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:	***2014.006a,hD***	(to be completed by ICTV officers)

Short title: Add 11 new species in the genus *Circovirus*
(e.g. 6 new species in the genus *Zetavirus*)

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

Author(s):

Mya Breitbart and Arvind Varsani on behalf of the *Circoviridae* SG

Corresponding author with e-mail address:

Mya Breitbart: mya@usf.edu

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:

EC46 decision on <2014.006a-gV.N.v2.Circoviridae>. Note that the version re-submitted for EC47 was divided into three separate proposals, <2014.006aD.U.v3.Circovirus_11sp>, <2014.006b-eD.U.v3.Cyclovirus> and <2014.006f,gD.N.v1.Gyrovirus_move>.

Decision: Ud. Need a phylogenetic tree that supports the 2 genera within one family – probably based on an aa alignment of the rep gene. Make clear the origin of the sequences; the EC doubts the need to classify as species sequences of unknown origin (particularly those from faeces) where there is no other information. A phylogenetic tree Is needed to support the movement of gyroviruses into *Anelloviridae*.

Date first submitted to ICTV: June 15, 2015
Date of this revision (if different to above): August 5, 2015

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	***2014.006aD***	(assigned by ICTV officers)

To create 11 new species within:

Genus:	***Circovirus***
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)**
Barbel circovirus	barbel circovirus	GU799606
Bat circovirus 1	bat circovirus 1 isolate XOR	JX863737
Bat circovirus 2	bat circovirus 2 isolate XOR7	KC339249
Bat circovirus 3	bat circovirus 3 (Rhinolophus ferrumequinum circovirus 1)	JQ814849
Canine circovirus	canine circovirus isolate UCD1-1698	KC241982
Chimpanzee faeces associated circovirus	chimpanzee faeces associated circovirus	GQ404851
Human faeces associated circovirus	human faeces associated circovirus	GQ404856
Mink circovirus	mink circovirus	KJ020099
Raven circovirus	raven circovirus	DQ146997
European catfish circovirus	European catfish circovirus isolate H5 (Silurus glanis circovirus)	JQ011377
Zebra finch circovirus	zebra finch circovirus	KP793918

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

- Explain how the proposed species differ(s) from all existing species.
  - If species demarcation criteria (see module 3) have previously been defined for the genus, **explain how the new species meet these criteria**.
  - If criteria for demarcating species need to be defined (because there will now be more than one species in the genus), please state the proposed criteria.
- Further material in support of this proposal may be presented in the Appendix, Module 9

The current criteria for species demarcation for circoviruses is 75% nt identity. However, we note that this was based on global alignment derived pairwise identities. These differ dramatically from pairwise identities derived from aligning each pair of genome sequences individually (see Muhire et al., 2013). We have hence reanalyzed all the full genomes of circoviruses available in public databases using SDT v1.2 (Muhire et al., 2014). Our analysis (Figure 1) shows that 80% pairwise identity species cut off is best suited for circoviruses and maintains the current classification of PCV-1 and PCV-2 as two species which share ~79% pairwise identity. Hence viruses with <80% pairwise identities coupled with phylogenetic support (Figures 2) should be considered as new species.

MODULE 8: **RENAME**

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

Renaming one or more taxa

Code	***2014.006hD***	(assigned by ICTV officers)

To rename the following taxon (or taxa):

Current name		**Proposed name**
Porcine circovirus-1		***Porcine circovirus 1***
Porcine circovirus-2		***Porcine circovirus 2***

Reasons to justify the renaming: Explain why the taxon (or taxa) should be renamed
To make species names similar and uniform across all members of the family *Circoviridae*.

MODULE 10: **APPENDIX**: supporting material

Table 1: Details of new viruses in the genus *Circovirus*

Virus	Acronym	Isolation source	Accession #	Reference
barbel circovirus	BarCV	*Barbus barbus*	GU799606	Lorincz et al., 2011
barbel circovirus	BarCV (isolate BaCV2)	*Barbus barbus*	JF279961	Lorincz et al., 2011
bat circovirus 1	BatCV-1	*Rhinolophus ferrumequinum*	JX863737	He et al., 2013
bat circovirus 2	BatCV-2	*Rhinolophus ferrumequinum*	KC339249	He et al., 2013
bat circovirus 3	BatCV-3	*Rhinolophus ferrumequinum*	JQ814849	Wu et al., 2012
canine circovirus	CanineCV (UCD1-1698)	*Canis lupus familiaris*	KC241982	Li et al., 2013
canine circovirus	CanineCV (UCD3-478)	*Canis lupus familiaris*	KC241983	Li et al., 2013
canine circovirus	CanineCV (UCD2-32162)	*Canis lupus familiaris*	KC241984	Li et al., 2013
chimpanzee faeces associated circovirus	ChfaCV	chimpanzee faeces	GQ404851	Li et al., 2010
human faeces associated circovirus	HufaCV	human faeces	GQ404856	Li et al., 2010
mink circovirus	MiCV	*Mustela* sp.	KJ020099	Lian et al., 2014
raven circovirus	RaCV	*Corvus coronoides*	DQ146997	Stewart et al., 2006
European catfish circovirus	EcatfishCV (H5)	*Silurus glanis*	JQ011377	Lorincz et al., 2012
European catfish circovirus	EcatfishCV (H6)	*Silurus glanis*	JQ011378	Lorincz et al., 2012
zebra finch circovirus	ZfiCV	*Taeniopygia guttata*	KP793918	Rinder et al., 2015

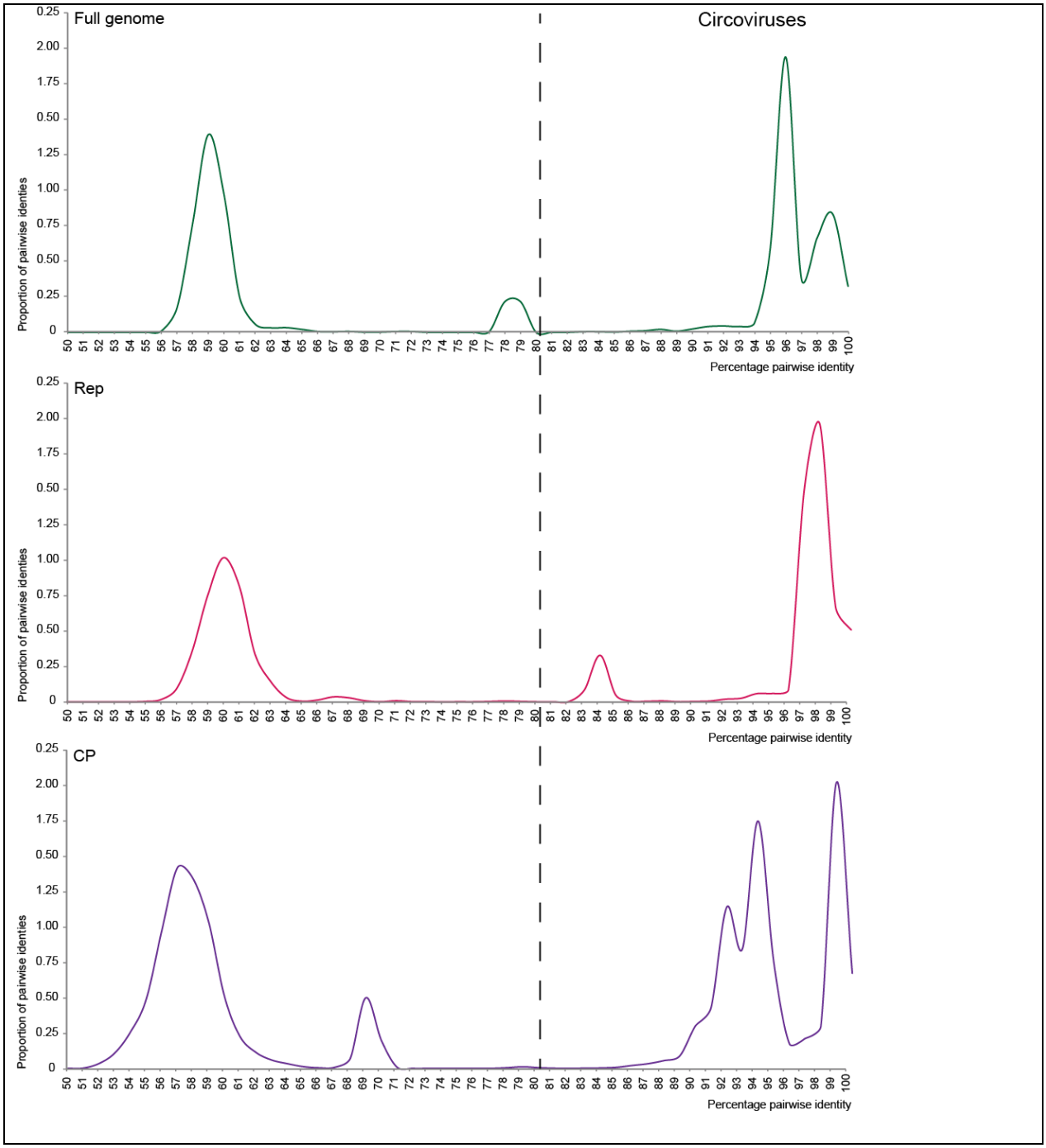

Figure 1: Distribution pairwise identity of circovirus genomes. The pairwise identities were calculated using SDT V1.2 (Muhire et al., 2014) with MUSCLE alignment algorithm (Edgar, 2004). Rep = replication associated protein gene; CP = capsid protein gene.

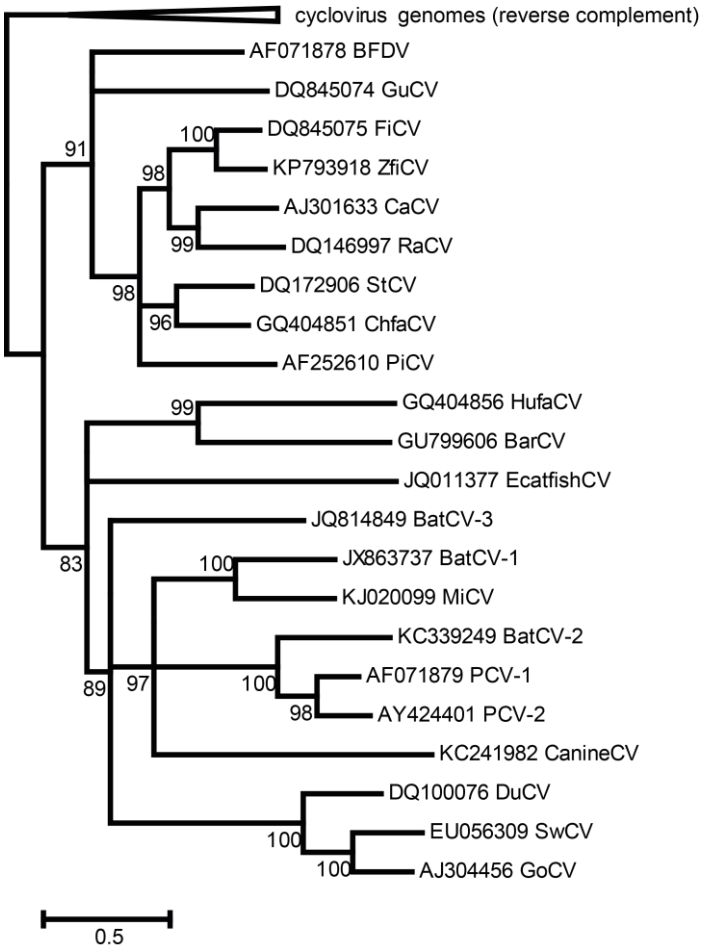

Figure 2: Maximum likelihood phylogenetic tree of the representative species full genome sequences inferred with PHYML using GTR model of substitution (with aLRT branch support). Branches with <80% support have been collapsed. Scale bar shows 0.5 nucleotide substitutions per site.

We have also double checked to make sure that variants within a species share >80% pairwise identity (Figure 3).

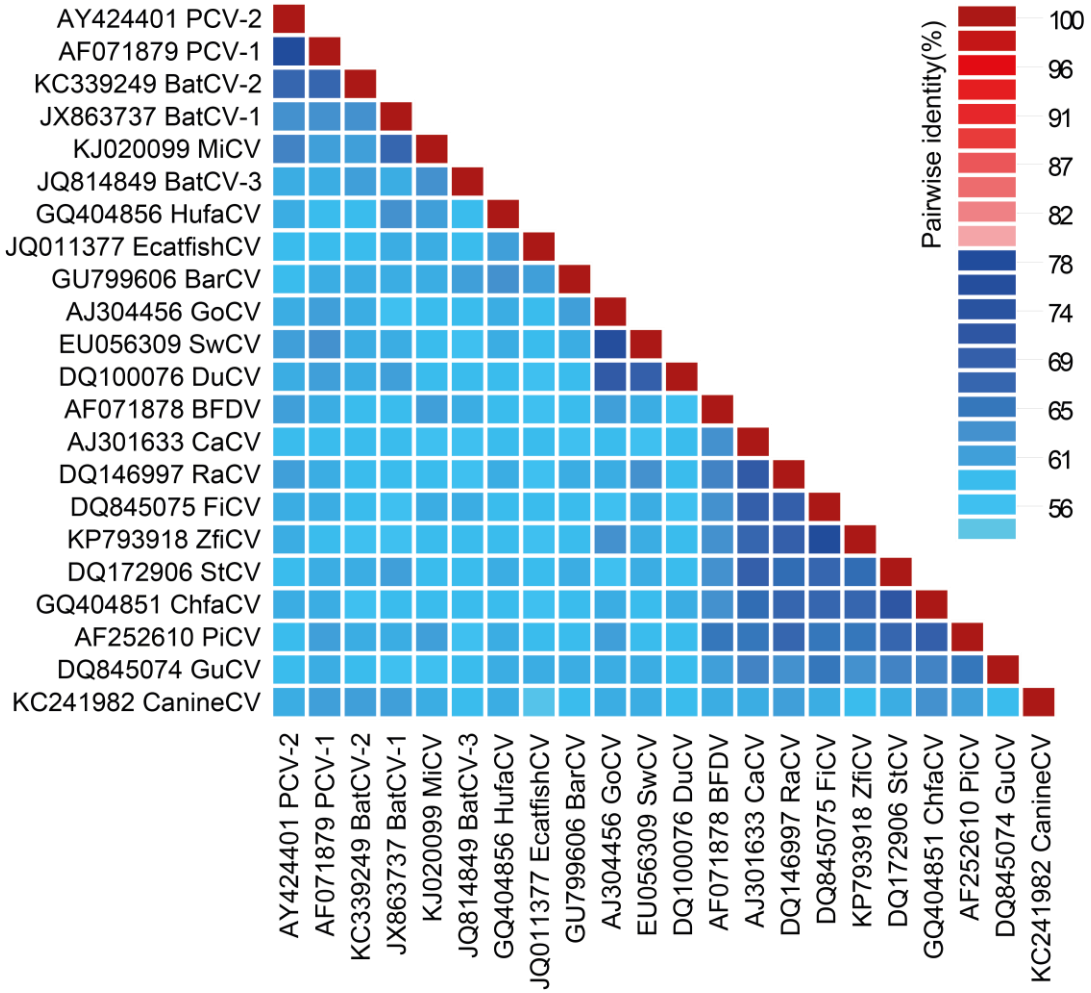

Figure 3: Genome-wide pairwise identities determined using SDT v1.2 (Muhire et al., 2014) with a 'two colour' profile highlighting that the 80% species demarcation threshold is valid.

We have also provided supporting analysis based on the replication associated protein (Figures 4 and 5) and the capsid protein sequences (Figures 6 and 7).

Figure 4: Maximum likelihood phylogenetic tree of the representative replication associated protein sequences inferred with PHYML using LG model of substitution (with aLRT branch support). Branches with <80% support have been collapsed. Scale bar shows 0.2 amino acid substitutions per site.

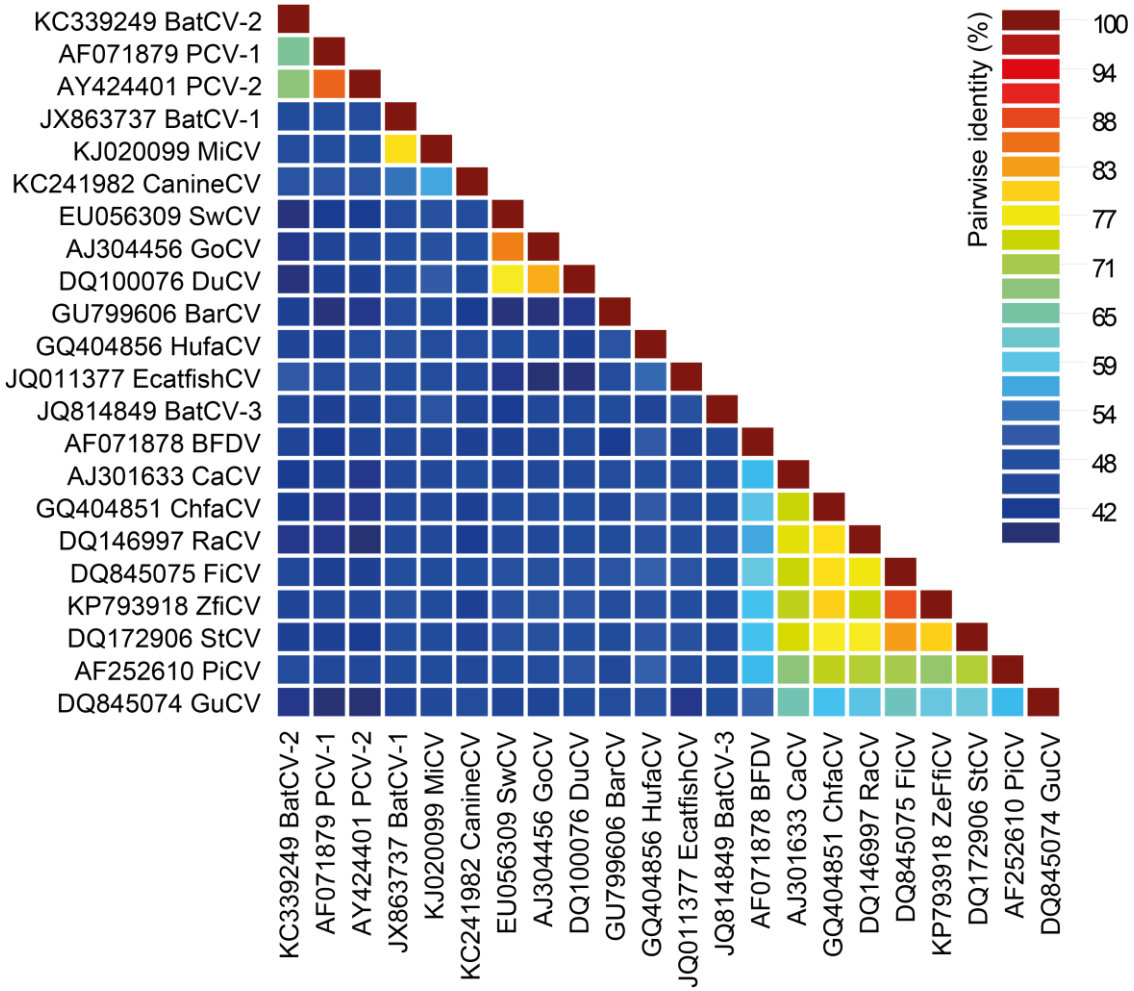

Figure 5: Replication associated protein sequence pairwise identities determined using SDT v1.2 (Muhire et al., 2014).

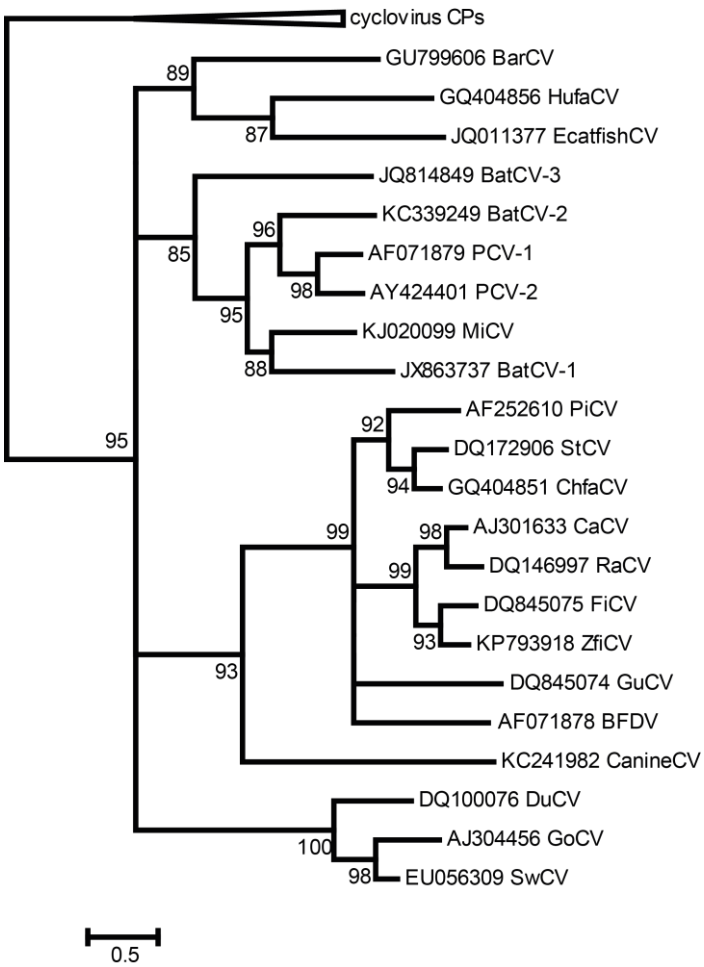

Figure 6: Maximum likelihood phylogenetic tree of the representative capsid protein sequences inferred with PHYML using LG model of substitution (with aLRT branch support). Branches with <80% support have been collapsed. Scale bar shows 0.5 amino acid substitutions per site.

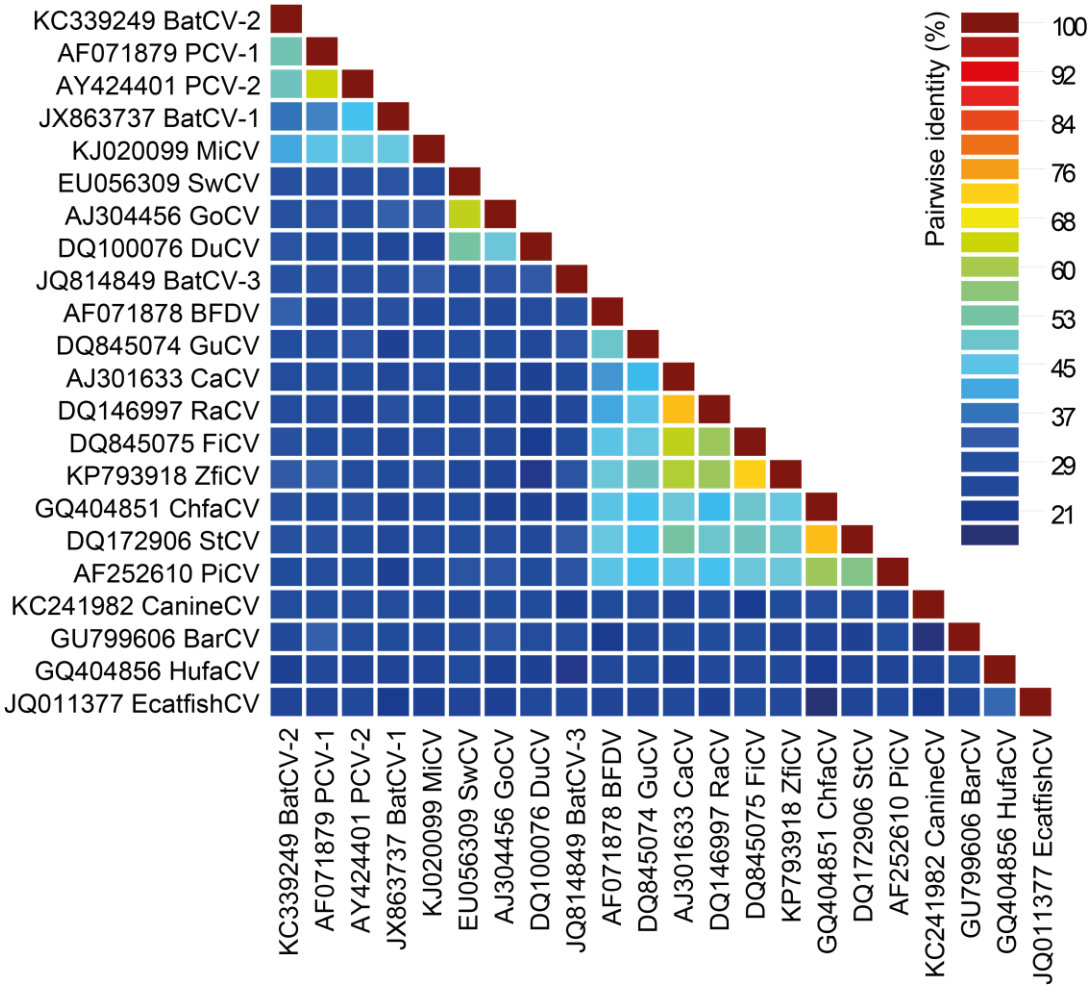

Figure 7: Capsid protein sequence pairwise identities determined using SDT v1.2 (Muhire et al., 2014) showing that in all cases the capsid protein sequences share <80% pairwise identity.

References

He, B., Li, Z., Yang, F., Zheng, J., Feng, Y., Guo, H., Li, Y., Wang, Y., Su, N., Zhang, F., Fan, Q. & Tu, C. (2013). Virome profiling of bats from Myanmar by metagenomic analysis of tissue samples reveals more novel mammalian viruses. PloS one 8, e61950.

Li, L., Kapoor, A., Slikas, B., Bamidele, O. S., Wang, C., Shaukat, S., Masroor, M. A., Wilson, M. L., Ndjango, J. B., Peeters, M., Gross-Camp, N. D., Muller, M. N., Hahn, B. H., Wolfe, N. D., Triki, H., Bartkus, J., Zaidi, S. Z. & Delwart, E. (2010). Multiple diverse circoviruses infect farm animals and are commonly found in human and chimpanzee feces. Journal of virology 84, 1674-1682.

Li, L., McGraw, S., Zhu, K., Leutenegger, C. M., Marks, S. L., Kubiski, S., Gaffney, P., Dela Cruz, F. N., Jr., Wang, C., Delwart, E. & Pesavento, P. A. (2013). Circovirus in tissues of dogs with vasculitis and hemorrhage. Emerging infectious diseases 19, 534-541.

Lian, H., Liu, Y., Li, N., Wang, Y., Zhang, S. & Hu, R. (2014). Novel circovirus from mink, China. Emerging infectious diseases 20, 1548-1550.

Lorincz, M., Csagola, A., Farkas, S. L., Szekely, C. & Tuboly, T. (2011). First detection and analysis of a fish circovirus. Journal of general virology 92, 1817-1821.

Lorincz, M., Dan, A., Lang, M., Csaba, G., Toth, A. G., Szekely, C., Csagola, A. & Tuboly, T. (2012). Novel circovirus in European catfish (*Silurus glanis*). Archives of virology 157, 1173-1176.

Muhire, B., Martin, D. P., Brown, J. K., Navas-Castillo, J., Moriones, E., Zerbini, F. M., Rivera-Bustamante, R., Malathi, V. G., Briddon, R. W. & Varsani, A. (2013). A genome-wide pairwise-identity-based proposal for the classification of viruses in the genus *Mastrevirus* (*Geminiviridae*). Archives of Virology. 158, 1411-1424.

Muhire, B.M., Varsani, A. & Martin, D.P. (2014) SDT: A virus classification tool based on pairwise sequence alignment and identity calculation. PLoS one, 9, e108277.

Rinder, M., Schmitz, A., Peschel, A. & Korbel, R. (2015). Complete genome sequence of a novel circovirus from zebra finch. Genome announcements 3, e 00560-15

Stewart, M. E., Perry, R. & Raidal, S. R. (2006). Identification of a novel circovirus in Australian ravens (*Corvus coronoides*) with feather disease. Avian pathology. 35, 86-92.

Wu, Z., Ren, X., Yang, L., Hu, Y., Yang, J., He, G., Zhang, J., Dong, J., Sun, L., Du, J., Liu, L., Xue, Y., Wang, J., Yang, F., Zhang, S. & Jin, Q. (2012). Virome analysis for identification of novel mammalian viruses in bat species from Chinese provinces. Journal of virology 86, 10999-11012.