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 new genera and seventy three species in the family *Genomoviridae*
(e.g. 6 new species in the genus *Zetavirus*)

Modules attached (modules 1 and 11 are required)	**1** ☒	**2** ☒	**3** ☒	**4** ☐	**5** ☐
	6 ☐	**7** ☐	**8** ☐	**9** ☐	**10** ☐
	11 ☒				

Author(s):

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List the ICTV study group(s) that have seen this proposal:

A list of study groups and contacts is provided at http://www.ictvonline.org/subcommittees.asp . If in doubt, contact the appropriate subcommittee chair (fungal, invertebrate, plant, prokaryote or vertebrate viruses)	

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

Date first submitted to ICTV: July 2016
Date of this revision (if different to above):

ICTV-EC comments and response of the proposer:

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	***2016.001aF***	(assigned by ICTV officers)

To create 42 new species within:

Genus:	***Gemycircularvirus***
Subfamily:	
Family:	***Genomoviridae***
Order:	

Fill in all that apply.

- If the higher taxon has yet to be created (in a later module, below) write "**(new)**" after its proposed name.
- If no genus is specified, enter "**unassigned**" in the genus box.

Name of new species:	**Representative isolate: (only 1 per species please)**	**GenBank sequence accession number(s)**
Blackbird associated gemycircularvirus 1	P9	KF371641
Bovine associated gemycircularvirus 1	52 Fec78023 cow	KT862253
Bromus associated gemycircularvirus 1	BasCV-3 NZ-NZG01 Sef-2012	KM510192
Cassava associated gemycircularvirus 1	G14	JQ412056
Chickadee associated gemycircularvirus 1	2.54E+08	KT309029
Chicken associated gemycircularvirus 1	27 Fec79971 chicken	KT862243
Chicken associated gemycircularvirus 2	27 Fec16497 chicken	KT862242
Dragonfly associated gemycircularvirus 1	FL2-5X-2010	JX185429
Equine associated gemycircularvirus 1	30 Fec80061 horse	KT862248
Fur seal associated gemycircularvirus 1	as50	KF371638
Gerygone associated gemycircularvirus 1	P24a	KF371636
Gerygone associated gemycircularvirus 2	P24b	KF371637
Gerygone associated gemycircularvirus 3	P24c	KF371639
Hypericum associated gemycircularvirus 1	VNHJ1W	KF413620
Lama associated gemycircularvirus 1	29 Fec80018 llama	KT862245
Mallard associated gemycircularvirus 1	as24	KF371635
Miniopterus associated gemycircularvirus 1	BtMf-CV-23/GD2012	KJ641719
Mongoose associated gemycircularvirus 1	478d	KP263547
Mosquito associated gemycircularvirus 1	SDBVL G	HQ335086
Odonata associated gemycircularvirus 1	OdaGmV-1-US-260BC-12	KM598385
Odonata associated gemycircularvirus 2	OdaGmV-2-US-1642KW-12	KM598387
Poaceae associated gemycircularvirus 1	PaGmV-1 TO STO14-29204 2014	KT253577
Porcine associated gemycircularvirus 1	49 Fec80061 pig	KT862250
Porcine associated gemycircularvirus 2	as5	KF371640
Pteropus associated gemycircularvirus 1	Tbat 45285	KT732804
Pteropus associated gemycircularvirus 2	Tbat 103791	KT732792
Pteropus associated gemycircularvirus 3	Tbat A 103852	KT732797
Pteropus associated gemycircularvirus 4	Tbat H 103806	KT732814
Pteropus associated gemycircularvirus 5	Tbat 12377	KT732801
Pteropus associated gemycircularvirus 6	Tbat 103951	KT732803
Pteropus associated gemycircularvirus 7	Tbat A 103746	KT732807
Pteropus associated gemycircularvirus 8	Tbat 31579	KT732806
Pteropus associated gemycircularvirus 9	Tbat 21383	KT732795
Pteropus associated gemycircularvirus 10	Tbat H 103958	KT732794
Rat associated gemycircularvirus 1	Ch-zjrat-01	KR912221
Sewage derived gemycircularvirus 1	BS3917	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.
  - 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 11

Currently the genus *Gemycircularvirus* contains a single species, *Sclerotinia gemycircularvirus 1*, 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).

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	***2016.001bF***	(assigned by ICTV officers)

To create 16 new species within:

Genus:	***Gemykibivirus (new)***
Subfamily:	
Family:	***Genomoviridae***
Order:	

Fill in all that apply.

- If the higher taxon has yet to be created (in a later module, below) write "**(new)**" after its proposed name.
- If no genus is specified, enter "**unassigned**" in the genus box.

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.
  - 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 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).

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	***2016.001cF***	(assigned by ICTV officers)

To create 5 new species within:

Genus:	***Gemygorvirus (new)***
Subfamily:	
Family:	***Genomoviridae***
Order:	

Fill in all that apply.

- If the higher taxon has yet to be created (in a later module, below) write "**(new)**" after its proposed name.
- If no genus is specified, enter "**unassigned**" in the genus box.

Name of new species:	**Representative isolate: (only 1 per species please)**	**GenBank sequence accession number(s)**
Canine associated gemygorvirus 1	53 Fec7 dog	KT862254
Mallard associated gemygorvirus 1	4 Fec7 duck	KT862238
Pteropus associated gemygorvirus 1	Tbat A 103952	KT732790
Sewage derived gemygorvirus 1	BS3963	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**.
  - 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).

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	***2016.001dF***	(assigned by ICTV officers)

To create 2 new species within:

Genus:	***Gemykolovirus (new)***
Subfamily:	
Family:	***Genomoviridae***
Order:	

Fill in all that apply.

- If the higher taxon has yet to be created (in a later module, below) write "**(new)**" after its proposed name.
- If no genus is specified, enter "**unassigned**" in the genus box.

Name of new species:	**Representative isolate: (only 1 per species please)**	**GenBank sequence accession number(s)**
Pteropus associated gemykolovirus 1	Tbat A 103779	KT732798
Pteropus associated gemykolovirus 2	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.
  - 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 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).

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	***2016.001eF***	(assigned by ICTV officers)

To create 1 new species within:

Genus:	***Gemyvongvirus (new)***
Subfamily:	
Family:	***Genomoviridae***
Order:	

Fill in all that apply.

- If the higher taxon has yet to be created (in a later module, below) write "**(new)**" after its proposed name.
- If no genus is specified, enter "**unassigned**" in the genus box.

Name of new species:	**Representative isolate: (only 1 per species please)**	**GenBank sequence accession number(s)**
Human associated gemyvongvirus 1	DB1	KP974693

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 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).

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	***2016.001fF***	(assigned by ICTV officers)

To create 3 new species within:

Genus:	***Gemykrogvirus (new)***
Subfamily:	
Family:	***Genomoviridae***
Order:	

Fill in all that apply.

- If the higher taxon has yet to be created (in a later module, below) write "**(new)**" after its proposed name.
- If no genus is specified, enter "**unassigned**" in the genus box.

Name of new species:	**Representative isolate: (only 1 per species please)**	**GenBank sequence accession number(s)**
Bovine associated gemykrogvirus 1	HCB19.212	LK931484
Caribou associated gemykrogvirus 1	FaGmCV-13	KJ938717
Sewage 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**.
  - 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).

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	***2016.001gF***	(assigned by ICTV officers)

To create 1 new species within:

Genus:	***Gemytondvirus (new)***
Subfamily:	
Family:	***Genomoviridae***
Order:	

Fill in all that apply.
- If the higher taxon has yet to be created (in a later module, below) write "**(new)**" after its proposed name.
- If no genus is specified, enter "**unassigned**" in the genus box.

Name of new species:	**Representative isolate: (only 1 per species please)**	**GenBank sequence accession number(s)**
Ostrich associated gemytondvirus 1	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**.
  - 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).

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	***2016.001hF***	(assigned by ICTV officers)

To create 1 new species within:

Genus:	***Gemykroznavirus (new)***
Subfamily:	
Family:	***Genomoviridae***
Order:	

Fill in all that apply.

- If the higher taxon has yet to be created (in a later module, below) write "**(new)**" after its proposed name.
- If no genus is specified, enter "**unassigned**" in the genus box.

Name of new species:	**Representative isolate: (only 1 per species please)**	**GenBank sequence accession number(s)**
Rabbit associated gemykroznavirus 1	as35	KF371631

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 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).

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	***2016.001iF***	(assigned by ICTV officers)

To create 1 new species within:

Genus:	***Gemyduguivirus (new)***
Subfamily:	
Family:	***Genomoviridae***
Order:	

Fill in all that apply.

- If the higher taxon has yet to be created (in a later module, below) write "**(new)**" after its proposed name.
- If no genus is specified, enter "**unassigned**" in the genus box.

Name of new species:	**Representative isolate: (only 1 per species please)**	**GenBank sequence accession number(s)**
Dragonfly associated gemyduguivirus 1	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.
  - 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 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).

MODULE 3: **NEW GENUS**

creating a new genus

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

Code	***2016.001jF***	(assigned by ICTV officers)

To create a new genus within:

Subfamily:	
Family:	***Genomoviridae***
Order:	

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

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	***2016.001lF***	(assigned by ICTV officers)

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

Dragonfly associated gemykibivirus 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:**

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)

MODULE 3: **NEW GENUS**

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:

Subfamily:	
Family:	***Genomoviridae***
Order:	

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

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

Starling associated gemygorvirus 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:**

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)

MODULE 3: **NEW GENUS**

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:

Subfamily:	
Family:	***Genomoviridae***
Order:	

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

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

Pteropus associated gemykolovirus 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:**

2

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)

MODULE 3: **NEW GENUS**

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:

Subfamily:	
Family:	***Genomoviridae***
Order:	

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

naming a new genus

Code	***2016.001tF***	(assigned by ICTV officers)

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

Human associated gemyvongvirus 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:**

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 *Human associated gemyvongvirus 1* 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.

Not applicable – only one species in the genus.

MODULE 3: **NEW GENUS**

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:

Subfamily:	
Family:	***Genomoviridae***
Order:	

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

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

Code	***2016.001xF***	(assigned by ICTV officers)

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).

MODULE 3: **NEW GENUS**

creating a new genus

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

Code	***2016.001yF***	(assigned by ICTV officers)

To create a new genus within:

Subfamily:	
Family:	***Genomoviridae***
Order:	

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

naming a new genus

Code	***2016.001zF***	(assigned by ICTV officers)

To name the new genus: *Gemytondvirus*

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

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.

Not applicable – only one species in the genus.

MODULE 3: **NEW GENUS**

creating a new genus

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

Code	***2016.001abF***	(assigned by ICTV officers)

To create a new genus within:

Subfamily:	
Family:	***Genomoviridae***
Order:	

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

naming a new genus

Code	***2016.001acF***	(assigned by ICTV officers)

To name the new genus: *Gemykroznavirus*

Assigning the type species and other species to a new genus

Code	***2016.001adF***	(assigned by ICTV officers)

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

Rabbit associated gemykroznavirus 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:**

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 *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.

Not applicable – only one species in the genus.

MODULE 3: **NEW GENUS**

creating a new genus

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

Code	***2016.001aeF***	(assigned by ICTV officers)

To create a new genus within:

Subfamily:	
Family:	***Genomoviridae***
Order:	

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

naming a new genus

Code	***2016.001afF***	(assigned by ICTV officers)

To name the 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

Dragonfly associated gemyduguivirus 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:**

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 *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.

Not applicable – only one species in the genus.

MODULE 11: **APPENDIX**: supporting material

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	KF371642	P22	*Turdus merula*	Blackbird	Faeces	New Zealand	Sikorski et al., 2013
Blackbird associated gemycircularvirus 1	KF371643	as41	*Ovis aries*	Sheep	Faeces	New Zealand	Sikorski et al., 2013
Bovine associated gemycircularvirus 1	KT862253	52 Fec78023 cow	*Bos taurus*	Cow	Faeces	New Zealand	Steel et al., 2016
Bromus associated gemycircularvirus 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	KT862243	27 Fec79971 chicken	*Gallus gallus domesticus*	Chicken	Faeces	New Zealand	Steel et al., 2016
Chicken associated gemycircularvirus 1	KT862244	29 Fec79971 llama	*Lama glama*	Llama	Faeces	New Zealand	Steel et al., 2016
Chicken associated gemycircularvirus 1	KT862246	30 Fec79971 horse	*Equus ferus caballus*	Horse	Faeces	New Zealand	Steel et al., 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	Abdomen	USA	Rosario et al., 2012
Equine associated gemycircularvirus 1	KT862248	30 Fec80061 horse	*Equus ferus caballus*	Horse	Faeces	New Zealand	Steel et al., 2016
Fur seal associated gemycircularvirus 1	KF371638	as50	*Arctocephalus forsteri*	New Zealand fur seal	Faeces	New Zealand	Sikorski et al., 2013
Fur seal associated gemycircularvirus 1	KT862241	27 Fec1 chicken	*Gallus gallus domesticus*	Chicken	Faeces	New Zealand	Steel et al., 2016
Gerygone associated gemycircularvirus 1	KF371636	P24a	*Gerygone albofrontata*	Chatham Island warbler	Faeces	New Zealand	Sikorski et al., 2013
Gerygone associated gemycircularvirus 2	KF371637	P24b	*Gerygone albofrontata*	Chatham Island warbler	Faeces	New Zealand	Sikorski et al., 2013
Gerygone associated gemycircularvirus 3	KF371639	P24c	*Gerygone albofrontata*	Chatham 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	KT862245	29 Fec80018 llama	*Lama glama*	Llama	Faeces	New Zealand	Steel et al., 2016
Lama associated gemycircularvirus 1	KT862247	30 Fec80018 horse	*Equus ferus caballus*	Horse	Faeces	New Zealand	Steel et al., 2016
Mallard associated gemycircularvirus 1	KF371635	as24	*Anas platyrhynchos*	Mallard duck	Faeces	New Zealand	Sikorski et al., 2013
Miniopterus associated gemycircularvirus 1	KJ641719	BtMf-CV-23/GD2012	*Miniopterus fuliginosus*	Bat	Pharyngeal & rectal swabs	China	Wu et al., 2015
Mongoose associated gemycircularvirus 1	KP263547	478d	*Herpestes ichneumon*	Egyptian mongoose	Faeces	Portugal	Conceicao-Neto et al., 2015
Mosquito associated gemycircularvirus 1	HQ335086	SDBVL G	*Culex erythrothorax*	Mosquito	Mosquito samples	USA	Ng et al., 2011

Odonata associated gemycircularvirus 1	KM598385	OdaGmV-1-US-260BC-12	*Ischnura posita*	Damselfly	Abdomen	USA	Dayaram et al., 2015
Odonata associated gemycircularvirus 1	KM598386	OdaGmV-1-US-260SR1-12	*Pantala hymenaea*	Dragonfly	Abdomen	USA	Dayaram et al., 2015
Odonata associated gemycircularvirus 2	KM598387	OdaGmV-2-US-1642KW-12	*Aeshna multicolor*	Dragonfly	Abdomen	USA	Dayaram et al., 2015
Odonata associated gemycircularvirus 2	KM598388	OdaGmV-2-US-1634LM2-12	*Libellula saturata*	Dragonfly	Abdomen	USA	Dayaram et al., 2015
Poaceae associated gemycircularvirus 1	KT253577	PaGmV-1 TO STO14-29204 2014	*Rattus norvegicus*	Rat	Blood	China	Li et al., 2015
Poaceae associated gemycircularvirus 1	KT253578	PaGmV-1 TO STO15-29204 2014	*Brachiaria deflexa*	Signalgrass	Leaf	Tonga	Male et al., 2015
Poaceae associated gemycircularvirus 1	KT253579	PaGmV-1 TO STO18-29204 2014	*Brachiaria deflexa*	Signalgrass	Leaf	Tonga	Male et al., 2015
Porcine associated gemycircularvirus 1	KT862250	49 Fec80061 pig	*Sus scrofa domestica*	Pig	Faeces	New Zealand	Steel et al., 2016
Porcine associated gemycircularvirus 2	KF371640	as5	*Sus scrofa*	Domestic pig	Faeces	New Zealand	Sikorski et al., 2013
Pteropus associated gemycircularvirus 1	KT732804	Tbat 45285	*Pteropus tonganus*	Bat	Faeces	Tonga	Male et al., 2016
Pteropus associated gemycircularvirus 1	KT732805	Tbat 47364	*Pteropus tonganus*	Bat	Faeces	Tonga	Male et al., 2016
Pteropus associated gemycircularvirus 2	KT732792	Tbat 103791	*Pteropus tonganus*	Bat	Faeces	Tonga	Male et al., 2016
Pteropus associated gemycircularvirus 2	KT732793	Tbat A 103791	*Pteropus tonganus*	Bat	Faeces	Tonga	Male et al., 2016
Pteropus associated gemycircularvirus 3	KT732797	Tbat A 103852	*Pteropus tonganus*	Bat	Faeces	Tonga	Male et al., 2016
Pteropus associated gemycircularvirus 4	KT732814	Tbat H 103806	*Pteropus tonganus*	Bat	Faeces	Tonga	Male et al., 2016
Pteropus associated gemycircularvirus 5	KT732801	Tbat 12377	*Pteropus tonganus*	Bat	Faeces	Tonga	Male et al., 2016
Pteropus associated gemycircularvirus 5	KT732802	Tbat H 12377	*Pteropus tonganus*	Bat	Faeces	Tonga	Male et al., 2016
Pteropus associated gemycircularvirus 6	KT732803	Tbat 103951	*Pteropus tonganus*	Bat	Faeces	Tonga	Male et al., 2016
Pteropus associated gemycircularvirus 6	KT732796	Tbat H 103639	*Pteropus tonganus*	Bat	Faeces	Tonga	Male et al., 2016
Pteropus associated gemycircularvirus 7	KT732807	Tbat A 103746	*Pteropus tonganus*	Bat	Faeces	Tonga	Male et al., 2016
Pteropus associated gemycircularvirus 7	KT732808	Tbat A 103909	*Pteropus tonganus*	Bat	Faeces	Tonga	Male et al., 2016
Pteropus associated gemycircularvirus 7	KT732809	Tbat H 103746	*Pteropus tonganus*	Bat	Faeces	Tonga	Male et al., 2016
Pteropus associated gemycircularvirus 7	KT732810	Tbat H 103909	*Pteropus tonganus*	Bat	Faeces	Tonga	Male et al., 2016
Pteropus associated gemycircularvirus 7	KT732811	Tbat L 103746	*Pteropus tonganus*	Bat	Faeces	Tonga	Male et al., 2016
Pteropus associated gemycircularvirus 7	KT732812	Tbat L 103909	*Pteropus tonganus*	Bat	Faeces	Tonga	Male et al., 2016
Pteropus associated gemycircularvirus 8	KT732806	Tbat 31579	*Pteropus tonganus*	Bat	Faeces	Tonga	Male et al., 2016
Pteropus associated gemycircularvirus 9	KT732795	Tbat 21383	*Pteropus tonganus*	Bat	Faeces	Tonga	Male et al., 2016
Pteropus associated gemycircularvirus 10	KT732794	Tbat H 103958	*Pteropus tonganus*	Bat	Faeces	Tonga	Male et al., 2016
Rat associated gemycircularvirus 1	KR912221	Ch-zjrat-01	*Homo sapiens*	Human	Plasma	France	Uch et al., 2015
Sclerotinia gemycircularvirus 1	GQ365709	SsHADV-1 CN	*Sclerotinia sclerotiorum*	Sclerotinia	Mycelial samples	China	Yu et al., 2010
Sclerotinia gemycircularvirus 1	KF268025	SsHADV-1 NZ H6 2012	River Sediments	-	River Sediments	New Zealand	Kraberger et al., 2013
Sclerotinia gemycircularvirus 1	KF268026	SsHADV-1 NZ SR1 2012	River Sediments	-	River Sediments	New Zealand	Kraberger et al., 2013
Sclerotinia gemycircularvirus 1	KF268027	SsHADV-1 NZ SR3 2012	River Sediments	-	River Sediments	New Zealand	Kraberger et al., 2013
Sclerotinia gemycircularvirus 1	KF268028	SsHADV-1 NZ SR5 2012	River Sediments	-	River Sediments	New Zealand	Kraberger et al., 2013
Sclerotinia gemycircularvirus 1	KM598382	SsHADV-1-US-549LB-12	*Ischnura ramburii*	Damselfly	Abdomen	USA	Dayaram et al., 2015

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

Table 2: Details of all isolates within the genus *Gemykibivirus*

Species	Accession	Isolate	Isolation source	Common Name	Sample type	Country	Reference
Badger associated gemykibivirus 1	KP263543	588t	*Meles meles*	European badger	Faeces	Portugal	Conceicao-Neto et al., 2015
Black robin associated gemykibivirus 1	KF371634	P21	*Petroica traversi*	Chatham Island black robin	Faeces	New Zealand	Sikorski et al., 2013
Blackbird associated gemykibivirus 1	KF371633	P22	*Turdus merula*	Blackbird	Faeces	New Zealand	Sikorski et al., 2013
Bovine associated gemykibivirus 1	LK931483	HCBI8.215	*Bos taurus*	Cow	Serum	Germany	Lamberto et al., 2014
Dragonfly associated gemykibivirus 1	JX185430	FL1-2X-2010	*Miathyria marcella*	Dragonfly	Abdomen	USA	Rosario et al., 2012
Human associated gemykibivirus 1	KJ547644	BS3980	Sewage oxidation pond	-	Sewage	New Zealand	Kraberger et al., 2015a
Human associated gemykibivirus 1	KJ547645	BS3849	Sewage oxidation pond	-	Sewage	New Zealand	Kraberger et al., 2015a
Human associated gemykibivirus 1	KP974694	DB2	*Homo sapiens*	Human	Plasma	Germany	unpublished
Human associated gemykibivirus 1	LK931485	MSSI2.225	*Homo sapiens*	Human	Blood	Germany	Lamberto et al., 2014
Human associated gemykibivirus 2	KP133075	SL1	*Homo sapiens*	Human	Cerebro spinal fluid	Sri Lanka	Phan et al., 2015
Human associated gemykibivirus 2	KP133076	SL2	*Homo sapiens*	Human	Cerebro spinal fluid	Sri Lanka	Phan et al., 2015
Human associated gemykibivirus 2	KP133077	SL3	*Homo sapiens*	Human	Cerebro spinal fluid	Sri Lanka	Phan et al., 2015
Human associated gemykibivirus 2	KP133078	BZ1	*Homo sapiens*	Human	Faeces	Brazil	Phan et al., 2015
Human associated gemykibivirus 2	KP133079	BZ2	*Homo sapiens*	Human	Faeces	Brazil	Phan et al., 2015
Human associated gemykibivirus 2	KP133080	NP	Untreated sewage	-	Sewage	Nepal	Phan et al., 2015
Human associated gemykibivirus 3	KP987887	GemyC1c	*Homo sapiens*	Human	Plasma	France	unpublished
Human associated gemykibivirus 3	KP263546	541c	*Herpestes ichneumon*	Egyptian mongoose	Faeces	Portugal	Conceicao-Neto et al., 2015
Human associated gemykibivirus 4	KT363839	GeTz1	*Poecile atricapillus*	Black-capped chickadee	Buccal and cloacal swab	USA	Hanna et al., 2015

Human associated gemykibivirus 5	KU343137	HV-GcV2	*Homo sapiens*	Human	Pericardial 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	KJ641737	BtRh-CV-6/Tibet2013	*Rhinolophus hipposideros*	Bat	Pharyngeal & rectal swabs	China	Wu et al., 2015
Rhinolophus associated gemykibivirus 1	KP263544	181a	*Herpestes ichneumon*	Egyptian mongoose	Faeces	Portugal	Conceicao-Neto et al., 2015
Rhinolophus associated gemykibivirus 2	KJ641726	BtRf-CV-8/NM2013	*Rhinolophus ferrumequinum*	Bat	Pharyngeal & rectal swabs	China	Wu et al., 2015
Sewage derived gemykibivirus 1	KJ547643	BS4149	Sewage oxidation pond	-	Sewage	New Zealand	Kraberger et al., 2015a
Sewage derived gemykibivirus 1	KT862240	27 BS14149 chicken	*Gallus gallus domesticus*	Chicken	Faeces	New Zealand	Steel et al., 2016
Sewage derived gemykibivirus 1	KT862252	52 BS14149 cow	*Bos taurus*	Cow	Faeces	New Zealand	Steel et al., 2016
Sewage derived gemykibivirus 1	KT862255	56 BS14149 hare	*Lepus europaeus*	Hare	Faeces	New Zealand	Steel et al., 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*

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

Table 4: Details of all isolates within the genus *Gemykolovirus*

Species	Accession	Isolate	Isolation source	Common Name	Sample type	Country	Reference
Pteropus associated gemykolovirus 1	KT732798	Tbat A 103779	*Pteropus tonganus*	Bat	Faeces	Tonga	Male et al., 2016
Pteropus associated gemykolovirus 1	KT732799	Tbat H 103779	*Pteropus tonganus*	Bat	Faeces	Tonga	Male et al., 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	Accession	Isolate	Isolation source	Common Name	Sample type	Country	Reference
Bovine associated gemykrogvirus 1	LK931484	HCBI9.212	*Bos taurus*	Cow	Serum	Germany	Lamberto et al., 2014
Caribou associated gemykrogvirus 1	KJ938717	FaGmCV-13	*Rangifer tarandus*	Caribou	Faeces	Canada	Ng et al., 2014
Sewage derived gemykrogvirus 1	KJ547634	BS3913	Sewage oxidation pond	-	Sewage	New Zealand	Kraberger et al., 2015a

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

Species	Accession	Isolate	Isolation source	Common Name	Sample 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*

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

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

Species	Accession	Isolate	Isolation source	Common Name	Sample type	Country	Reference
Rabbit associated gemykroznavirus 1	KF371631	as35	*Oryctolagus cuniculus*	Rabbit	Faeces	New Zealand	Sikorski et 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 gemyduguivirus 1	JX185428	TO-DFS3B2-2010	*Pantala flavescens*	Dragonfly	Abdomen	Tonga	Rosario et al., 2012

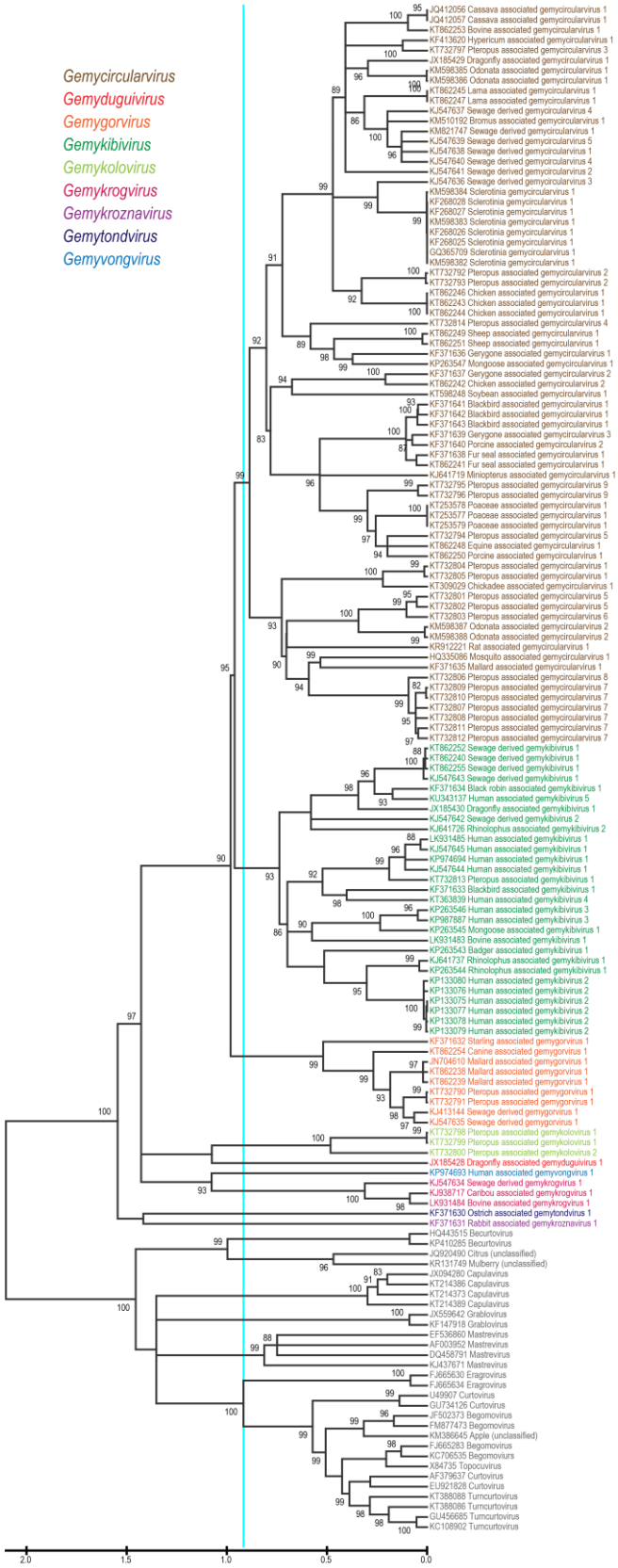

Figure 1: Maximum likelihood phylogenetic tree of the Rep amino acid sequences inferred using PHYML with LG+G+I substitution model and rooted with geminivirus sequences. The sequences of geminiviruses labelled with the corresponding genera names are used as a guide to identify genera within the *Genomoviridae*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

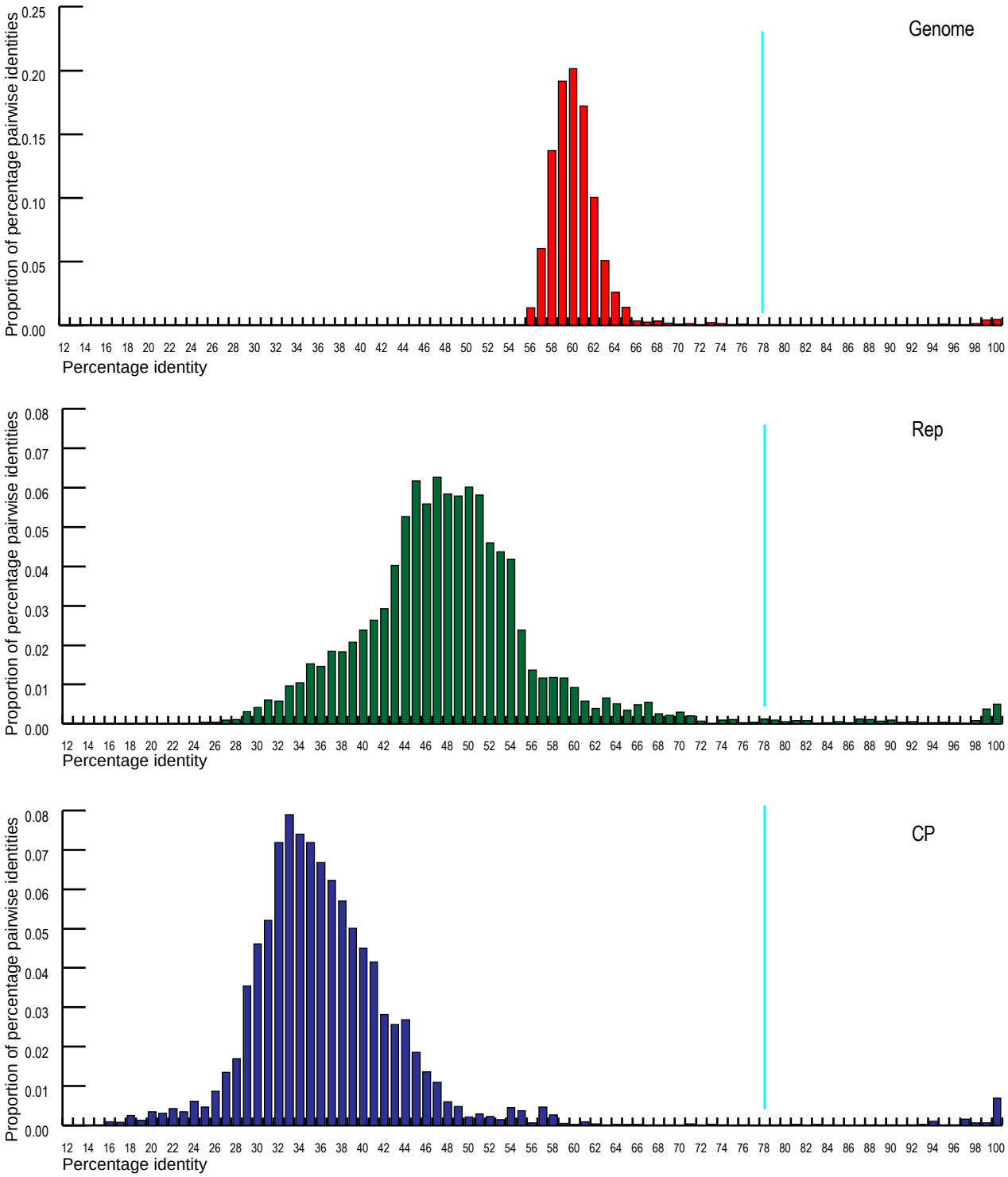

Figure 2: Distribution of (A) genome-wide, (B) Rep and (C) CP pairwise identities (121 taxa) of genomoviruses calculated using SDT v1.2 (Muhire et al., 2014).

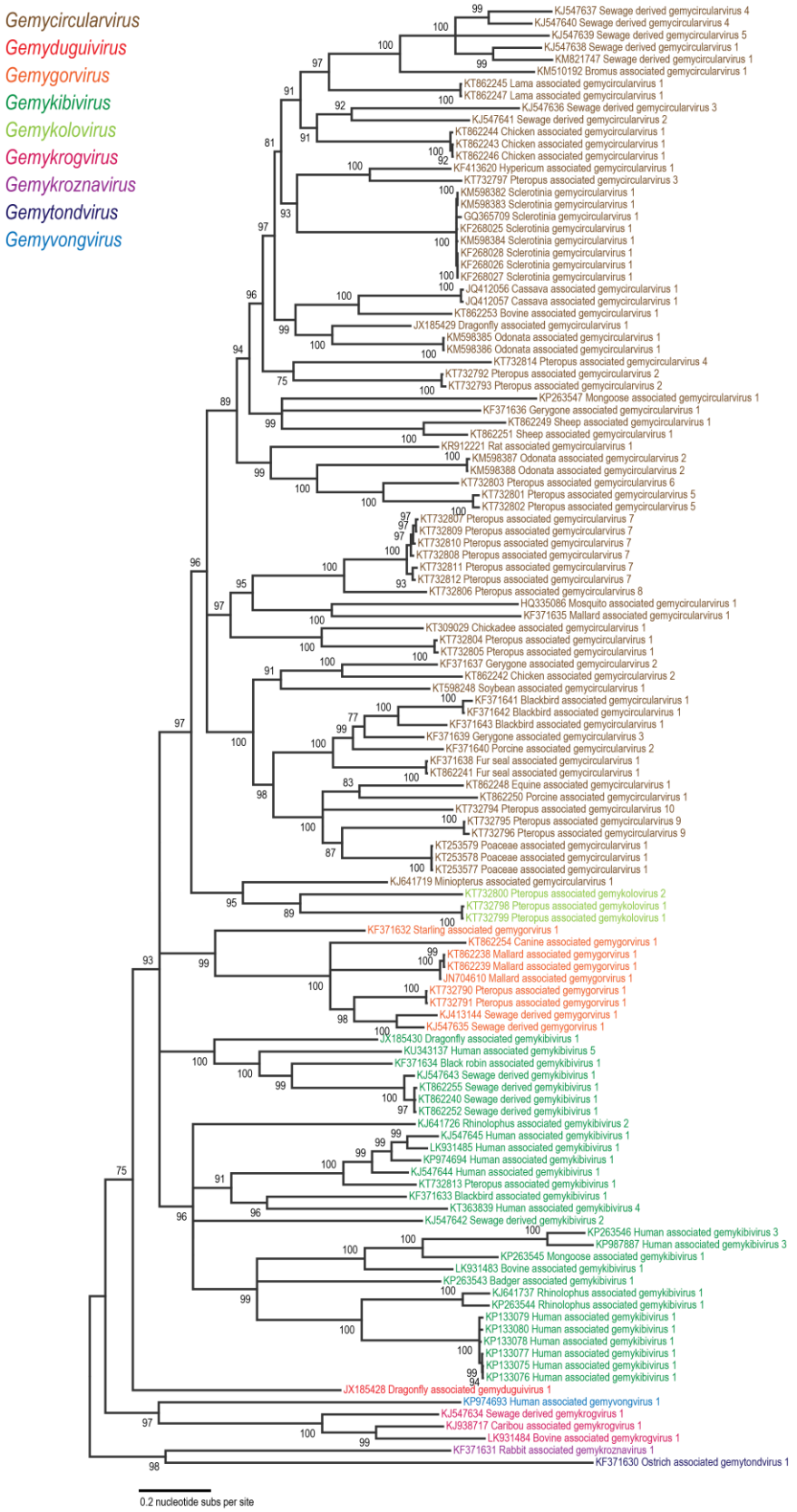

Figure 3: Maximum likelihood phylogenetic tree (GTR+CAT) with SH-like support of the genomes of isolates in the *Genomoviridae* family supporting that the genera demarcation is supported at the genome level as well despite there being evidence of recombination within the genomes. Branches with <75% SH-like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

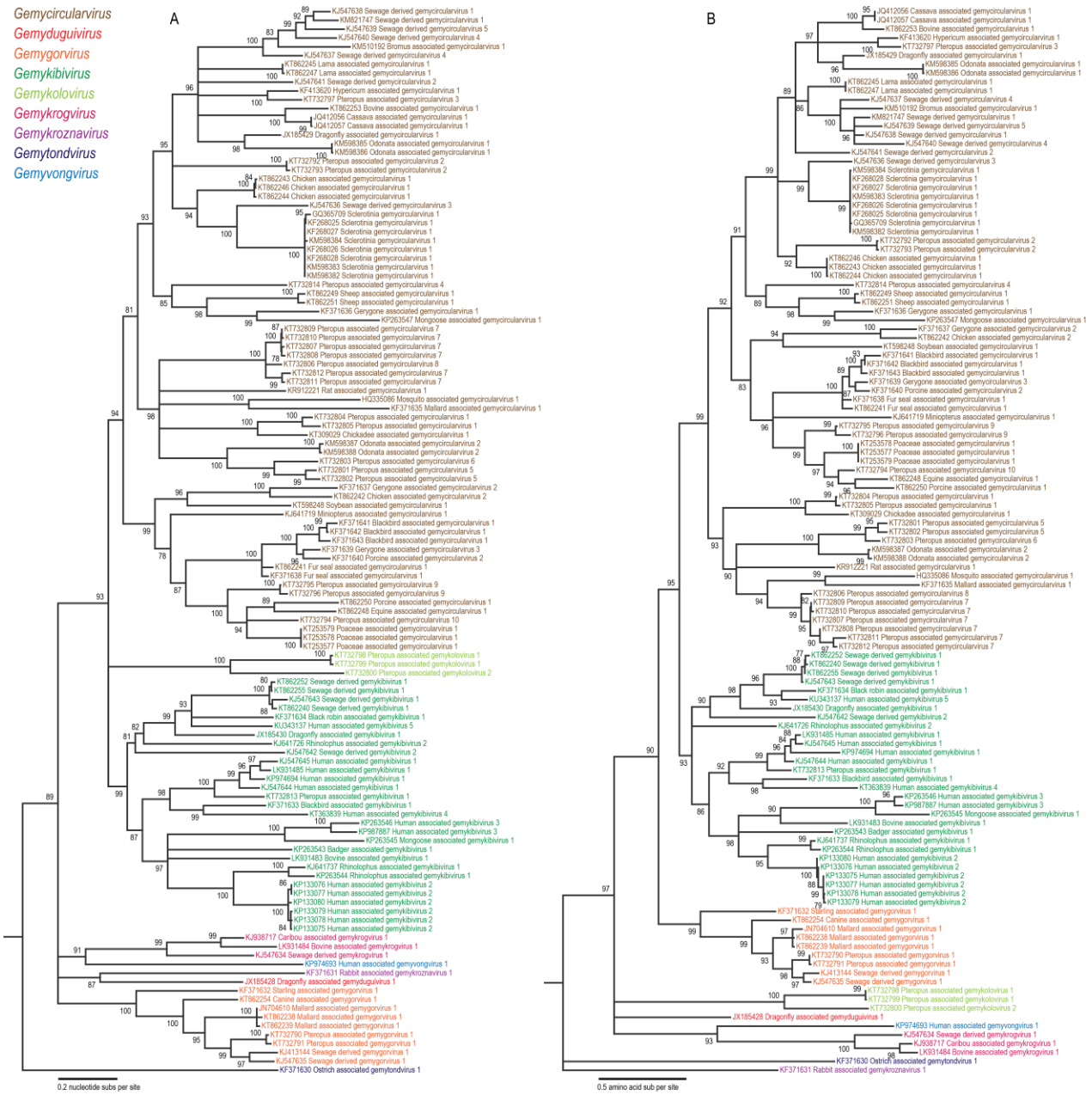

Figure 4: Maximum likelihood phylogenetic tree of (A) the *rep* gene sequences and (B) the Rep amino acid sequences inferred using PHYML with GTR+G and LG+G+I substitution models and rooted with geminivirus sequences. The genera demarcation that is Rep-sequence driven for the family *Genonoviridae* is 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.

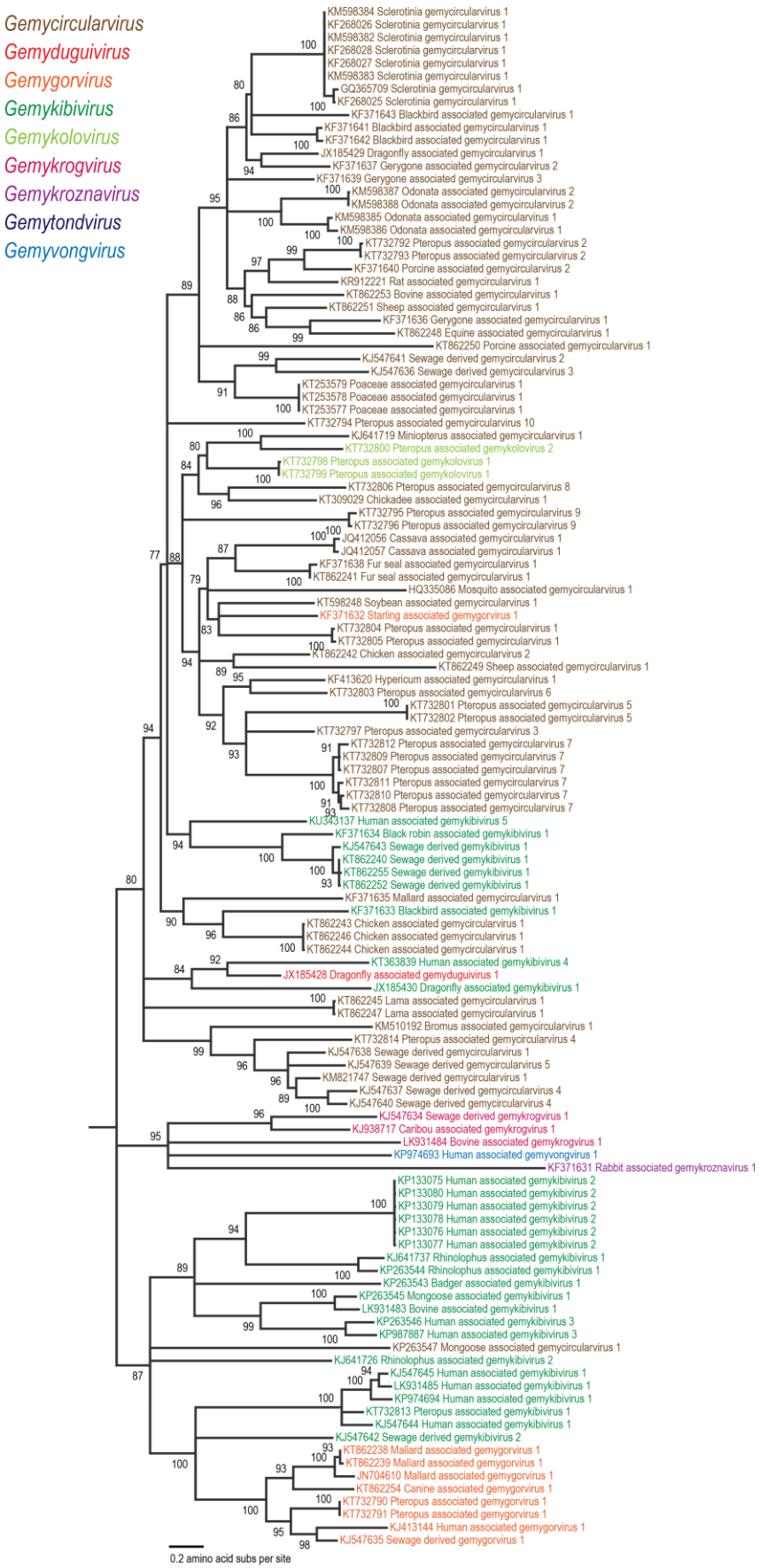

Figure 5: Maximum likelihood phylogenetic tree of the CP amino acid sequences inferred using PHYML with LG+G+I substitution models and rooted with geminivirus sequences. Branches with <75% SH-like branch support have been collapsed.

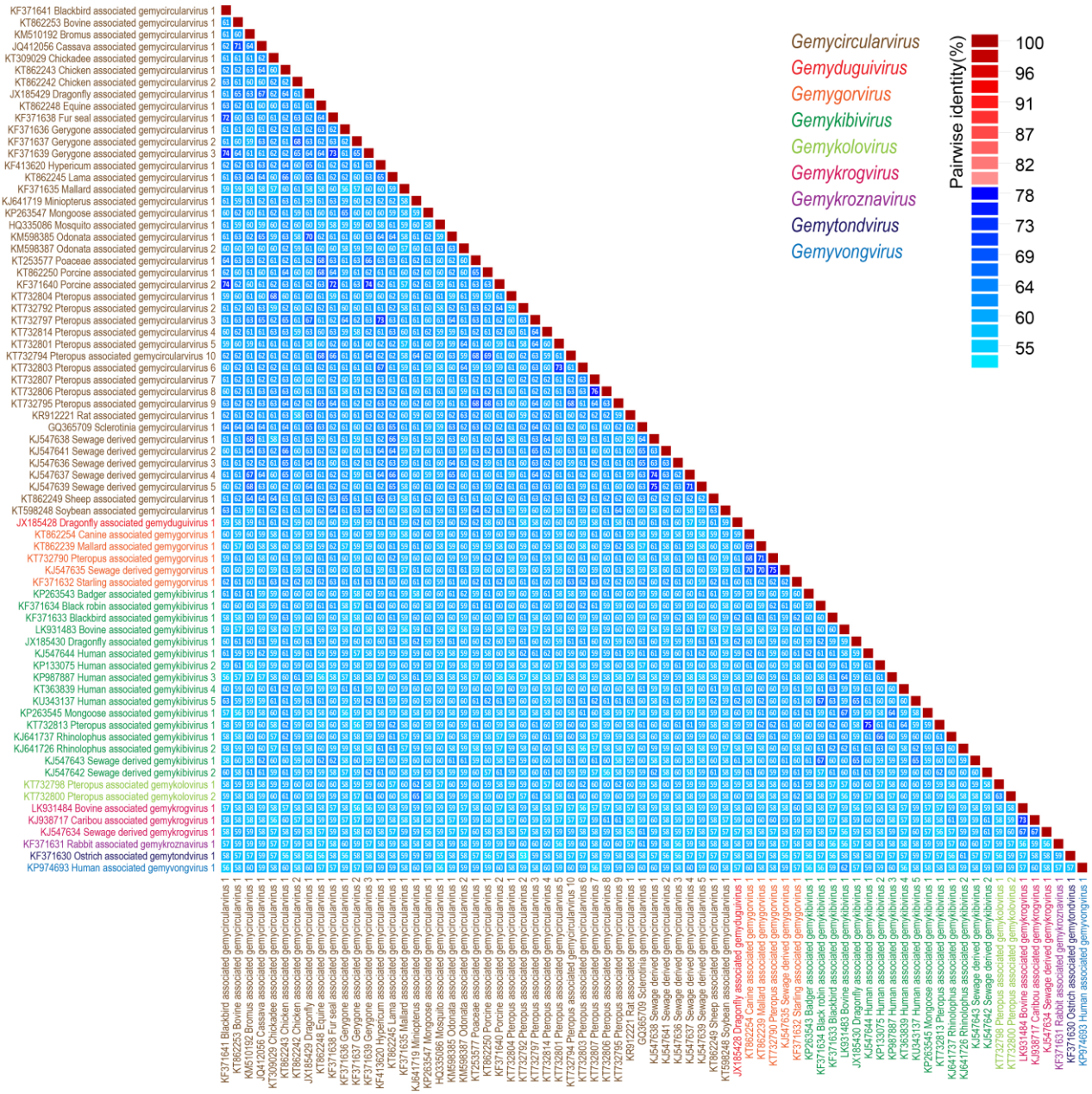

Figure 6: Genome-wide pairwise identities representative isolates of each species within the *Genomoviridae* family determined using SDT v1.2 (Muhire et al., 2014). The 'two colour' profile highlights that the 78% species demarcation threshold is valid for the proposed species in the *Genomoviridae*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

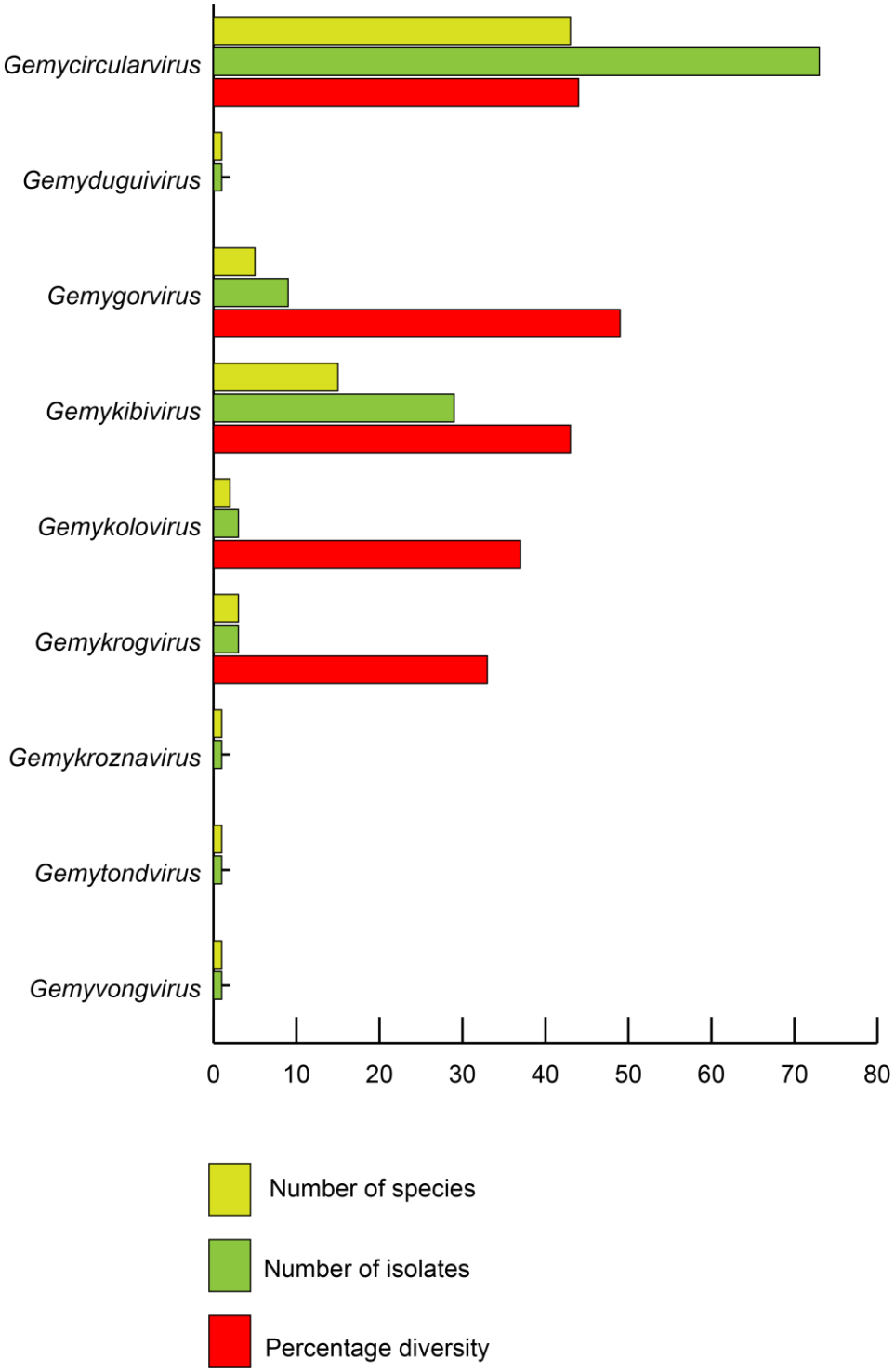

Figure 7: Summary of genera and the associated species and their diversity (within genera) within the *Genomoviridae* family.