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:	***2014.006f,gD***	(to be completed by ICTV officers)

Short title: Move genus *Gyrovirus* from the family *Circoviridae* to the family *Anelloviridae*
(e.g. 6 new species in the genus *Zetavirus*)

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

Author(s):

Mya Breitbart on behalf of the *Circoviridae* SG

Corresponding author with e-mail address:

Mya Breitbart on behalf of the *Circoviridae* SG; email: 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* SG, *Anelloviridae* SG

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

Date first submitted to ICTV:	June 15, 2015
Date of this revision (if different to above):	June 29, 2015

ICTV-EC comments and response of the proposer:

MODULE 7: **REMOVE and MOVE**

Use this module whenever an existing taxon needs to be removed:

- *Either* to abolish a taxon entirely (when only part (a) needs to be completed)
- *Or* to move a taxon and re-assign it e.g. when a species is moved from one genus to another (when BOTH parts (a) and (b) should be completed)

Part (a) taxon/taxa to be removed or moved

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

To remove the following taxon (or taxa) from their present position:

genus ***Gyrovirus*** and its constituent species

The present taxonomic position of these taxon/taxa:

Genus:	***Gyrovirus***	Fill in all that apply.
Subfamily:		
Family:	***Circoviridae***	
Order:		

If the taxon/taxa are to be abolished (i.e. not reassigned to another taxon) write “yes” in the box on the right	**NO**

Reasons to justify the removal:

Explain why the taxon (or taxa) should be removed

The genus *Gyrovirus* (species *Chicken anemia virus*, CAV) is currently classified in the family *Circoviridae*. However, CAV exhibits a very high sequence divergence when compared to circoviruses and, unlike other members of the family *Circoviridae*, gyroviruses have features in common with anelloviruses (family *Anelloviridae*). According to the current virus taxonomy release (Report 9): “Analysis of the genome structure, the origin of replication and the Rep proteins of viruses of the genus *Circovirus* show similarity to members of the plant virus family *Nanoviridae* and less pronounced similarity to members of the plant virus family *Geminiviridae*. CAV has features in common with viruses such as Torque Teno virus (TTV) and Torque Teno mini virus (TTMV), which are members of the genus *Anellovirus*.” This misplacement of the genus *Gyrovirus* in the *Circoviridae* is exemplified by the fact that the CAV genome does not contain a recognizable replication protein that can be aligned with members of the *Circovirus* genus to produce a reliable phylogeny. As early as 2009, Hino and Prasetyo proposed moving the genus *Gyrovirus* into the *Anelloviridae*, and as more genomes of both circoviruses and anelloviruses are sequenced, the rationale for moving the *Gyrovirus* genus still holds firm. It is not logical to keep CAV within the *Circoviridae*.

Part (b) re-assign to a higher taxon

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

To re-assign the taxon (or taxa) listed in Part (a) as follows:

Genus:	***Gyrovirus***
Subfamily:	
Family:	***Anelloviridae***
Order:	

Fill in all that apply.

- If the higher taxon has yet to be created write "**(new)**" after its proposed name and complete relevant module to create it.

If no genus is specified, enter "**unassigned**" in the genus box.

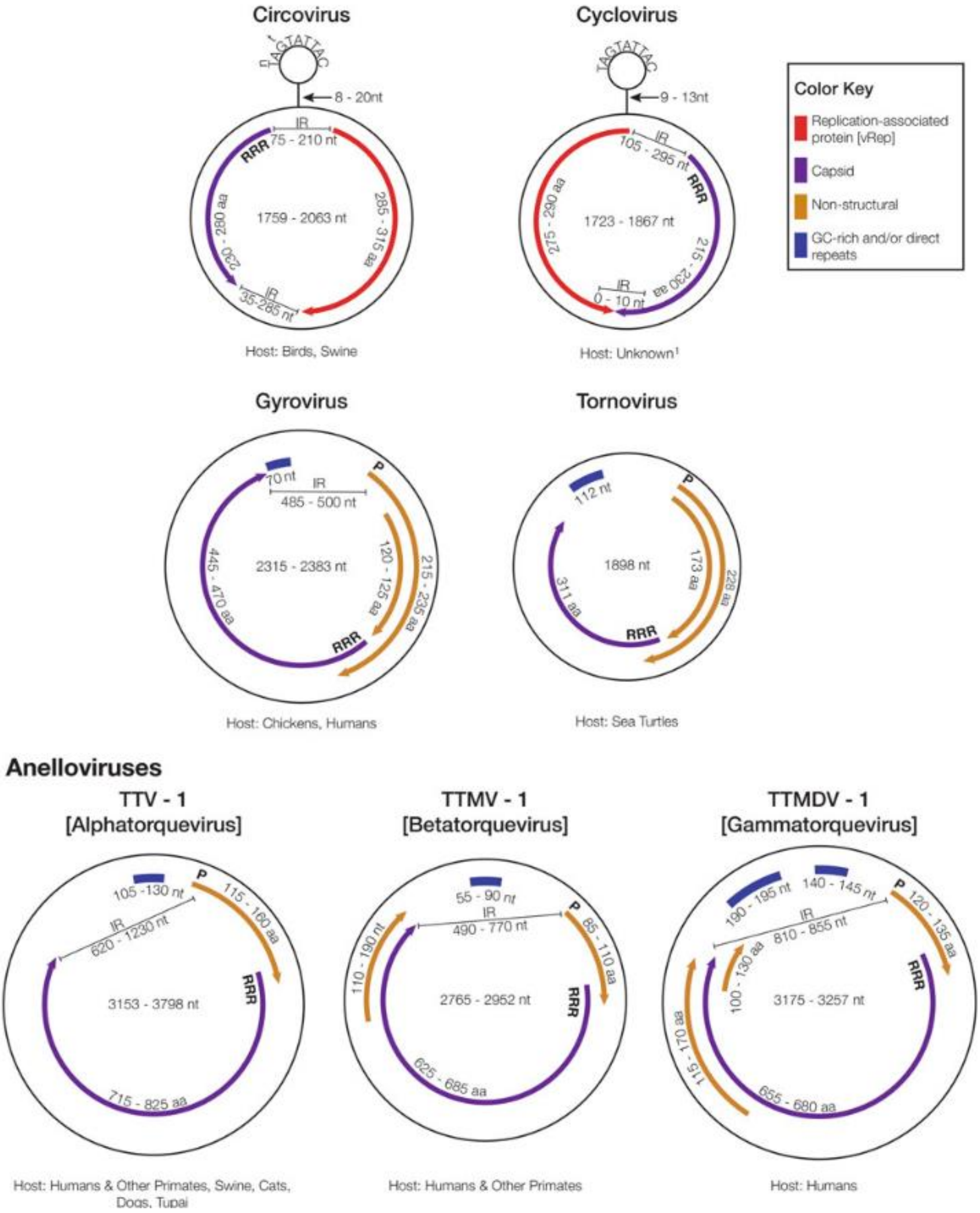
Reasons to justify the re-assignment:

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

Similar to anelloviruses, gyroviruses possess circular ssDNA genomes with a negative-sense genome organization. The non-coding regions of CAV and most of the anellovirus genomes are G+C-rich. The CP of CAV and the putative CPs of anelloviruses possess amino acid sequence motifs that are typical of RCR Rep proteins. Proteins encoded by the ORF2s of CAV and some anelloviruses contain amino acid sequences that are characteristic of protein tyrosine phosphatases (PTPases). ORF2s of CAV and anelloviruses have a common motif WX7HX3CXCX5H. Spliced transcripts have been detected for CAV and some anelloviruses, along with peptides able to induce apoptosis in human hepatocellular carcinoma cell lines.

MODULE 10: **APPENDIX**: supporting material

The figure below is taken from Rosario et al. (2012) and shows genome schematics for animal circular ssDNA viruses.



Each circle summarizes the size range of the genome, open reading frames (ORFs; shown with arrows), and intergenic regions (IR) for the different genera. The color legend indicates the different proteins encoded by each ORF. The stem-loop and nonanucleotide motif sequence are also shown when applicable. If more than one nucleotide is present for a given position of the nonamer, the most common nucleotide is indicated with a capital letter, and the other with lowercase (‘N’ represents any nucleotide and is used when more than two nucleotides were observed at a given position). Genomic features were extracted from genomes found in the literature. For anelloviruses, only the three genera containing the most members were included. In addition, only the major ORFs common to the majority of analyzed genomes are illustrated. ORF and IR sizes for groups with more than one member were approximated to the nearest multiple of five. ‘RRR’ on top of an arrow indicates the presence of a N-terminal region rich in basic amino acids, while ‘P’ refers to the presence of a phosphatase motif conserved in gyroviruses and anelloviruses (i.e., WX7HX3CXCX5H, where ‘X’ represents any residue). Note that the putative capsid of cycloviruses, anelloviruses, and tornovirus has not been confirmed. Known hosts for each viral genus are shown below the genome schematics. Members of the proposed genus ‘‘Cyclovirus’’ have been discovered through metagenomic analysis in various organisms, and a definitive host range has not been confirmed.

Based on these genome schematics showing conserved features (such as ORF directionality), the lack of a viral replication-associated protein (Rep), and the lack of a stem-loop with conserved nonanucleotide motif for rolling circle replication, it is clear that the genus *Gyrovirus* belongs in the family *Anelloviridae*.

References:

Hino, S, AA Prasetyo (2009). Relationship of Torque teno virus to chicken anemia virus. Current Topics in Microbiology and Immunology. 331. 117-130.

Rosario, K, S Duffy, M Breitbart (2012). A field guide to eukaryotic circular single-stranded DNA viruses: Insights gained from metagenomics. Archives of Virology. 157: 1851-1871.