

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

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| **Code assigned:** | **2021.003D** |  |
| **Short title:** Abolish one genus and reassign two species (*Anelloviridae*) | | |
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**Author(s) and email address(es)**

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| Varsani A |

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

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| *Anelloviridae* 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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| --- | --- |
| **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 | 28th May 2021 |
| 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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| 2021.003D.A.v1.Anelloviridae\_1abgen\_2spmv.xlsx |

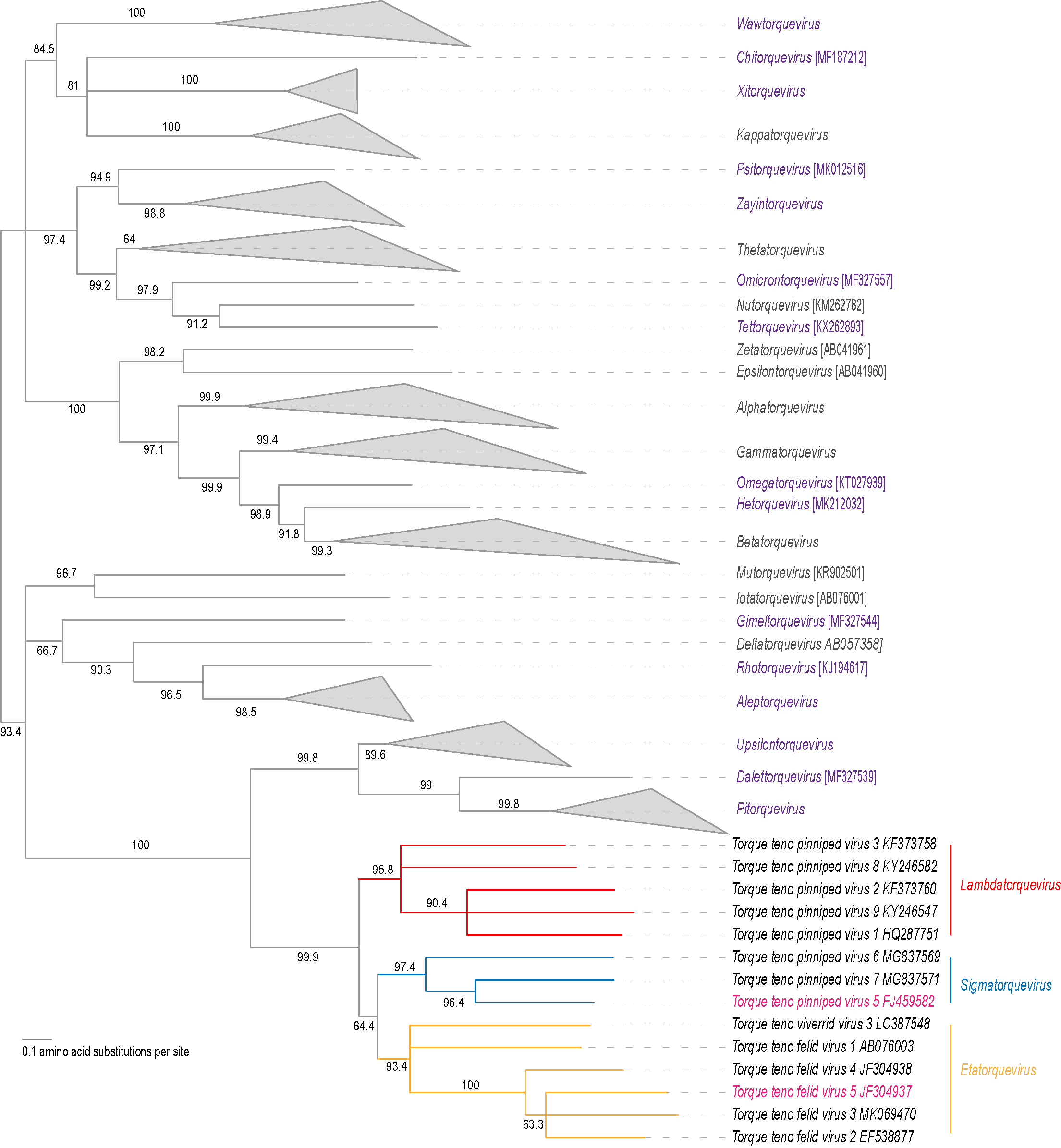
**Abstract**

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| The family *Anelloviridae* is composed of negative single-stranded circular DNA viruses that have been identified infecting mammal and avian species. Here we propose to abolish a genus and reassign two species to currently established genera. |

**Text of proposal**

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| |  | | --- | | The family *Anelloviridae* is composed of negative single-stranded circular DNA viruses that have been identified infecting various mammal and avian species.  Analyzing large datasets of new anelloviruses based on the phylogeny of the ORF1 sequences, we notice two discrepancies which we propose to correct with this proposal. The ORF1 amino acid sequences of representative anelloviruses were aligned using MAFFT [2]. The alignment was trimmed with TrimAL [1] using the gappyout option and the alignment was used to infer a maximum likelihood tree with IQTree [3] with LG+F+G4 substitution model. Based on our analysis (Figure 1):   1. We propose to abolish the genus *Tautorquevirus* and move the sole member of this genus, species *Torque teno felid virus 5* (GenBank Accession # JF304937 for exemplar virus), to genus *Etatorquevirus*. The sequence of JF304937 clusters with those in the genus *Etatorquevirus* (Figure 1). 2. We propose to reassign the species *Torque teno pinniped virus* *5* (GenBank Accession # FJ459582 for exemplar virus) from genus *Lambdatorquevirus* to the genus *Sigmatorquevirus* given that the sequence FJ459582 is nested with other members (Figure 1). | |

**Supporting evidence**

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**Figure 1:** Maximum likelihood phylogenetic tree of the ORF1 amino acid sequences of representative member of each species in the family *Anelloviridae*. Representative sequences of species in the genus *Gyrovirus* are not included as their VP1 is divergent from ORF1.Numbers at the nodes represent aLRT branch support values. Branches with less than 60% support have been collapsed with TreeGraph2 [4]. Species to be reassigned are highlighted in pink and the reassignment genera colour coded and named to the right of the taxa names.

**References**

1. Capella-Gutierrez S, Silla-Martinez JM, Gabaldon T (2009) trimAl: a tool for automated alignment trimming in large-scale phylogenetic analyses. Bioinformatics 25:1972-1973. PMID: 19505945; DOI: 10.1093/bioinformatics/btp348

2. Katoh K, Standley DM (2016) A simple method to control over-alignment in the MAFFT multiple sequence alignment program. Bioinformatics 32:1933-1942. PMID: 27153688; DOI: 10.1093/bioinformatics/btw108

3. Minh BQ, Schmidt HA, Chernomor O, Schrempf D, Woodhams MD, von Haeseler A, Lanfear R (2020) IQ-TREE 2: New Models and Efficient Methods for Phylogenetic Inference in the Genomic Era. Mol Biol Evol 37:1530-1534. PMID: 32011700; DOI: 10.1093/molbev/msaa015

4. Stover BC, Muller KF (2010) TreeGraph 2: combining and visualizing evidence from different phylogenetic analyses. BMC Bioinformatics 11:7. PMID: 20051126; DOI: 10.1186/1471-2105-11-7