

**Part 1:** **TITLE, AUTHORS, APPROVALS, etc**

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| **Code assigned:** | ***2023.003D*** |  |
| **Short title:** Two new species in the genus *Circovirus* (*Cirlivirales*: *Circoviridae*) |
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**Author(s) and email address(es)**

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**List the ICTV Study Group(s) that have seen this proposal**

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| Circoviridae Study Group |

**ICTV Study Group comments and response of proposer**

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**ICTV Study Group votes on proposal**

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| **Study Group** | **Number of members** |
| **Votes support** | **Votes against** | **No vote** |
| Circoviridae SG | 8 |  | 2 |
|  |  |  |  |

**Authority to use the name of a living person**

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| --- | --- |
| **Is any taxon name used here derived from that of a living person (Y/N)** | N |

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| **Taxon name** | **Person from whom the name is derived** | **Permission attached (Y/N)** |
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**Submission dates**

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| Date first submitted to SC Chair | 21 May 2023 |
| Date of this revision (if different to above) |  |

**ICTV-EC comments and response of the proposer**

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**Part 2:** **NON-TAXONOMIC PROPOSAL**

**Text of proposal**

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**Part 3:** **TAXONOMIC PROPOSAL**

**Name of accompanying Excel module**

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| 2023.003D.A.v2.Circoviridae\_2nsp.xlsx |

**Abstract**

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| Two novel circoviruses have been detected in organ samples (kidney, liver, bursa of Fabricius) of a little bittern (*Ixobrychus minutus*) and a European bee-eater (*Merops apiaster*) in Hungary. The genome length is 1935 nt and 1960 nt for the little bittern circovirus (TorCV) and European bee-eater circovirus (GyurCV), respectively (Fehér et al., 2022). The genomic structure of both viruses (GenBank accession numbers MZ710934 and MZ710935) corresponds to that of other circoviruses (Figure 1). Phylogenetic analysis and pairwise identity comparisons suggest that the two novel viruses belong to two distinct species of the *Circovirus* genus, *Circoviridae* family (Fehér et al., 2022), that were tentatively named *Circovirus torpegem* and *Circovirus gyurgyalag.* |

**Text of proposal**

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| The genome of the TorCV and GyurCV contain putative ORFs of the replication-associated protein (Rep) in the viral DNA strand and the capsid protein in the replicative complementary DNA strand. The nonanucleotide motif (TAGTATTAC) locates upstream of the *rep* in the 5’ intergenic region (Figure 1) (Fehér et al., 2022). Phylogenetic analysis of complete circovirus genome sequences (Figure 2) suggests that the TorCV and GyurCV represent two novel species within the *Circovirus* genus, *Circoviridae* family. The genome of the novel viruses show <41.5% genome-wide nt identitiy with that of other circoviruses (Figure 3) (Fehér et al., 2022). Genome-wide sequence pairwise identity <80% meets the criterion set by the ICTV for species demarcation of circoviruses, thus the TorCV and GyurCV are proposed as members of two novel species named *Circovirus torpegem* and *Circovirus gyurgyalag*, respectively. |

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**Supporting evidence**



**Figure 1.** Schematic representation of the genomic structure of the little bittern circovirus (TorCV) and European bee-eater (GyurCV) circovirus. The TAGTATTAC nonanucleotide motif and the flanking inverted repeats are labelled as stem-loops (Fehér et al., 2022).



**Figure 2.** Maximum likelihood phylogenetic tree of complete circovirus genome sequences. The tree was generated with the PhyML software, GTR+G+I model and aLRT SH-like branch support (values lower than 80 are hidden). Reverse complement sequence of the duck associated cyclovirus 1 (GenBank accession no. KY851116) was used as root of the tree. The scale bar shows substitutions per site. The little bittern circovirus (TorCV) and European bee-eater circovirus (GyurCV) are highlighted with black triangles (Fehér et al., 2022).

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**Figure 3.** Pairwise identity matrix of complete circovirus genome sequences using SDT v1.2 software. The little bittern circovirus (TorCV) and European bee-eater circovirus (GyurCV) are highlighted with red font (Fehér et al., 2022).

**References**

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