

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

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| **Code assigned:** | **2020.010D** |  |
| **Short title:** Create six new species in the genus *Circovirus* and one new species in the genus *Cyclovirus* (*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* 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 | July 10, 2020 |
| 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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| 2020.010D.R.Circoviridae\_7nsp.xlsx |

**Abstract**

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| We provide support for the classification of 10 new viruses in the family *Circoviridae* into 6 species within the genus *Circovirus* and one in the genus *Cyclovirus*. The classification is based on the guidelines set forward ie., 80% genome-wide pairwise identity species threshold. |

**Text of proposal**

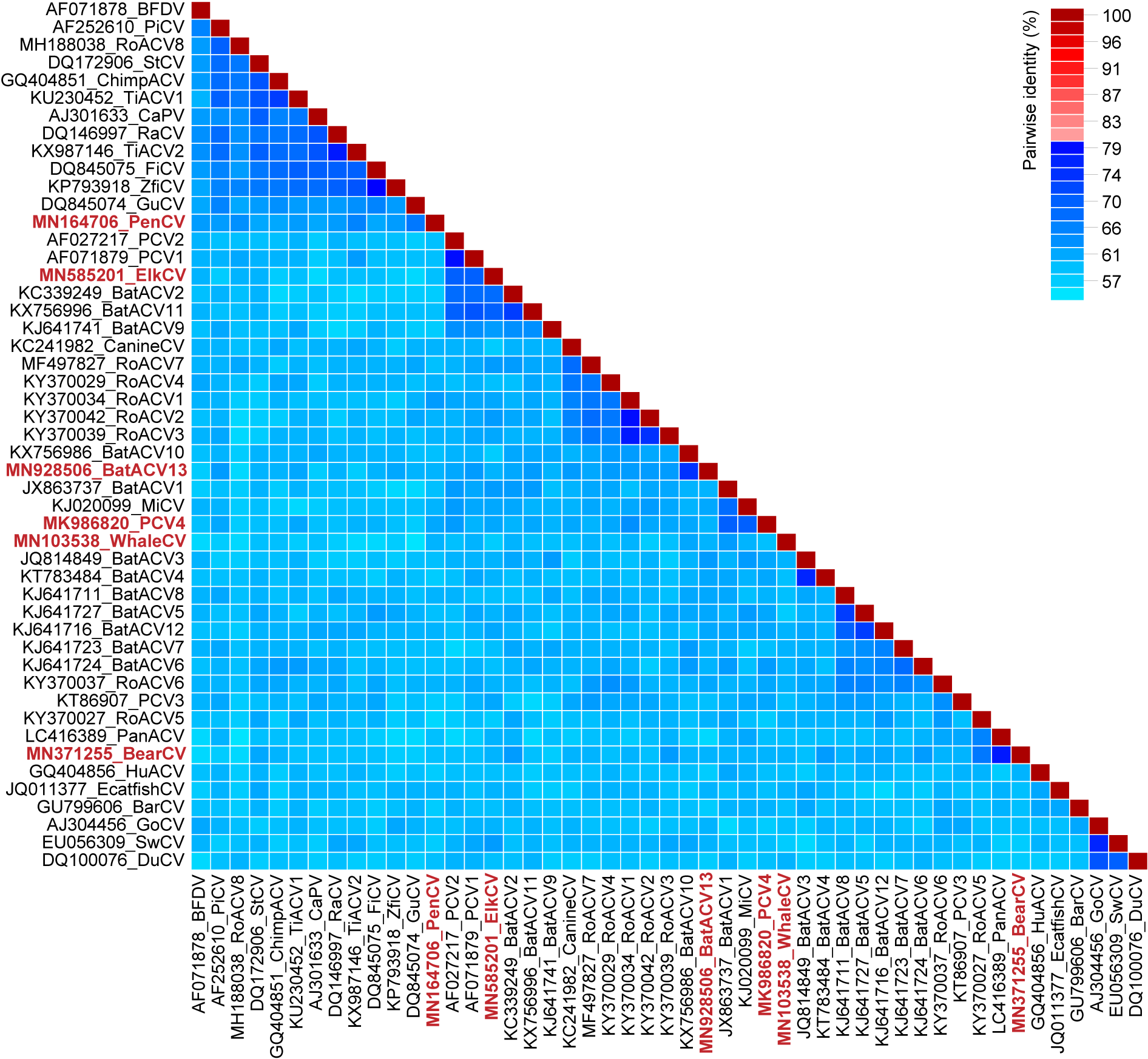
|  |  |
| --- | --- |
| |  | | --- | | The family *Circoviridae* (phylum *Cressdnaviricota*; order *Cirlivirales*) has two established genera (*Circovirus* and *Cyclovirus*). Viruses within these two genera are classified into species based on genome-wide pairwise identities with 80% species demarcation threshold [3].  Over the last year, 10 new viruses have been identified that fall within the *Circoviridae* family. These viruses represent seven new species within this family.  Based on the species demarcation threshold coupled with phylogenetic support, 6 new species for the genus *Circovirus* (Table 1, Figure 1-2) and 1 new species for the genus *Cyclovirus* (Table 2, Figure 3-4) are proposed.  Details of viruses belonging to these species are summarized in Tables 1 and 2. The term ‘associated’ is used when the host is unknown to maintain consistency with the past species nomenclature.  Please note that an independent proposal has been put forward for elk circovirus (ElkCV; MN585201) by the research team that identified it and here we provide additional evidence for it being classified into a new species. | |

**Supporting evidence**

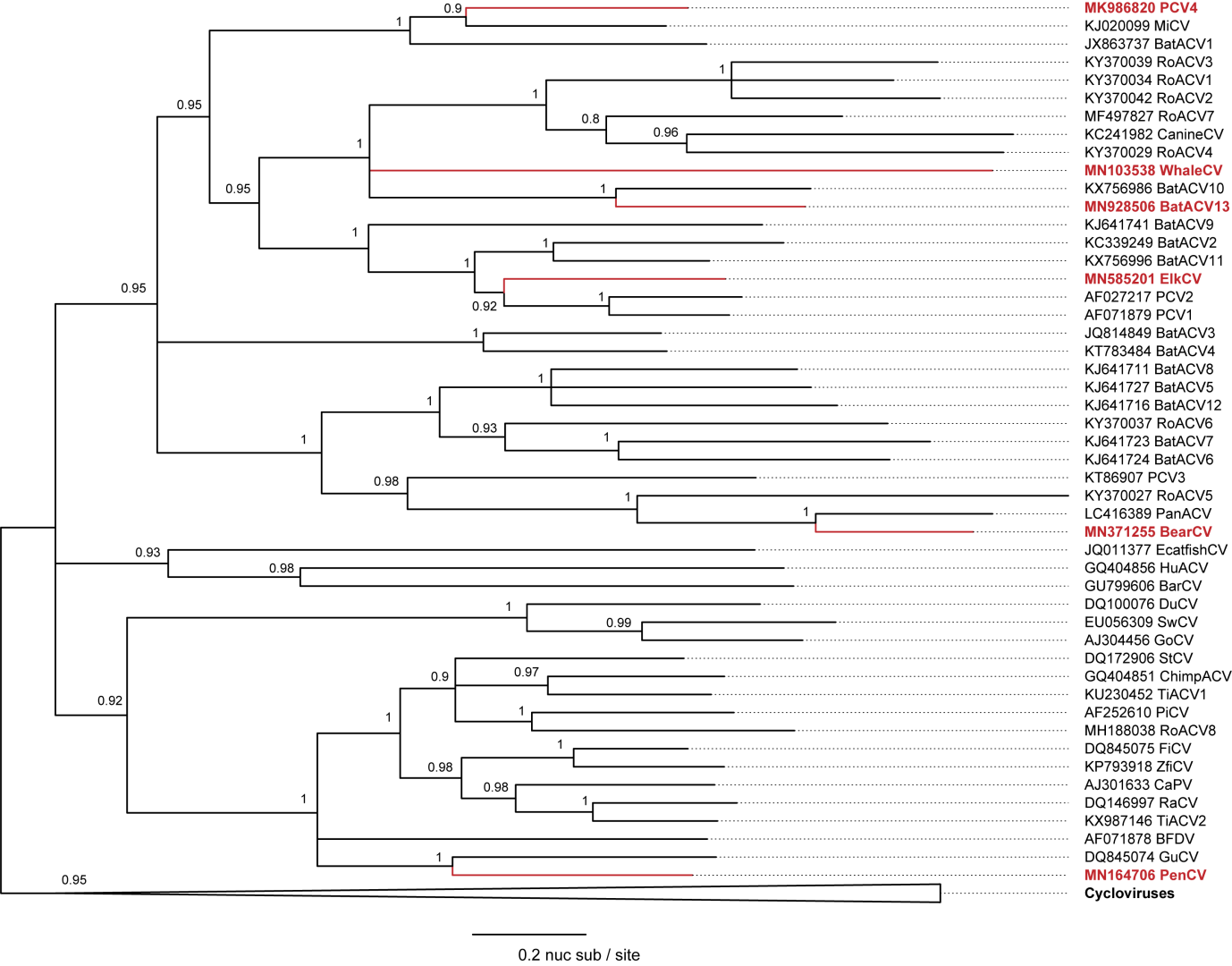
**Table 1:** Summary of new species and their members in the genus *Circovirus*

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| --- | --- | --- | --- | --- | --- | --- |
| **Species** | **Accession** | **Virus name** | **Virus acronym** | **Country** | **Host / isolation source** | **Isolate** |
| *Elk circovirus*\* | MN585201 | elk circovirus | ElkCV | Canada | *Cervus canadensis* | Banff/2019 |
| *Whale circovirus* | MN103538 | beaked whale circovirus | WhaleCV | USA | *Indopacetus pacificus* | IP13001 |
| *Porcine circovirus 4* | MK986820 | porcine circovirus 4 | PCV4 | China | *Sus scrofa* | HNU-AHG1-2019 |
| *Bear circovirus* | MN371255 | Ursus americanus circovirus | BearCV | USA | *Ursus americanus americanus* | UaCV/Reno/2014 |
| *Bat associated circovirus 13* | MN928506 | bat circovirus | BatACV13 | Italy | *Miniopterus schreibersii* | Sardinia BatACV |
| *Penguin circovirus* | MN164703 | penguin circovirus | PenCV | Antarctica | *Pygoscelis adeliae* | Croz\_chick |
|  | MN164704 | penguin circovirus | PenCV | Antarctica | *Pygoscelis adeliae* | Crc4 |
|  | MN164705 | penguin circovirus | PenCV | Antarctica | *Pygoscelis adeliae* | Crc17 |
|  | MN164706 | penguin circovirus | PenCV | Antarctica | *Pygoscelis adeliae* | Crc18 |

\* An independent proposal has been put forward by the research team that identified this virus.

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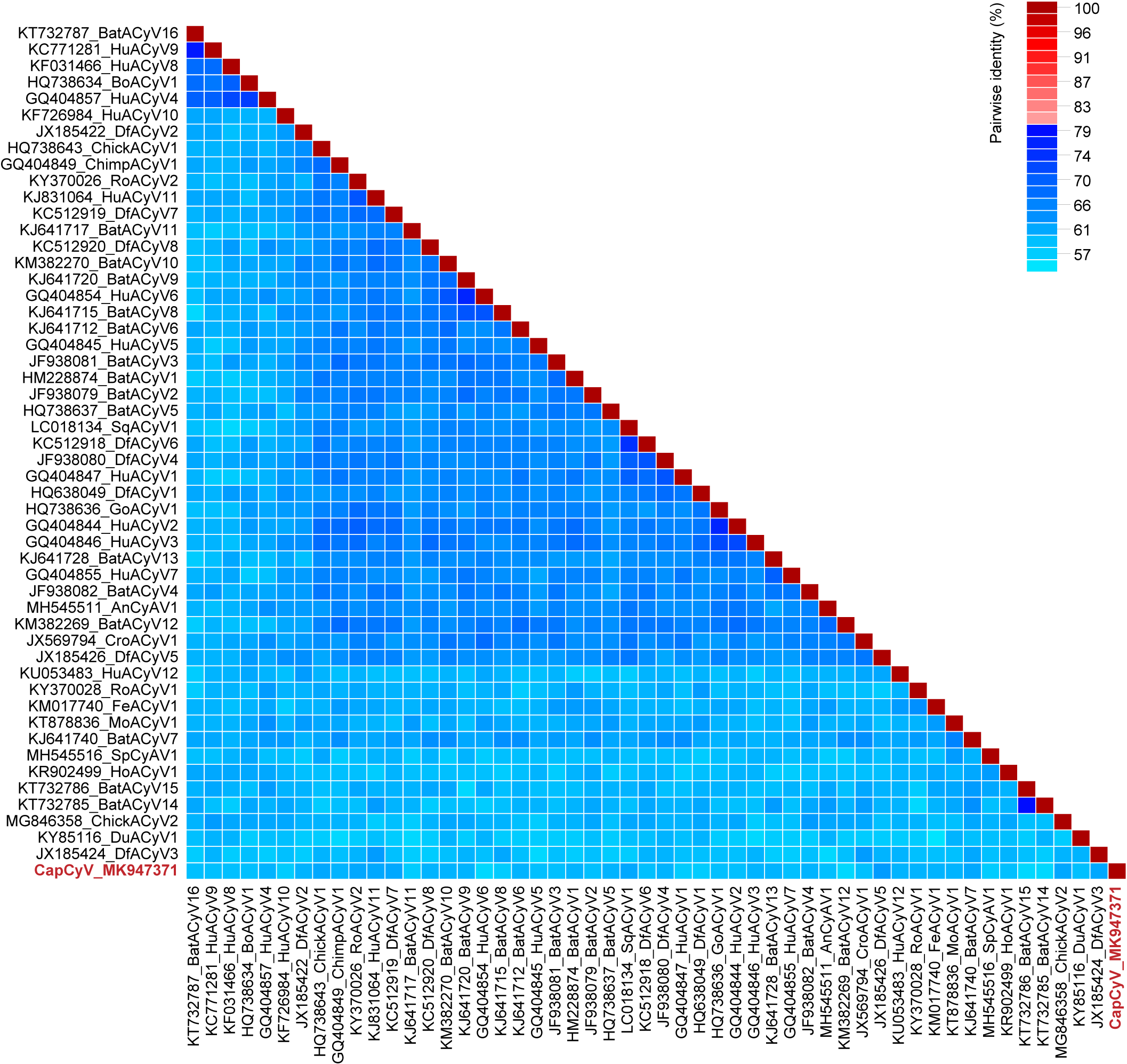
**Figure 1:** A ‘two colour’ pairwise identity matrix of representative genome-wide comparisons among sequences in the genus *Circovirus* inferred using SDT v1.2 [2]. Representative sequences from the proposed new species (n=6) are highlighted in red font.

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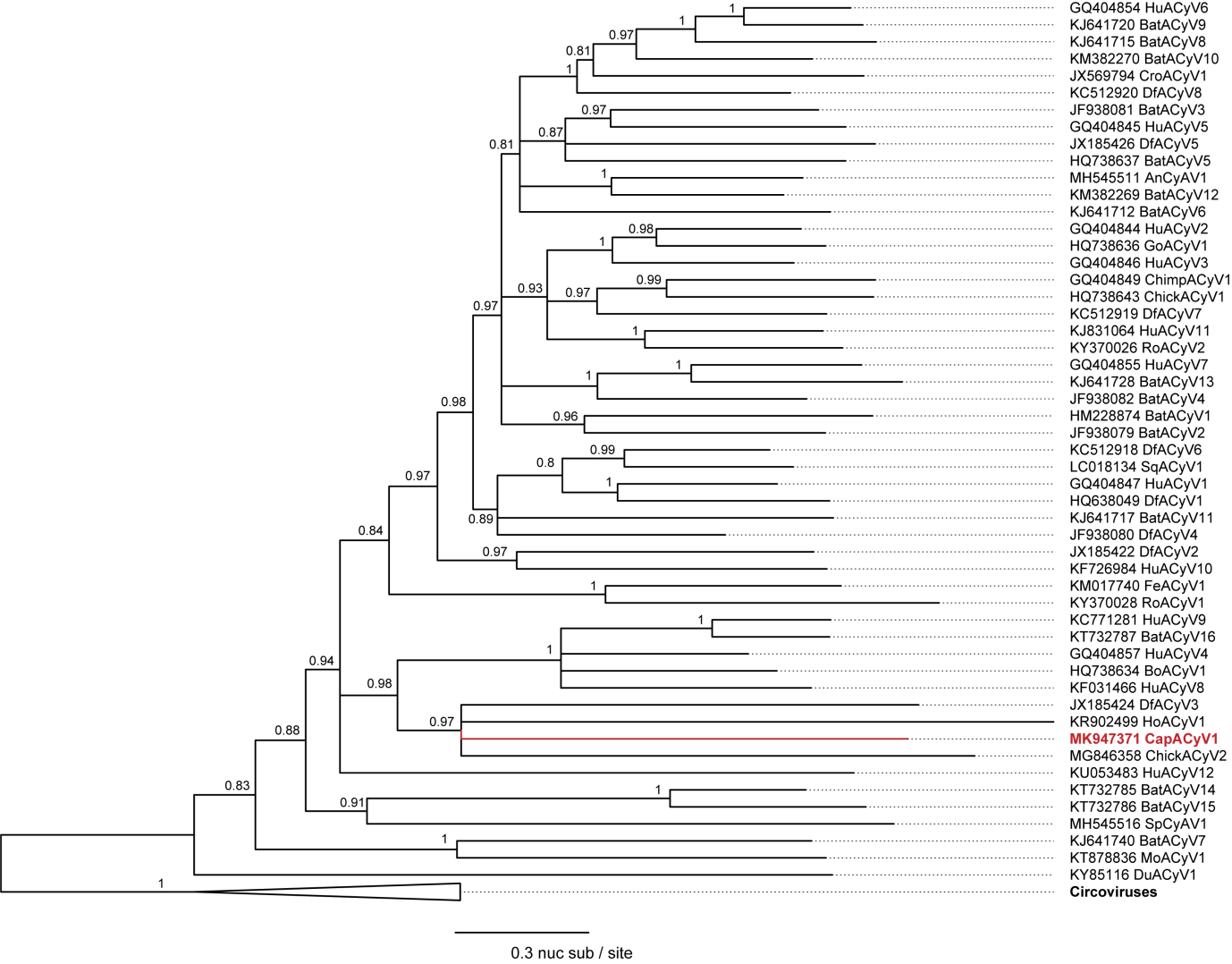
**Figure 2:** Maximum likelihood phylogenetic tree (rooted with reverse complement sequences of cycloviruses) of representative genomes from each circovirus species inferred using PHYML [1] with GTR+I+G4 chosen as the best fit model. Branches with <0.8 aLRT (approximate likelihood ratio test) branch support have been collapsed.

**Table 1:** Summary of new species and its member in the genus *Cyclovirus*

|  |  |  |  |  |  |  |
| --- | --- | --- | --- | --- | --- | --- |
| **Species** | **Accession** | **Virus name** | **Virus acronym** | **Country** | **Host / isolation source** | **Isolate** |
| *Capybara associated cyclovirus* | MK947371 | capybara associated cyclovirus 1 | CapCV | Brazil | *Hydrochoerus hydrochaeri* | Cap1\_365 |

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**Figure 3:** A ‘two colour’ pairwise identity matrix of representative genome-wide comparisons among cyclovirus sequences inferred using SDT v1.2 [2]. Representative sequence from the proposed new species is highlighted in red font.

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**Figure 4:** Maximum likelihood phylogenetic tree (rooted with reverse complement sequences of circoviruses) of representative genomes from each cyclovirus species inferred using PHYML [1] with GTR+I+G4 chosen as the best fit model. Branches with <0.8 aLRT (approximate likelihood ratio test) branch support have been collapsed.

**References**

1. 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

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. 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