

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

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| **Code assigned:** | **2020.009D** |  |
| **Short title:** Create one new species in the genus *Circovirus* (*Cirlivirales*: *Circoviridae*) | | |
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**Author(s) and email address(es)**

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| Lung O |

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

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| *Circoviridae* SG |

**ICTV study group comments and response of proposer**

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

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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 | October 24, 2019 |
| Date of this revision (if different to above) | November 24, 2020 |

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

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

**Name of accompanying Excel module**

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| 2020.009D.R.v1.Circovirus\_1nsp.xlsx |

**Abstract**

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| Here we propose the addition of a new species to genus *Circovirus,* family *Circoviridae*, which we have tentatively named *Elk circovirus*. The 1,787 nucleotide complete circular genome was sequenced from the tissue of a Rocky Mountain elk (*Cervus canadensis nelsoni*), assembled and compared to other publicly available sequences. It was determined that the closest match was a PCV1 sequence (CT-PCV-P7 accession AY099501.1) with a pairwise genome-wide nucleotide identity of 65.7%. The annotated complete elk circovirus genome has been uploaded to NCBI with accession number MN585201. To the best of our knowledge, this is the first circovirus reported in a cervid host. |

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| --- | --- |
| **Text of proposal**   |  | | --- | | The complete 1,787 nucleotide elk circovirus genome sequence described here (Table 1) showed the highest degree of nucleotide identity to sequences representing porcine circovirus 1 (AY099501), porcine circovirus 2 (MK424116), bat-associated circovirus 2 (KC339249) and bat-associated circovirus 11 (KX756996). These showed, respectively, only 65.7%, 64.7%, 61.9% and 64.3% genome-wide pairwise nucleotide identity to the elk circovirus sequence (Table 2). When queried against the NCBI nr/nt database no other significant matches with higher percent identity were observed. Viruses within the genus *Circovirus* are classified into distinct species using a threshold of 80% genome-wide nucleotide identity [1]. Based on the nucleotide identity values and phylogenetic support presented here (Figure 1), this novel virus should be classified as member of a new species within the genus *Circovirus*. | |

**Supporting evidence [8]**

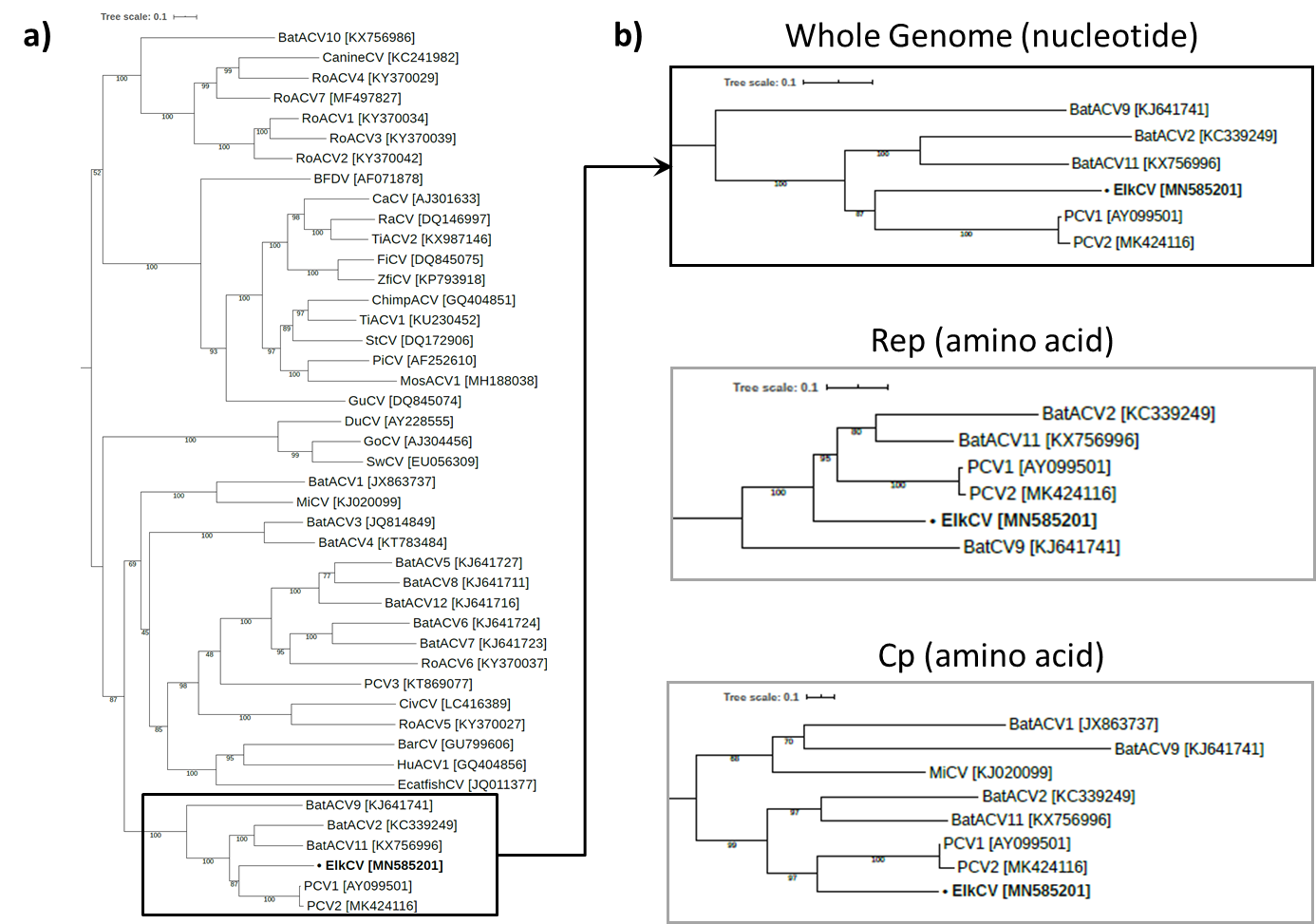
**Table 1.** Summary of details regarding the proposed novel species belonging to the genus *Circovirus*

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| --- | --- | --- | --- | --- | --- |
| **Virus name**  **(species name)** | **GenBank accession** | **Virus acronym** | **Isolate ID** | **Country of isolation** | **Host/isolation source** |
| elk circovirus  (*Elk circovirus*) | MN585201 | ElkCV | Banff/2019 | Canada | *Cervus canadensis nelsoni* |

**Table 2.** Comparison of the elk circovirus Banff/2019 genome to genomes of the most closely related circovirus genomes currently known

|  |  |  |  |  |  |  |  |
| --- | --- | --- | --- | --- | --- | --- | --- |
| **Species [Accession]** | **Percent Identity** | | | | | | |
| **WG** |  | **Rep** | |  | **Cp** | |
| **nt** |  | **nt** | **aa** |  | **nt** | **aa** |
| ElkCV [MN585201] | - |  | - | - |  | - | - |
| BatACV2 [KC339249] | 61.9 |  | 69.6 | 68.7 |  | 52.7 | 47.1 |
| BatACV11 [KX756996] | 64.3 |  | 72.4 | 74.2 |  | 54.6 | 52.7 |
| PCV1 [AY099501] | 65.7 |  | 71.5 | 72.9 |  | 58.2 | 59.2 |
| PCV2 [MK424116] | 64.7 |  | 70.9 | 73.2 |  | 55.6 | 58.3 |

Percent identity is shown between elk circovirus genome and the genomes of closely related circoviruses based on EMBOSS Needle [2] pairwise nucleotide alignments for the whole genome (WG) as well as nucleotide (nt) and amino acid (aa) alignments of the Rep and Cp genes.



**Figure 1.** Maximum likelihood phylogenetic trees of representative sequences within the genus *Circovirus*. Sequences were aligned using MAFFT [3], trees generated using IQ-Tree [4] on find best model setting with ModelFinder [5] with 1,000 ultrafast bootstraps [6] and visualized with iTOL [7]. In all trees ElkCV is indicated in bold text and with “•” before the sequence name. (a) Full mid-point rooted phylogenetic tree generated from representative circovirus complete genome nucleotide sequences (model TIM+F+R5). (b) Pruned trees showing only ElkCV and sequences on closely related branches from complete genome nucleotide sequences (top black box), Rep protein amino acid sequences (middle gray box, model LG+I+G4) and Cp protein amino acid sequences (bottom gray box, model PMB+R3).

**References**

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