

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

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| **Code assigned:** | ***2023.014S*** |  |
| **Short title:** Create one new species in the genus *Senecavirus* (*Picornavirales*: *Picornaviridae*) | | |
|  | | |

**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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| Picornavirus Study Group |

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

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| Suggestions from the Study group indicated below were all incorporated :   1. The suggested species designation 2. The common name of the cetacean picornavirus and Seneca Valley virus 3. The inclusion of the recently described Seneca-like viruses from pangolins and other genera in the phylogenetic analysis 4. Missing extreme 5’ and 3’ end of the genome 5. Adding a cartoon diagram of the genome layout of the new sequence |

**ICTV Study Group votes on proposal**

|  |  |  |  |
| --- | --- | --- | --- |
| **Study Group** | **Number of members** | | |
| **Votes support** | **Votes against** | **No vote** |
| *Picornaviridae* SG | 6 | 0 | 6 |
|  |  |  |  |

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

|  |  |
| --- | --- |
| **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**

|  |  |
| --- | --- |
| Date first submitted to SC Chair | 22 February 2023 |
| Date of this revision (if different to above) | 16 August 2023 |

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

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

**Text of proposal**

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

**Name of accompanying Excel module**

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| --- |
| 2023.014S.N.v2.Senecavirus\_1nsp.xlsx |

**Abstract**

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| We propose the creation of a new species in the *Senecavirus* genus, which would include the recently isolated and sequenced cetacean picornavirus 1 (CPv1). We suggest the species name *Senecavirus cetus* in line with the new binomial species nomenclature. The complete genome (7455nt) and coding genome (6645nt / 2215aa) was sequenced from post-mortem brain tissue of a stranded Beluga Whale (*Delphinapterus leucas*). The resulting assembled contig was compared to publicly available sequences and it was found that the closest match was the only member of the *Senecavirus* genus, Seneca Valley virus (SVV; species *Senecavirus* A), accession KY618836.1) having an ORF1 pairwise nucleotide identity of 58.29% and ORF1 amino acid identity of 51.32%. Sequence divergence between the new species and SVV was 40.5% and 44.5% nucleotide identity for the 3Dpol and P1 regions, respectively. This would make CPv1 the first virus in the *Senecavirus* genus that is isolated from a cetacean. |

**Text of proposal**

|  |  |
| --- | --- |
| |  | | --- | | A new virus, tentatively named cetacean picornavirus 1 (CPv1) was isolated from the brain of a stranded dead beluga whale (*Delphinapterus leucas*) from Alaska, USA in 2019 and sequenced (**Table 1**). The 7455nt complete genome and 6645nt / 2215aa complete coding genome of the named CPv1 showed the greatest degree of similarity to Seneca Valley virus (species *Senecavirus A*, accession MN812958.1) which is currently the sole member of the *Senecavirus* genus. CPv1 showed an ORF1 pairwise nucleotide identity of 58.29% and ORF1 amino acid identity of 51.32% to its top BLAST match (**Table 2**). Additionally, sequence divergence between the new species and Senecavirus A was 40.5% and 44.5% nucleotide identity for the 3Dpol and P1 protein coding regions, respectively. When compared with the next closest match from an adjacent genus (species *Cardiovirus C*, accession JQ864242), CPv1 continued to show the greatest degree of similarity to members of the *Senecavirus* genus (**Figure 1**). When queried against the NCBI nr/nt database, no other matches with a higher percent identity were found. Based on the nucleotide and amino acid identity, as well as the results of the genome layout (**Figure 2**) and phylogenetic analysis (**Figure 3**), we propose that CPv1 should be classified as a new member within the *Senecavirus* genus and suggest the species name *Senecavirus cetus* in line with the new binomial species nomenclature. The name Cetus, is Latin for whale, and is referenced as a sea monster in Greek mythology  Comparative genomic analysis of the complete coding genome for CPv1 found that conserved motifs present within members of the *Picornaviridae* family were present including the Walker A motif (GxxGxGKS/T), 3C proteinase motif (GxCGx10-15GxH) and 3D polymerase motifs (KDE, DxxxxD, PSG, YGDD, FLKR).  A virus isolate very similar to our novel CPv1 was also isolated and sequenced from a stranded dead harbor porpoise (*Phocoena phocoena*). *Senecavirus cetus* (porpoise rectal) isolate showed an ORF1 pairwise nucleotide identity of 100% and ORF1 amino acid identity of 100% to CPv1 and *Senecavirus cetus* (porpoise brain) isolate showed an ORF1 pairwise nucleotide identity of 98.8% and ORF1 amino acid identity of 99.0% to CPv1. | |

**Supporting evidence**

**Table 1:** Summary of details regarding the proposed novel *Picornavirus* species

|  |  |  |  |  |  |
| --- | --- | --- | --- | --- | --- |
| **Species name** | **GenBank accession** | **Virus acronym** | **Isolate ID** | **Country of Isolate** | **Host/isolation source** |
| *Senecavirus cetus* | OR416239 | CPv1 | Alaska /  2019 | USA | *Delphinapterus leucas* (Beluga whale) / Brain |

**Table 2:** Comparison of novel *Picornavirus* species to closest BLAST matches

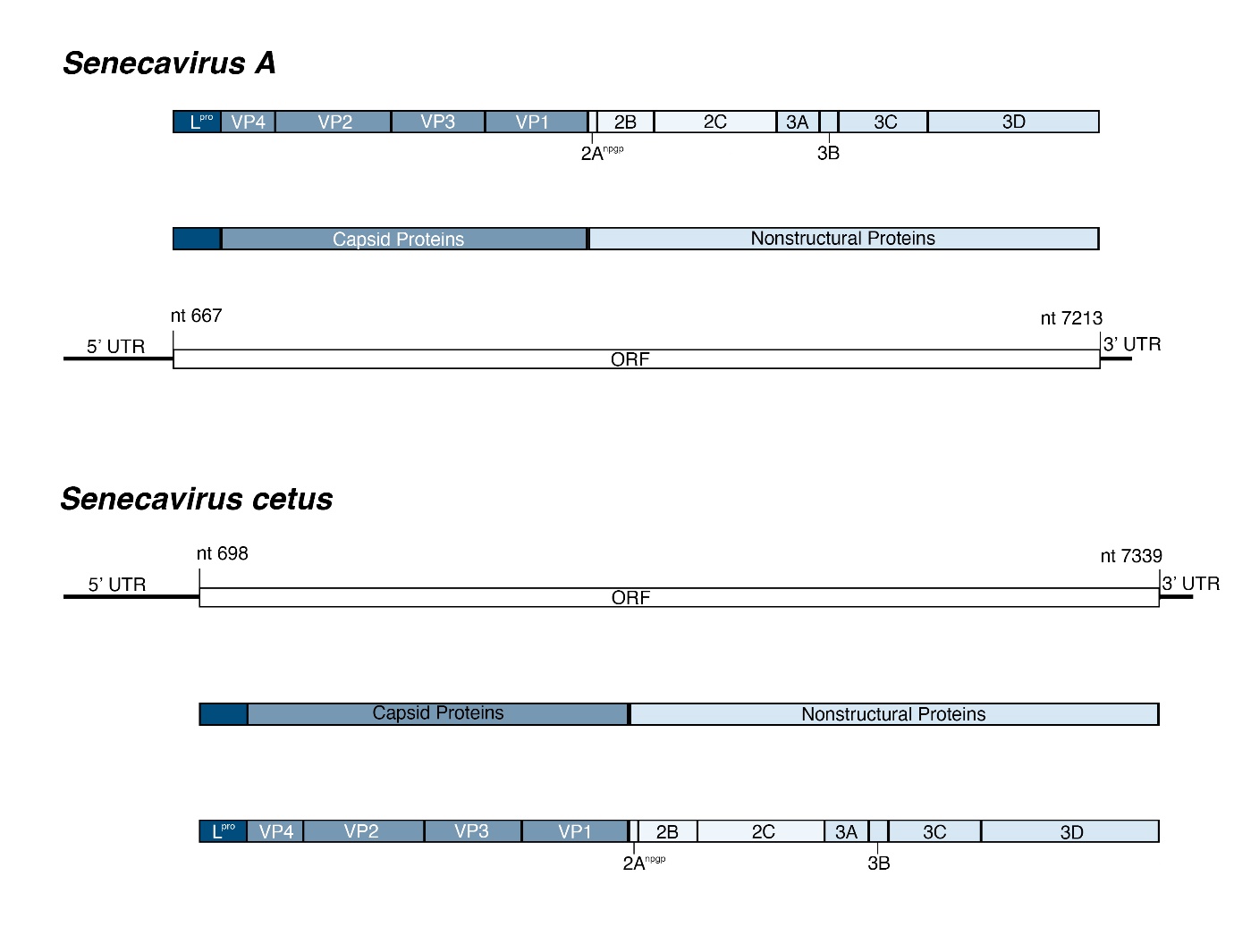
|  |  |  |  |
| --- | --- | --- | --- |
| **Species name** | **GenBank accession** | **Percent Identity** | |
| **Nucleotide** | **Amino Acid** |
| *Senecavirus cetus* | OR416239 | - | - |
| *Senecavirus A* | MN812958 | 58.3 | 51.8 |
| Pangolin senecavirus | OL519620 | 53.7 | 49.7 |

**A**

**B**

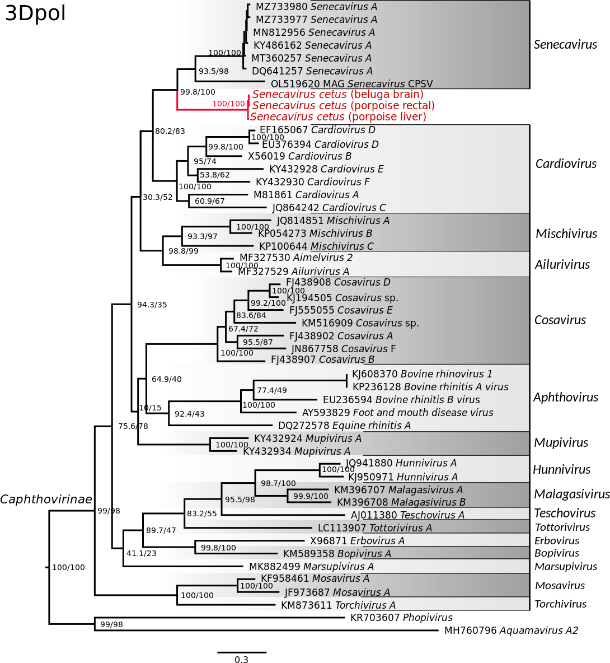
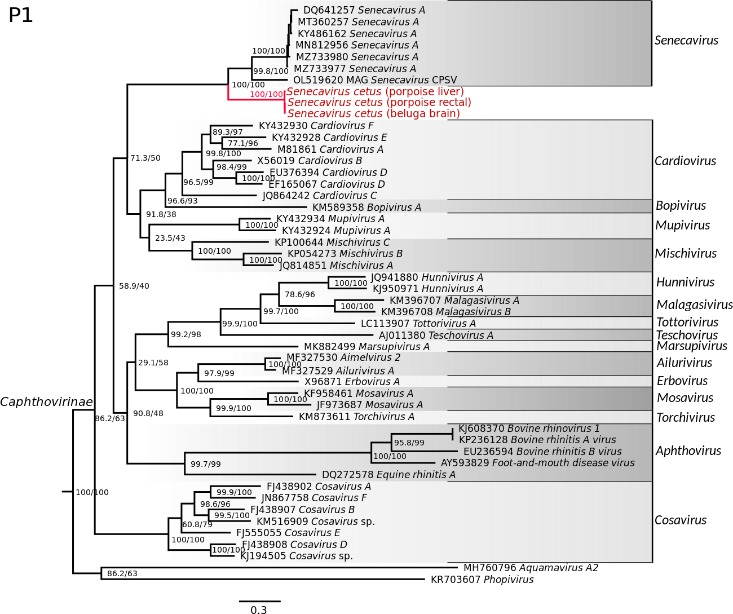


**Figure 1:** Percent identity matrix based on picornavirus polyprotein gene pairwise nucleotide (**A**) and amino acid sequences (**B**).

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**Figure 2:** *Senecavirus cetus*genome layout and organization compared to *Senecavirus A*.



**Figure 3:** Maximum likelihood phylogenetic trees of picornaviruses in the subfamily *Caphthovirinae* reconstructed based on the nucleotide sequences of the P1 (left) and 3Dpol (right) genes. Sequences of the novel picornavirus is shown in red (GenBank accession numbers are OR416237-liver; OR416238-rectal; and OR416239-brain); the most closely related lineage, genus *Senecavirus*, includes a Senecavirus identified in pangolin, OL519620 MAG Senecavirus CPSV (Ning et al., 2022). Phylogenetic analysis was performed using IQ-Tree web server 1.6.12 (Nguyen et al., 2015; Trifinopoulos et al., 2016). The best-fit model of sequence evolution was selected based on the Bayesian information criterion (BIC) score (Schwarz, 1978) calculated by ModelFinder (Kalyaanamoorthy et al., 2017), GTR+F+I+G4 model was selected as the best-fitting for P1 and 3Dpol data sets. Node support was estimated by ultrafast bootstrap (Hoang et al., 2018) and the SH-aLRT test (Guindon et al., 2010) with 1,000 replicates each. Support values are shown at the nodes (SSH-LRT/Ultrafast bootstrap). The trees were rooted to the outgroups, Phopivirus and Aquamavirus A2, members of the subfamilies *Heptrevirinae* and *Paavivirinae*, respectively. Scale bars represent estimated average number of substitutions per site.

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