Conceicao- Neto et al., 2015
Pteropus associated gemykibivirus 1	KT732813	Tbat A 64418	Pteropus tonganus	Bat	Faeces	Tonga	Male et al., 2016
Rhinolophus associated gemykibivirus 1 Rhinolophus associated	KJ641737	BtRh-CV- 6/Tibet2013	Rhinolophus hipposideros	Bat Egyptian	Pharyng eal & rectal swabs	China	Wu et al., 2015 Conceicao- Neto et al.,
gemykibivirus 1	KP263544	181a	Herpestes ichneumon	mongoose	Faeces	Portugal	2015
Rhinolophus associated gemykibivirus 2	KJ641726	BtRf-CV-8/NM2013	Rhinolophus ferrumequinum	Bat	Pharyng eal & rectal swabs	China	Wu et al., 2015
Sewage derived gemykibivirus 1 Sewage derived	KJ547643	BS4149 27 BS14149	Sewage oxidation pond	-	Sewage	New Zealand	Kraberger et al., 2015a Steel et al.,
gemykibivirus 1 Sewage derived	KT862240	chicken	Gallus gallus domesticus	Chicken	Faeces	New Zealand	2016 Steel et al.,
gemykibivirus 1 Sewage derived	KT862252	52 BS14149 cow	Bos taurus	Cow	Faeces	New Zealand	2016 Steel et al.,
gemykibivirus 1	KT862255	56 BS14149 hare	Lepus europaeus	Hare	Faeces	New Zealand	2016
Sewage derived gemykibivirus 2	KJ547642	BS3911	Sewage oxidation pond	-	Sewage	New Zealand	Kraberger et al., 2015a

Table 3: Details of all isolates within the genus Gemygorvirus

				Common	Sample		
Species	Accession	Isolate	Isolation source	Name	type	Country	Reference
Canine associated							Steel et al.,
gemygorvirus 1	KT862254	53 Fec7 dog	Canis lupus familiaris	Dog	Faeces	New Zealand	2016
Mallard associated							Steel et al.,
gemygorvirus 1	KT862238	4 Fec7 duck	Anas platyrhynchos	Duck	Faeces	New Zealand	2016
Mallard associated							Steel et al.,
gemygorvirus 1	KT862239	24 Fec7 duck	Anas platyrhynchos	Duck	Faeces	New Zealand	2016
							van den
Mallard associated				European	Rectal		Brand et al.,
gemygorvirus 1	JN704610	VS4700006	Meles meles	badger	swab	Netherlands	2012
Pteropus associated							Male et al.,
gemygorvirus 1	KT732790	Tbat A 103952	Pteropus tonganus	Bat	Faeces	Tonga	2016
Pteropus associated			, ,			Ü	Male et al.,
gemygorvirus 1	KT732791	Tbat H 103952	Pteropus tonganus	Bat	Faeces	Tonga	2016
Sewage derived							Kraberger et
gemygorvirus 1	KJ547635	BS3963	Sewage oxidation pond	-	Sewage	New Zealand	al., 2015a
Sewage derived			,		Cervical		
gemygorvirus 1	KJ413144	349	Homo sapiens	Human	sample	South Africa	unpublished
Starling associated			•	European			Sikorski et
gemygorvirus 1	KF371632	P14	Sturnus vulgaris	starling	Faeces	New Zealand	al., 2013

Table 4: Details of all isolates within the genus Gemykolovirus

				Common	Sample		
Species	Accession	Isolate	Isolation source	Name	type	Country	Reference
Pteropus associated gemykolovirus 1 Pteropus associated	KT732798	Tbat A 103779	Pteropus tonganus	Bat	Faeces	Tonga	Male et al., 2016 Male et al.,
gemykolovirus 1	KT732799	Tbat H 103779	Pteropus tonganus	Bat	Faeces	Tonga	2016
Pteropus associated gemykolovirus 2	KT732800	Tbat H 103921	Pteropus tonganus	Bat	Faeces	Tonga	Male et al., 2016

Table 5: Details of all isolates within the genus Gemykrogvirus

Species				Common	Sample		
	Accession	Isolate	Isolation source	Name	type	Country	Reference
Bovine associated							Lamberto et
gemykrogvirus 1	LK931484	HCBI9.212	Bos taurus	Cow	Serum	Germany	al., 2014
Caribou associated							Ng et al.,
gemykrogvirus 1	KJ938717	FaGmCV-13	Rangifer tarandus	Caribou	Faeces	Canada	2014
Sewage derived							Kraberger et
gemykrogvirus 1	KJ547634	BS3913	Sewage oxidation pond	-	Sewage	New Zealand	al., 2015a

## Table 6: Details of all isolates within the genus Gemyvongvirus

				Common	Sample		
Species	Accession	Isolate	Isolation source	Name	type	Country	Reference
Human associated							
gemyvongvirus 1	KP974693	DB1	Homo sapiens	Human	Plasma	Germany	unpublished

## **Table 7:** Details of all isolates within the genus *Gemytondvirus*

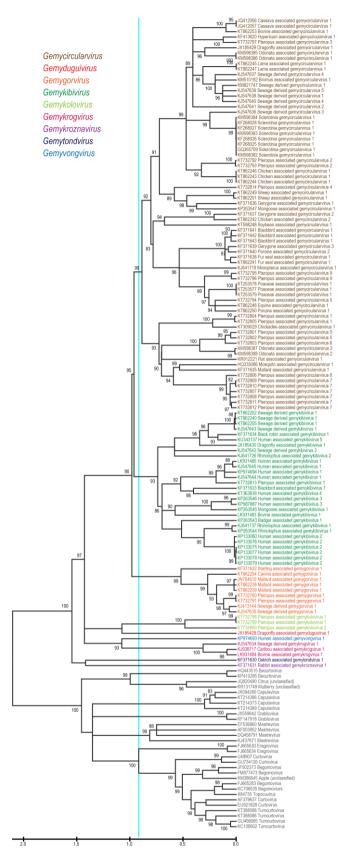
				Common	Sample		
Species	Accession	Isolate	Isolation source	Name	type	Country	Reference
Ostrich associated						-	Sikorski et
gemytondvirus 1	KF371630	as3	Struthio camelus	Ostrich	Faeces	New Zealand	al., 2013

## Table 8: Details of all isolates within the genus Gemykroznavirus

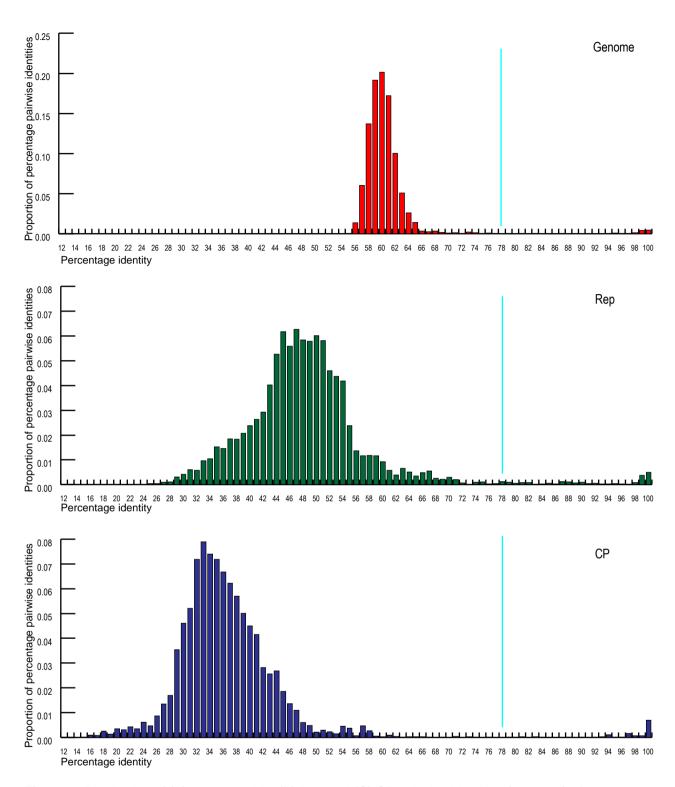
				Common	Sample		
Species	Accession	Isolate	Isolation source	Name	type	Country	Reference
Rabbit associated							Sikorski et
gemykroznavirus 1	KF371631	as35	Oryctolagus cuniculus	Rabbit	Faeces	New Zealand	al., 2013

## **Table 9:** Details of all isolates within the genus *Gemyduguivirus*

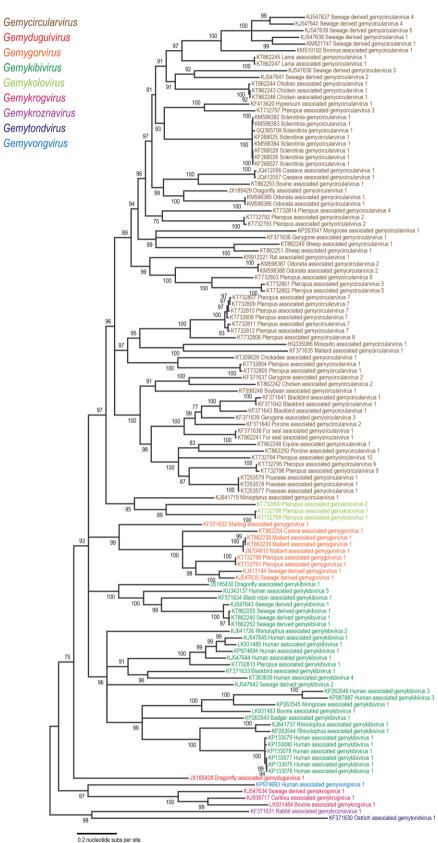
Species	Accession	Isolate	Isolation source	Common Name	Sample type	Country	Reference
Dragonfly associated					Abdome		Rosario et
gemyduguivirus 1	JX185428	TO-DFS3B2-2010	Pantala flavescens	Dragonfly	n	Tonga	al., 2012



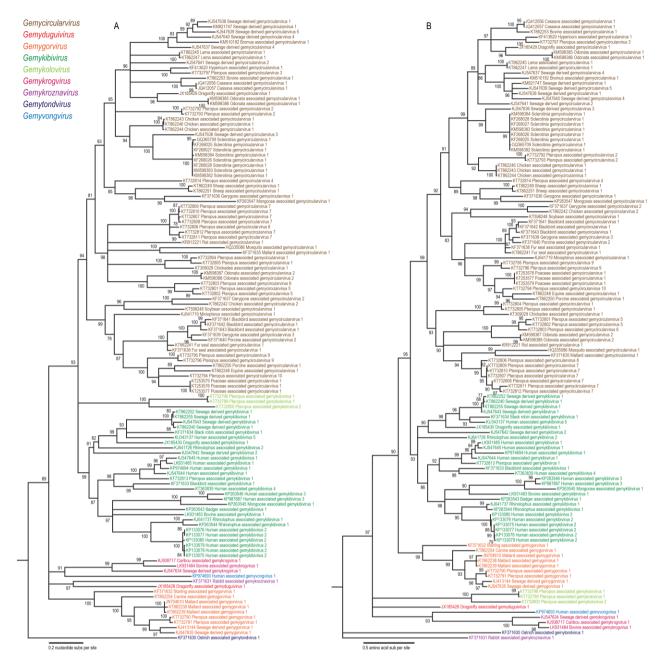
**Figure 1:** Maximum likelihood phylogenetic tree of the Rep amino acid sequences inferred using PHYML with LG+G+I substitution model and rooted with geminivirus sequences. The sequences of geminiviruses labelled with the corresponding genera names are used as a guide to identify genera within the *Genomoviridae* family. The cyan line shows a rough genera demarcation for both *Genomoviridae* and *Geminiviridae*. Branches with <75% SH-like branch support have been collapsed.



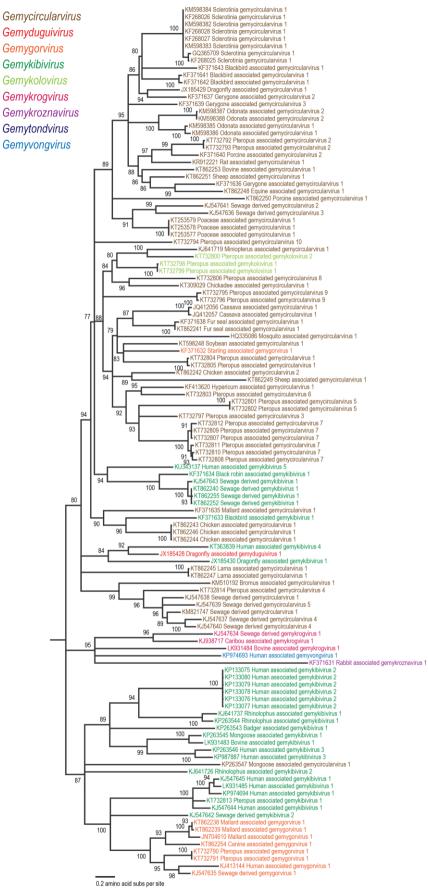
**Figure 2:** Distribution of (A) genome-wide, (B) Rep and (C) CP pairwise identities (121 taxa) of genomoviruses calculated using SDT v1.2 (Muhire et al., 2014).



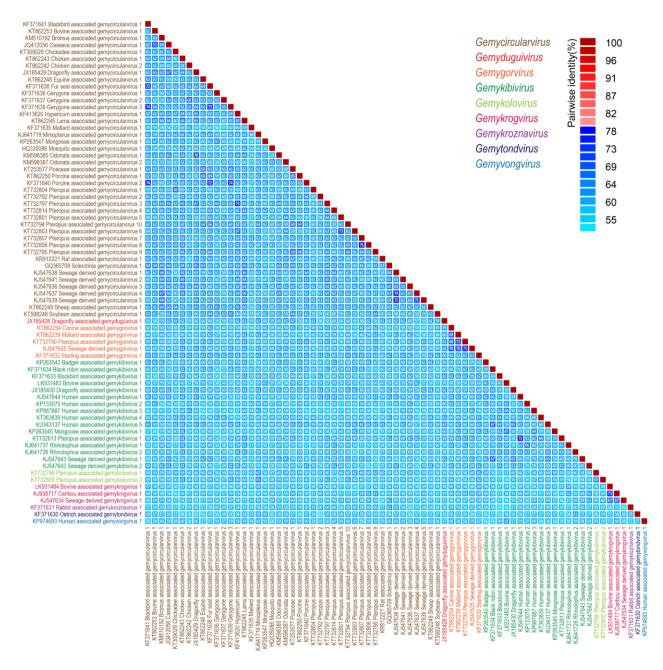
**Figure 3:** Maximum likelihood phylogenetic tree (GTR+CAT) with SH-like support of the genomes of isolates in the *Genomoviridae* family supporting that the genera demarcation is supported at the genome level as well despite there being evidence of recombination within the genomes. Branches with <75% SH-like branch support have been collapsed.



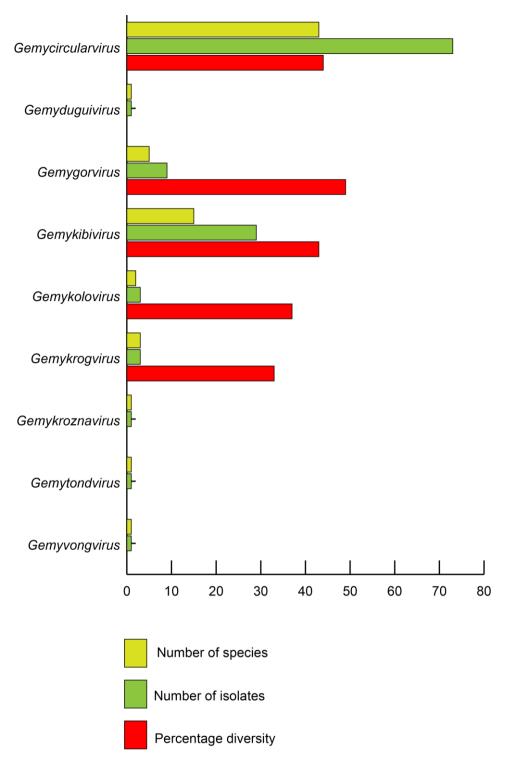
**Figure 4:** Maximum likelihood phylogenetic tree of (A) the *rep* gene sequences and (B) the Rep amino acid sequences inferred using PHYML with GTR+G and LG+G+I substitution models and rooted with geminivirus sequences. The genera demarcation that is Rep-sequence driven for the family *Genonoviridae* is supported at both nucleotide and protein level as illustrated by the *rep* and Rep sequence inferred ML phylogenetic trees. Branches with <75% SH-like branch support have been collapsed.



**Figure 5:** Maximum likelihood phylogenetic tree of the CP amino acid sequences inferred using PHYML with LG+G+I substitution models and rooted with geminivirus sequences. Branches with <75% SH-like branch support have been collapsed.



**Figure 6:** Genome-wide pairwise identities representative isolates of each species within the *Genomoviridae* family determined using SDT v1.2 (Muhire et al., 2014). The 'two colour' profile highlights that the 78% species demarcation threshold is valid for the proposed species in the *Genomoviridae* family.



**Figure 7:** Summary of genera and the associated species and their diversity (within genera) within the *Genomoviridae* family.