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:	***2016.008a,bD***	(to be completed by ICTV officers)
Short title: 15 new species in the genus *Cyclovirus* (e.g. 6 new species in the genus *Zetavirus*)		
Modules attached (modules 1 and 11 are required)	**..** **2** ☒ **3** ☐ **4** ☐ **5** ☐ **6** ☐ **7** ☐ **8** ☐ **9** ☒ **10** ☐	

Author(s):

Arvind Varsani, Karyna Rosario and Mya Breitbart on behalf of study group

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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)	Circoviridae Study Group

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

Date first submitted to ICTV:	July 18, 2016
Date of this revision (if different to above):	27 November 2016

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	***2016.008aD***	(assigned by ICTV officers)

To create 15 new species within:

Genus:	*Cyclovirus*
Subfamily:	
Family:	*Circoviridae*
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)**
Bat associated cyclovirus 6	BtRp-CV-14/GD2012	KJ641712
Bat associated cyclovirus 7	BtRf-CV-24/YN2010	KJ641740
Bat associated cyclovirus 8	BtRp-CV-52/GD2012	KJ641715
Bat associated cyclovirus 9	BtTp-CV-2/GX2012	KJ641720
Bat associated cyclovirus 10	POA/2012/VI	KM382270
Bat associated cyclovirus 11	BtMspp-CV/GD2012	KJ641717
Bat associated cyclovirus 12	POA/2012/II	KM382269
Bat associated cyclovirus 13	BtPa-CV-2/NX2013	KJ641728
Bat associated cyclovirus 14	Tbat_H_103699	KT732785
Bat associated cyclovirus 15	Tbat_H_88317	KT732786
Bat associated cyclovirus 16	Tbat_H_103923	KT732788
Feline associated cyclovirus 1	feline cyclovirus	KM017740
Horse associated cyclovirus 1	cyclovirus Equ1	KR902499
Squirrel associated cyclovirus 1	TsCyV-1_JP-NUBS-2014	LC018134
Human associated cyclovirus 11	SL-108277	KJ831064

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

The current species demarcation for members of the genus Cyclovirus is 80%, i.e. cyclovirus sequences that share <80% genome-wide pairwise identity are classified as new species. We have analyzed new full genomes of cycloviruses available in public databases using SDT v1.2 (Muhire et al., 2014). Our analysis reveals that 18 virus genomes (see Table 1 for details) represent 15 new species, based on genome-wide pairwise identities (Figure 1) coupled with phylogenetic support, and should be classified accordingly (Figure 2). Analysis of the Rep and CP amino acid sequences (Figures 3 and 4) provide additional support for the classification.

MODULE 9: **RENAME**

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

Renaming one or more taxa

Code	***2016.008bD***	(assigned by ICTV officers)

To rename the following taxon (or taxa):

Current name	**Proposed name**
Bat faeces associated cyclovirus 1	*Bat associated cyclovirus 1*
Bat faeces associated cyclovirus 2	*Bat associated cyclovirus 2*
Bat faeces associated cyclovirus 3	*Bat associated cyclovirus 3*
Bat faeces associated cyclovirus 4	*Bat associated cyclovirus 4*
Bat cyclovirus	*Bat associated cyclovirus 5*
Bovine cyclovirus	*Bovine associated cyclovirus 1*
Chimpanzee faeces associated cyclovirus	*Chimpanzee associated cyclovirus 1*
Dragonfly cyclovirus 1	*Dragonfly associated cyclovirus 1*
Dragonfly cyclovirus 2	*Dragonfly associated cyclovirus 2*
Dragonfly cyclovirus 3	*Dragonfly associated cyclovirus 3*
Dragonfly cyclovirus 4	*Dragonfly associated cyclovirus 4*
Dragonfly cyclovirus 5	*Dragonfly associated cyclovirus 5*
Dragonfly cyclovirus 6	*Dragonfly associated cyclovirus 6*
Dragonfly cyclovirus 7	*Dragonfly associated cyclovirus 7*
Dragonfly cyclovirus 8	*Dragonfly associated cyclovirus 8*
Florida wood cockroach cyclovirus	*Cockroach associated cyclovirus 1*
Gallus cyclovirus	*Chicken associated cyclovirus 1*
Goat cyclovirus	*Goat associated cyclovirus 1*
Human faeces associated cyclovirus 1	*Human associated cyclovirus 1*
Human faeces associated cyclovirus 2	*Human associated cyclovirus 2*
Human faeces associated cyclovirus 3	*Human associated cyclovirus 3*
Human faeces associated cyclovirus 4	*Human associated cyclovirus 4*
Human faeces associated cyclovirus 5	*Human associated cyclovirus 5*
Human faeces associated cyclovirus 6	*Human associated cyclovirus 6*
Human faeces associated cyclovirus 8	*Human associated cyclovirus 7*
Human cyclovirus 1	*Human associated cyclovirus 8*
Human cyclovirus 2	*Human associated cyclovirus 9*
Human cyclovirus 3	*Human associated cyclovirus 10*

Reasons to justify the renaming:
Explain why the taxon (or taxa) should be renamed

The genus *Cyclovirus* accommodates a group of phylogenetically related viruses discovered through metagenomic analysis and degenerate PCR. Therefore, it has been difficult to identify a definitive host for most, if not all, cyclovirus species described to date. Since their detection in a given organism does not grant their infectivity to the organism, it is important to make this distinction in cyclovirus species names. We propose adding the word ‘associated’ as a modifier to cyclovirus species for which replication within a given organism has not been reported. In addition, it is important to make species names similar and uniform across all members of the family *Circoviridae.* We propose removing any specific tissue or source name used for virus isolation, such as faeces, from species names representing members of the *Circoviridae* (i.e., circovirus and cyclovirus species).

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 isolates in the genus *Cyclovirus*. New species are highlighted in red font. Note that the table lists new cyclovirus species names proposed here.

Species	Accession #	Acronym	Country of isolate	Isolation source (Common name)	Sample type	References
Bat associated cyclovirus 1	HM228874	BatACyV-1	USA	*Antrozous pallidus* (Bat)	Faeces	Li et al., 2010a
Bat associated cyclovirus 2	JF938079	BatACyV-2	China	*Myotis* spp. (Bat)	Faeces	Ge et al., 2011
Bat associated cyclovirus 3	JF938081	BatACyV-3	China	*Myotis* spp. (Bat)	Faeces	Ge et al., 2011
Bat associated cyclovirus 4	JF938082	BatACyV-4	China	*Myotis* spp. (Bat)	Faeces	Ge et al., 2011
Bat associated cyclovirus 5	HQ738637	BatACyV-5	USA	*Tadarida brasiliensis* (Bat)	Muscle	Li et al., 2011
Bat associated cyclovirus 6	KJ641712	BatACyV-6	China	*Rhinolophus pusillus* (Bat)	Pharyngeal & rectal swabs	Wu et al.,2015
Bat associated cyclovirus 7	KJ641740	BatACyV-7	China	*Rhinolophus pusillus* (Bat)	Pharyngeal & rectal swabs	Wu et al.,2015
	KJ641714	BatACyV-7	China	*Rhinolophus ferrumequinum* (Bat)	Pharyngeal & rectal swabs	Wu et al.,2015
Bat associated cyclovirus 8	KJ641715	BatACyV-8	China	*Rhinolophus pusillus* (Bat)	Pharyngeal & rectal swabs	Wu et al.,2015
	KJ641734	BatACyV-8	China	*Vespertilio superans* (Bat)	Pharyngeal & rectal swabs	Wu et al.,2015

Bat associated cyclovirus 9	KJ641720	BatACyV-9	China	*Tylonycteris pachypus* (Bat)	Pharyngeal & rectal swabs	Wu et al.,2015
Bat associated cyclovirus 10	KM382270	BatACyV-10	Southern Brazil	*Molossus molossus, Tadarida brasiliensis* (Bat)	Faeces	Lima et al., 2015
Bat associated cyclovirus 11	KJ641717	BatACyV-11	China	*Myotis spp.* (Bat)	Pharyngeal & rectal swabs	Wu et al.,2015
Bat associated cyclovirus 12	KM382269	BatACyV-12	Southern Brazil	*Molossus molossus, Tadarida brasiliensis* (Bat)	Faeces	Lima et al., 2015
Bat associated cyclovirus 13	KJ641728	BatACyV-13	China	*Plecotus auritus* (Bat)	Pharyngeal & rectal swabs	Wu et al.,2015
Bat associated cyclovirus 14	KT732785	BatACyV-14	Tonga	*Pteropus tonganus* (Bat)	Faeces	Male et al. 2016
Bat associated cyclovirus 15	KT732786	BatACyV-15	Tonga	*Pteropus tonganus* (Bat)	Faeces	Male et al. 2016
Bat associated cyclovirus 16	KT732787	BatACyV-16	Tonga	*Pteropus tonganus* (Bat)	Faeces	Male et al. 2016
	KT732788	BatACyV-16	Tonga	*Pteropus tonganus* (Bat)	Faeces	Male et al. 2016
	KT732789	BatACyV-16	Tonga	*Pteropus tonganus* (Bat)	Faeces	Male et al. 2016
Bovine associated cyclovirus 1	HQ738634	BoACyV-1	Pakistan	*Bos taurus* (Cow)	Muscle	Li et al., 2011
	HQ738635	BoACyV-1	Pakistan	*Bos taurus* (Cow)	Muscle	Li et al., 2011
Feline associated cyclovirus 1	KM017740	FeACyV-1	USA	*Felis catus* (Cat)	Faeces	Zhang et al., 2014
Chicken associated cyclovirus 1	HQ738643	ChickACyV-1	Nigeria	*Gallus gallus* (Chicken)	Muscle	Li et al., 2011
	HQ738644	ChickACyV-1	Nigeria	*Gallus gallus* (Chicken)	Muscle	Li et al., 2011
Chimpanzee associated cyclovirus 1	GQ404849	ChimpACyV-1	Central Africa	*Pan troglodytes* (Chimpanzee)	Faeces	Li et al., 2010b
	GQ404850	ChimpACyV-1	Central Africa	*Pan troglodytes* (Chimpanzee)	Faeces	Li et al., 2010b
Dragonfly associated cyclovirus 1	HQ638049	DfACyV-1	Tonga	*Tholymis tillarga* (Dragonfly)	Abdomen	Rosario et al., 2011
	HQ638050	DfACyV-1	Tonga	*Tholymis tillarga* (Dragonfly)	Abdomen	Rosario et al., 2011
	HQ638051	DfACyV-1	Tonga	*Tholymis tillarga* (Dragonfly)	Abdomen	Rosario et al., 2011
	HQ638052	DfACyV-1	Tonga	*Pantala flavescens* (Dragonfly)	Abdomen	Rosario et al., 2011
	HQ638053	DfACyV-1	Tonga	*Diplacodes bipunctata* (Dragonfly)	Abdomen	Rosario et al., 2011
	HQ638054	DfACyV-1	Tonga	*Diplacodes bipunctata* (Dragonfly)	Abdomen	Rosario et al., 2011
	HQ638055	DfACyV-1	Tonga	*Pantala flavescens* (Dragonfly)	Abdomen	Rosario et al., 2011
	HQ638056	DfACyV-1	Tonga	*Pantala flavescens* (Dragonfly)	Abdomen	Rosario et al., 2011
	HQ638057	DfACyV-1	Tonga	*Tholymis tillarga* (Dragonfly)	Abdomen	Rosario et al., 2011
	HQ638058	DfACyV-1	Tonga	*Pantala flavescens* (Dragonfly)	Abdomen	Rosario et al., 2011
	HQ638059	DfACyV-1	Tonga	*Pantala flavescens* (Dragonfly)	Abdomen	Rosario et al., 2011
	HQ638060	DfACyV-1	Tonga	*Diplacodes bipunctata* (Dragonfly)	Abdomen	Rosario et al., 2011
	HQ638061	DfACyV-1	Tonga	*Diplacodes bipunctata* (Dragonfly)	Abdomen	Rosario et al., 2011
	HQ638062	DfACyV-1	Tonga	*Diplacodes bipunctata* (Dragonfly)	Abdomen	Rosario et al., 2011
	HQ638063	DfACyV-1	Tonga	*Diplacodes bipunctata* (Dragonfly)	Abdomen	Rosario et al., 2011
	HQ638064	DfACyV-1	Tonga	*Diplacodes bipunctata* (Dragonfly)	Abdomen	Rosario et al., 2011

	HQ638065	DfACyV-1	Tonga	*Pantala flavescens* (Dragonfly)	Abdomen	Rosario et al., 2011
	HQ638066	DfACyV-1	Tonga	*Pantala flavescens* (Dragonfly)	Abdomen	Rosario et al., 2011
	HQ638067	DfACyV-1	Tonga	*Pantala flavescens* (Dragonfly)	Abdomen	Rosario et al., 2011
	HQ638068	DfACyV-1	Tonga	*Diplacodes bipunctata* (Dragonfly)	Abdomen	Rosario et al., 2011
	HQ638069	DfACyV-1	Tonga	*Tholymis tillarga* (Dragonfly)	Abdomen	Rosario et al., 2011
	JX185419	DfACyV-1	Tonga	*Pantala flavescens* (Dragonfly)	Abdomen	Rosario et al., 2012a
	JX185420	DfACyV-1	Tonga	*Pantala flavescens* (Dragonfly)	Abdomen	Rosario et al., 2012a
	JX185421	DfACyV-1	Tonga	*Pantala flavescens* (Dragonfly)	Abdomen	Rosario et al., 2012a
Dragonfly associated cyclovirus 2	JX185422	DfACyV-2	USA	*Pantala flavescens* (Dragonfly)	Abdomen	Rosario et al., 2012a
	JX185423	DfACyV-2	USA	*Anax junius* (Dragonfly)	Abdomen	Rosario et al., 2012a
Dragonfly associated cyclovirus 3	JX185424	DfACyV-3	USA	*Erythemis simplicicollis* (Dragonfly)	Abdomen	Rosario et al., 2012a
Dragonfly associated cyclovirus 4	JF938080	DfACyV-4	China	*Myotis* spp. (Bat)	Faeces	Ge et al., 2011
	JN377566	DfACyV-4	China	*Myotis* spp. (Bat)	Faeces	Ge et al., 2011
	JX185425	DfACyV-4	Bulgaria	*Somatochlora meridionalis* (Dragonfly)	Abdomen	Rosario et al., 2012a
	KC512916	DfACyV-4	USA	*Aeshna multicolor* (Dragonfly)	Abdomen	Dayaram et al., 2013
	KC512917	DfACyV-4	USA	*Aeshna multicolor* (Dragonfly)	Abdomen	Dayaram et al., 2013
	KJ641710	DfACyV-4	China	*Myotis blythii* (Bat)	Pharyngeal & rectal swabs	Wu et al.,2015
Dragonfly associated cyclovirus 5	JX185426	DfACyV-5	Puerto Rico	*Erythrodiplax umbrata* (Dragonfly)	Abdomen	Rosario et al., 2012a
	JX185427	DfACyV-5	Puerto Rico	*Erythrodiplax umbrata* (Dragonfly)	Abdomen	Rosario et al., 2012a
Dragonfly associated cyclovirus 6	KC512918	DfACyV-6	USA	*Aeshna multicolor* (Dragonfly)	Abdomen	Dayaram et al., 2013
Dragonfly associated cyclovirus 7	KC512919	DfACyV-7	New Zealand	*Xanthocnemis zealandica* (Dragonfly)	Abdomen	Dayaram et al., 2013
Dragonfly associated cyclovirus 8	KC512920	DfACyV-8	Australia	*Orthetrum Sabina* (Dragonfly)	Abdomen	Dayaram et al., 2013
Cockroach associated cyclovirus 1	JX569794	CroACyV-1	USA	*Eurycotis floridana* (Cockroach)	Abdomen	Padilla-Rodriguez et al., 2013
Goat associated cyclovirus 1	HQ738636	GoACyV-1	Pakistan	*Capra aegagrus hircus* (Goat)	Muscle	Li et al., 2011
Horse associated cyclovirus 1	KR902499	HoACyV-1	USA	*Equus caballus* (Horse)	Nasal secretions	Li et al., 2015
Human associated cyclovirus 1	GQ404847	HuACyV-1	Pakistan	*Homo sapiens* (Human)	Faeces	Li et al., 2010b
Human associated cyclovirus 2	GQ404844	HuACyV-2	Pakistan	*Homo sapiens* (Human)	Faeces	Li et al., 2010b
Human associated cyclovirus 3	GQ404846	HuACyV-3	Pakistan	*Homo sapiens* (Human)	Faeces	Li et al., 2010b
	GQ404848	HuACyV-3	Pakistan	*Homo sapiens* (Human)	Faeces	Li et al., 2010b
Human associated cyclovirus 4	GQ404857	HuACyV-4	Tunisia	*Homo sapiens* (Human)	Faeces	Li et al., 2010b
	GQ404858	HuACyV-4	Tunisia	*Homo sapiens* (Human)	Faeces	Li et al., 2010b
Human associated cyclovirus 5	GQ404845	HuACyV-5	Pakistan	*Homo sapiens* (Human)	Faeces	Li et al., 2010b
Human associated cyclovirus 6	GQ404854	HuACyV-6	Nigeria	*Homo sapiens* (Human)	Faeces	Li et al., 2010b

Human associated cyclovirus 7	GQ404855	HuACyV-7	Nigeria	*Homo sapiens* (Human)	Faeces	Li et al., 2010b
Human associated cyclovirus 8	AB937980	HuACyV-8	Zambia	*Mastomys natalensis* (African rat)	Faeces	Sasaki et al., 2015
	AB937981	HuACyV-8	Zambia	*Crocidura hirta* (shrew)	Faeces	Sasaki et al., 2015
	AB937982	HuACyV-8	Zambia	*Crocidura hirta* (shrew)	Faeces	Sasaki et al., 2015
	AB937983	HuACyV-8	Zambia	*Crocidura hirta* (shrew)	Faeces	Sasaki et al., 2015
	AB937984	HuACyV-8	Zambia	*Crocidura hirta* (shrew)	Faeces	Sasaki et al., 2015
	AB937985	HuACyV-8	Zambia	*Crocidura hirta* (shrew)	Faeces	Sasaki et al., 2015
	AB937986	HuACyV-8	Zambia	*Crocidura hirta* (shrew)	Faeces	Sasaki et al., 2015
	AB937987	HuACyV-8	Zambia	*Crocidura hirta* (shrew)	Faeces	Sasaki et al., 2015
	KF031465	HuACyV-8	Vietnam	*Homo sapiens* (Human)	Cerebrospinal fluid	Tan et al., 2013
	KF031466	HuACyV-8	Vietnam	*Homo sapiens* (Human)	Cerebrospinal fluid	Tan et al., 2013
	KF031467	HuACyV-8	Vietnam	*Homo sapiens* (Human)	Cerebrospinal fluid	Tan et al., 2013
	KF031468	HuACyV-8	Vietnam	*Homo sapiens* (Human)	Cerebrospinal fluid	Tan et al., 2013
	KF031469	HuACyV-8	Vietnam	*Homo sapiens* (Human)	Cerebrospinal fluid	Tan et al., 2013
	KF031470	HuACyV-8	Vietnam	*Sus scrofa* (Wild pig)	Faeces	Tan et al., 2013
	KF031471	HuACyV-8	Vietnam	*Gallus gallus* (Chicken)	Faeces	Tan et al., 2013
	KM392284	HuACyV-8	Cameroon	*Sus scrofa* (Wild pig)	Faeces	Garigliany et al., 2014
	KM392285	HuACyV-8	Cameroon	*Sus scrofa* (Wild pig)	Faeces	Garigliany et al., 2014
	KM392286	HuACyV-8	Cameroon	*Sus scrofa* (Wild pig)	Faeces	Garigliany et al., 2014
	KM392287	HuACyV-8	Madagascar	*Homo sapiens* (Human)	Faeces	Garigliany et al., 2014
	KM392288	HuACyV-8	Madagascar	*Homo sapiens* (Human)	Faeces	Garigliany et al., 2014
	KM392289	HuACyV-8	Madagascar	*Homo sapiens* (Human)	Faeces	Garigliany et al., 2014
Human associated cyclovirus 9	KC771281	HuACyV-9	Malawi	*Homo sapiens* (Human)	Blood serum	Smits et al., 2013
Human associated cyclovirus 10	KF726984	HuACyV-10	Chile	*Homo sapiens* (Human)	Respiratory secretion	Phan et al., 2014
	KF726985	HuACyV-10	Chile	*Homo sapiens* (Human)	Respiratory secretion	Phan et al., 2014
	KF726986	HuACyV-10	Chile	*Homo sapiens* (Human)	Respiratory secretion	Phan et al., 2014
	KF726987	HuACyV-10	Chile	*Homo sapiens* (Human)	Respiratory secretion	Phan et al., 2014
Human associated cyclovirus 11	KJ831064	HuACyV-5	Sri Lanka	*Homo sapiens* (Human)	Cerebrospinal fluid	Phan et al., 2015
	KP151567	HuACyV-5	Nicaragua	*Homo sapiens* (Human)	Faeces	Phan et al., 2015
Squirrel associated cyclovirus 1	LC018134	SqACyV-1	Japan	*Callosciurus erythraeus thaiwanensis* (Taiwan Squirrel)	Stomach contents	Sato et al., 2015

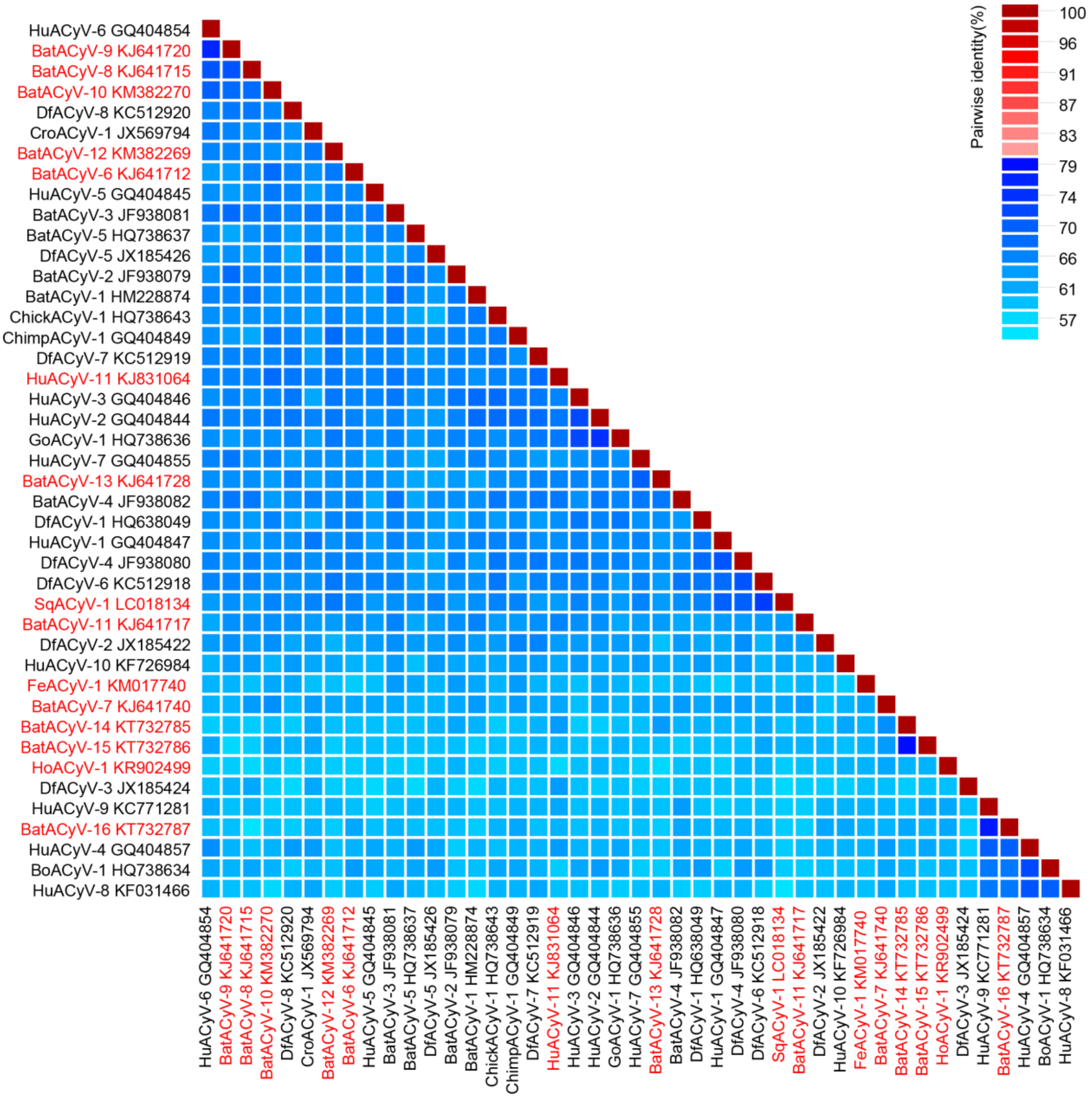

Figure 1: Genome-wide pairwise identities determined using SDT v1.2 (Muhire et al., 2014) with a 'two colour' profile highlighting that the 14 new taxa, which are highlighted in red, share < 80% identity with classified cyclovirus species. Note that all acronyms used in this figure represent new cyclovirus species names proposed here.

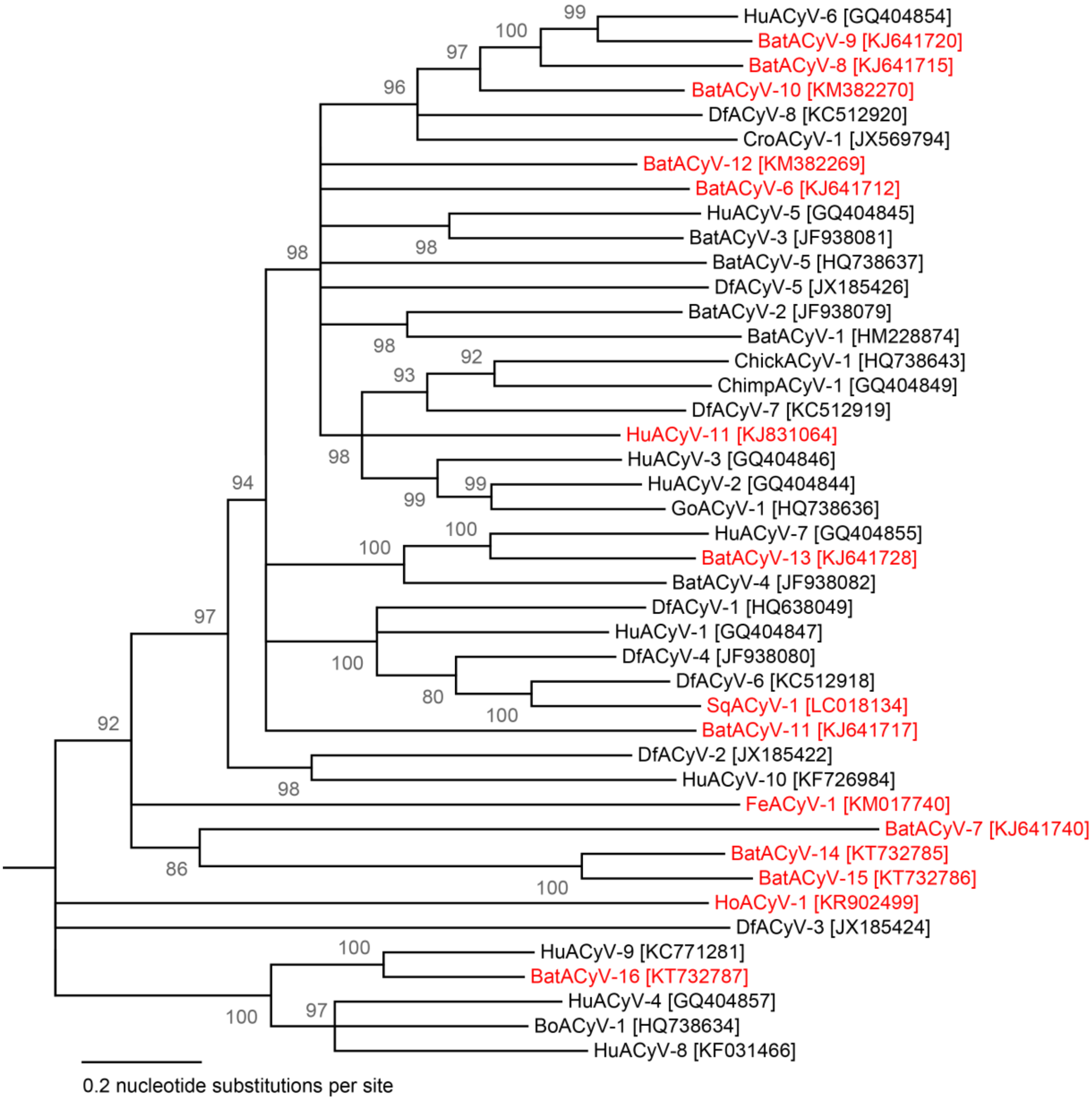

Figure 2: Maximum likelihood phylogenetic tree of representative cyclovirus species. The ML tree was constructed after aligning complete genome sequences and inferred using PHYML with GTR+G model of substitution (with SH-like branch support). Branches with <80% support have been collapsed. The phylogenetic tree was rooted after using circovirus reverse complemented genome sequences as an outgroup. New species are highlighted in red font. Note that all acronyms used in this figure represent new cyclovirus species names proposed here.

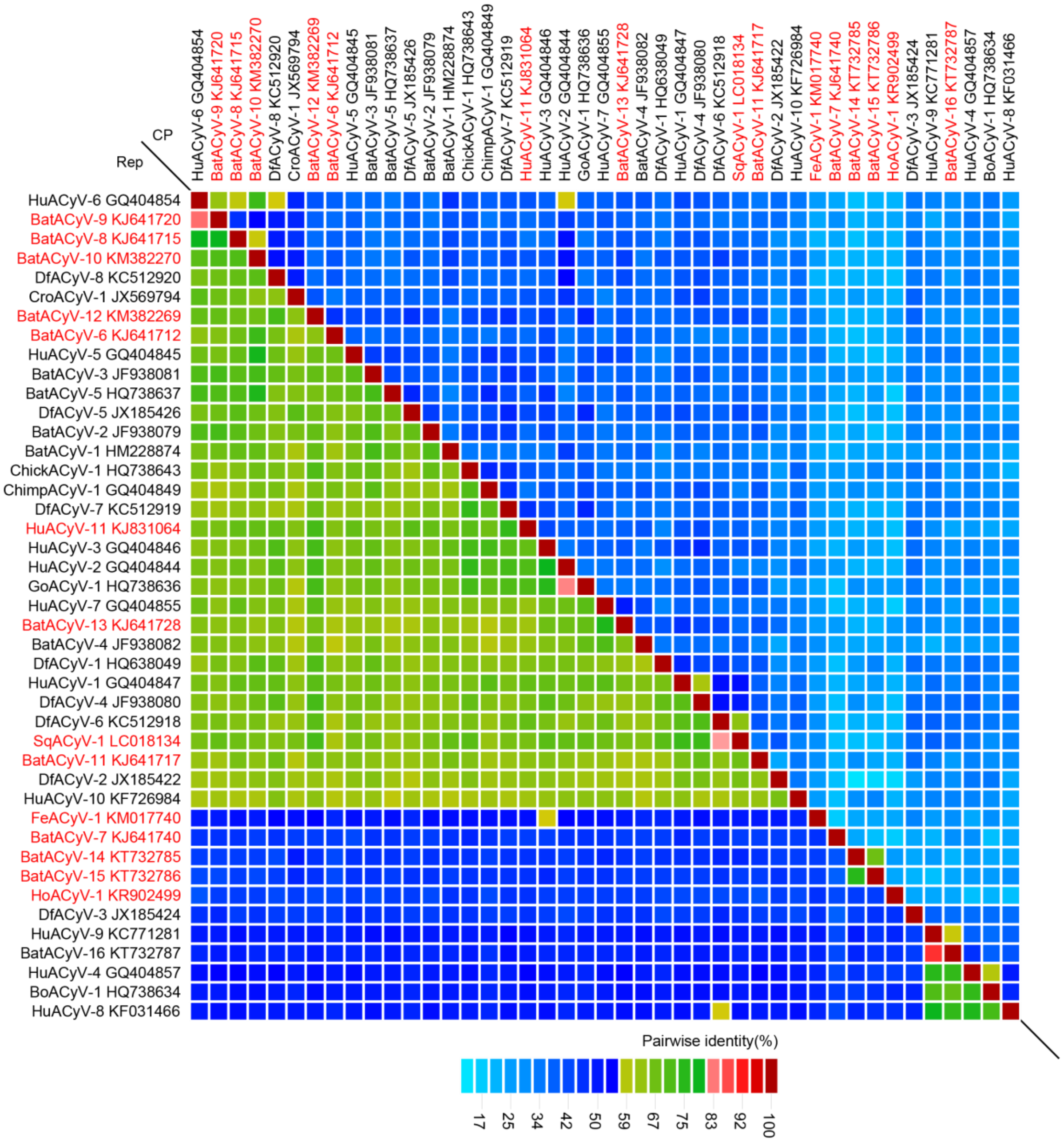

Figure 3: Two-by-two pairwise identity plot of the replication-associated (Rep) and capsid (CP) protein amino acid sequences constructed using SDT v1.2 (Muhire et al., 2014) with a 'three colour' profile. New species are highlighted in red font. Note that all acronyms used in this figure represent new cyclovirus species names proposed here.

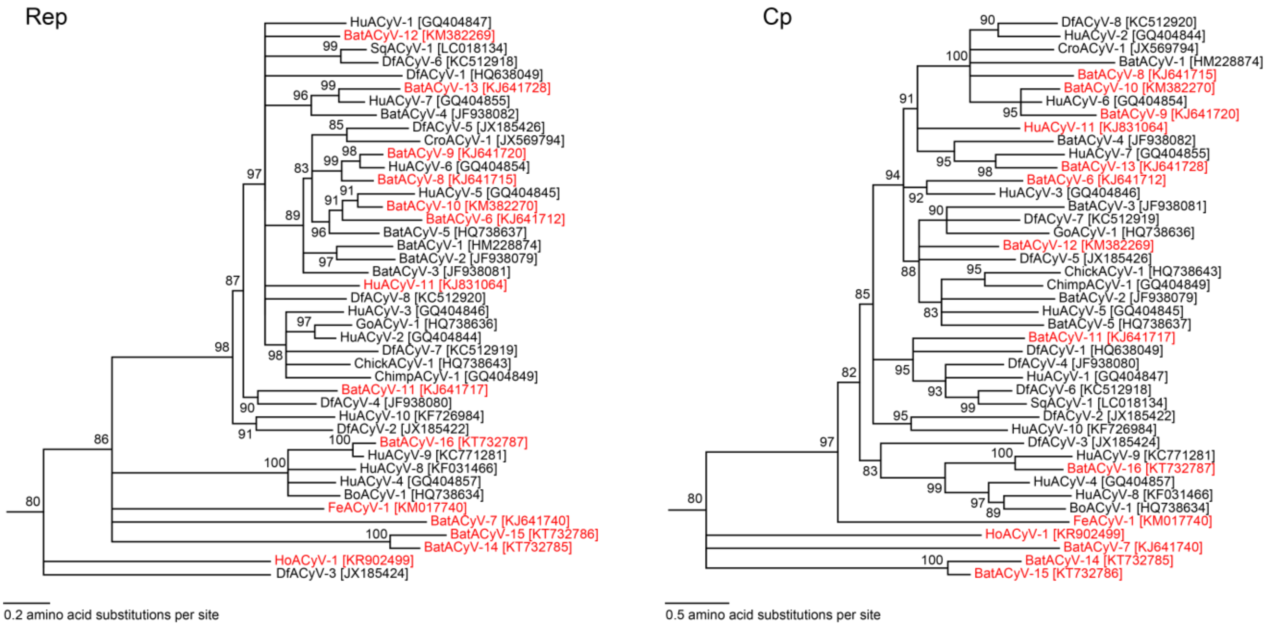

Figure 4: Maximum likelihood phylogenetic trees of representative cyclovirus replication-associated (Rep) and capsid (CP) protein amino acid sequences inferred with PHYML using LG model of substitution (with SH-like branch support). Branches with <80% support have been collapsed. Rep and CP phylogenetic trees were rooted using circovirus sequences. New species are highlighted in red font. Note that all acronyms used in this figure represent new cyclovirus species names proposed here.