Template for Taxonomic Proposal to the ICTV Executive Committee
Creating Species in an existing genus

Code †2007.081V.04 To designate the following as species in the genus:

**Circovirus**

belonging to the family°:

**Circoviridae**

† Assigned by ICTV officers
° leave blank if inappropriate or in the case of an unassigned genus

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Old Taxonomic Order
Order
Family
Genus
Type Species
Species in the Genus

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<th>Genus</th>
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Tentative Species in the Genus
Unassigned Species in the family

New Taxonomic Order
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ICTV-EC comments and response of the SG
Species demarcation criteria in the genus

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 new species in the genus

Finch circovirus (FiCV) was characterized by Todd et al (2007) from a Gouldian finch (Chloebia gouldiae), following a previous report of the virus, and the genome sequence determined. The sequence demonstrates that FiCV is related to existing members of the genus Circovirus, with whole genome alignment showing identities to eight circoviruses in the range ***n to n%***, and capsid protein identities in the range 21 to 63%.

Gull circovirus (GuCV) was characterized by Todd et al (2007) from a herring gull (Larus argentatus), following previous reports of the virus, and the genome sequence determined. The sequence demonstrates that GuCV is related to existing members of the genus Circovirus, with whole genome alignment showing identities to eight circoviruses in the range ***n to n%***, and capsid protein identities in the range 17 to 41%.

Starling circovirus (StCV) was detected and characterized by Johne et al (2006) in European starlings (Sturnus vulgaris) and spotless starlings (Sturnus unicolor), and genome sequences determined. The sequence demonstrates that StCV is related to existing members of the genus Circovirus, with whole genome alignment showing identities to eight circoviruses in the range 15 to 67%, and capsid protein identities in the range 22 to 52%.

Relationships in the genus are summarized by the tree in annex 1.

List of created Species in the genus

Finch circovirus
Gull circovirus
Starling circovirus

References


Annexes:

**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).*