

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

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| **Code assigned:** | ***2023.002D*** |  |
| **Short title:** Establishing 3 new species in the family *Circoviridae* | | |
|  | | |

**Author(s) and email address(es)**

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**Corresponding author**

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| Arvind Varsani |

**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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| All who responded in agreement is an author on this TP |

**ICTV Study Group votes on proposal**

|  |  |  |  |
| --- | --- | --- | --- |
| **Study Group** | **Number of members** | | |
| **Votes support** | **Votes against** | **No vote** |
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**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 |

|  |  |  |
| --- | --- | --- |
| **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 | 16 June 2023 |
| Date of this revision (if different to above) | 28 July 2023 |

**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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| 2023.002D.N.v2.Circoviridae\_3nsp.xlsx |

**Abstract**

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| Circoviruses have small circular single-stranded DNA genomes. They are classified within two genera, *Circovirus* and *Cyclovirus*, in the family *Circoviridae* (phylum *Cressdnaviricota*, class *Arfiviricetes*, order *Circlivirales*). The classification of species is based on the guidelines set forward, i.e., 80% genome-wide pairwise identity species threshold and based on this we propose 3 new species to classify 3 new viruses in the genus *Circovirus*. |

**Text of proposal**

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| |  | | --- | | *Circovirus* and *Cyclovirus* are the two genera in the family *Circoviridae* (phylum *Cressdnaviricota,* class *Arfiviricetes* order *Circlivirales*). Viruses within these two genera are classified into species based on genome-wide pairwise identities, with a species demarcation threshold of 80% identity [1].  Over the last the last year various new circovirus genomes have been identified from various organisms and represent 5 new species. Two of these are described in a separate TP and here we address the classification of 3 circoviruses identified in human (n=1) and coyote (n=2) samples.  The proposed classification of the three viruses that represent new species is supported by phylogenetic analysis of the genome nucleotide sequences and pairwise nucleotide sequence identity analysis of the (Figure 1-2). | |

**Supporting evidence**

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| **Accession** | **Virus name** | **Host /source** | **Country** | **New species name** | **Epithet notes** |
| OQ599922 | banfec circovirus 1 | *Canis latrans* | USA | *Circovirus kukwuria* | Coyote, Scavenger in comanche |
| OQ599924 | banfec circovirus 2 | *Canis latrans* | USA | *Circovirus ban* | Coyote in Tohono O’odham |
| ON677309 | human circovirus 1 | *Homo sapiens* | France | *Circovirus human* | Virus identified in human tissue |

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Description automatically generated**

**Figure 1:** Maximum likelihood phylogenetic tree (rooted with reverse complement sequences of cycloviruses) of representative genomes from each circovirus species (aligned with MAFFT v7 [3]) inferred using PHYML [4] with GTR+I+G4 chosen as the best fit model.

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**Figure 2:** A ‘two color’ pairwise identity matrix of representative genome-wide comparisons among sequences in the genus *Circovirus* inferred using SDT v1.2 [2]. Representative sequences from the proposed new species (n=3) are highlighted in blue font and the two in purple font represent two additional species and are addressed in a separate proposal.

**References**

1. Rosario K, Breitbart M, Harrach B, Segales J, Delwart E, Biagini P, Varsani A (2017) Revisiting the taxonomy of the family *Circoviridae*: establishment of the genus *Cyclovirus* and removal of the genus *Gyrovirus*. Arch Virol 162:1447-1463. PMID: 28155197; DOI: 10.1007/s00705-017-3247-y
2. Muhire BM, Varsani A, Martin DP (2014) SDT: a virus classification tool based on pairwise sequence alignment and identity calculation. PLoS One 9:e108277. PMID: 25259891; DOI: 10.1371/journal.pone.0108277
3. Katoh K, Rozewicki J, Yamada KD (2019) MAFFT online service: multiple sequence alignment, interactive sequence choice and visualization. Brief Bioinform 20:1160-1166. PMID: 28968734; DOI: 10.1093/bib/bbx108
4. Guindon S, Dufayard JF, Lefort V, Anisimova M, Hordijk W, Gascuel O (2010) New algorithms and methods to estimate maximum-likelihood phylogenies: assessing the performance of PhyML 3.0. Syst Biol 59:307-321. PMID: 20525638; DOI: 10.1093/sysbio/syq010