MODULE 1: **1 new species (Swan circovirus) in the genus *Circovirus*. Ph. Biagini, Chair.**

Code assigned:	***2009.006a,bV***				
Short title: create new species in the genus Circovirus, family Circoviridae					
Modules attached	**1** ☒	**2** ☒	**3** ☐	**4** ☐	**5** ☐
	6 ☐	**7** ☐	**8** ☐	**9** ☒	

Author(s) with e-mail address(es) of the proposer:

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Has this proposal has been seen and agreed by the relevant study group(s)? Please select answer in the box on the right — **YES**

ICTV-EC or Study Group comments and response of the proposer:

Date first submitted to ICTV: **11 May 2009**
Date of this revision (if different to above):

MODULE 2: **NEW SPECIES**

Part (a) to create and name one or more new species.
If more than one, they should be a group of related species belonging to the same genus (see Part b)

Code	*2009.006aV*	(assigned by ICTV officers)

To create 1 new species with the name :

Swan circovirus

Part (b) assigning new species to higher taxa
All new species must be assigned to a higher taxon. This is usually a genus although it is also permissible for species to be "unassigned" within a subfamily or family.

Code	*2009.006bV*	(assigned by ICTV officers)

To assign the species listed in section 2(a) as follows:

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.

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

Species demarcation criteria:

The suggested criteria demarcating species in the genus are (i) complete genome nucleotide sequence identity less than 75%, and (ii) capsid protein amino acid sequence identity less than 70%.

Argumentation to justify the designation of the new species in the genus:

Swan circovirus (SwCV) was characterized by Halami et al (2008) from a mute swan (*Cygnus olor*), and the genome sequence determined (GenBank accession number EU056309).
The sequence demonstrates that SwCV is related to existing members of the genus *Circovirus*, with whole genome alignment showing identities to ten circoviruses in the range 42 to 73%, and capsid protein identities in the range 21 to 65%.
According to this data, SwCV fits both criteria of demarcation of a new species in the genus *Circovirus*.

Relationships in the genus are summarized by the phylogenetic tree in annex 1 (Module 9).

additional material in support of this proposal

References:

Halami, M.Y., Nieper, H., Müller, H. & Johne, R. (2008). Detection of a novel circovirus in mute swans (*Cygnus olor*) by using nested broad-spectrum PCR. *Virus Res* **132**, 208-12.

Todd, D., Bendinelli, M., Biagini, P., Hino, S., Mankertz, A., Mishiro, S., Niel, C., Okamoto, H., Raidal, S., Ritchie, B.W & Teo, G.C. (2005). *Circoviridae*. In: *Virus Taxonomy*, VIIIth Report of the International Committee for the Taxonomy of Viruses (C.M. Fauquet, M.A. Mayo, J. Maniloff, U. Desselberger, and L.A. Ball, eds), 327-334. Elsevier/Academic Press, London.

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.

Annex 1: Neighbour-joining phylogenetic tree built with CP amino acid sequences (*Beak and feather disease virus* **BFDV,** *Canary circovirus* **CaCV,** *Duck circovirus* **DuCV,** *Finch circovirus* **FiCV,** *Goose circovirus* **GoCV,** *Gull circovirus* **GuCV,** *Pigeon circovirus* **PiCV,** *Porcine circovirus-1* **PCV-1,** *Porcine circovirus-2* **PCV-2,** *Starling circovirus* **StCV,** *Swan circovirus* **SwCV).**