

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

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| **Code assigned:** | **2021.002D** |  |
| **Short title:** Create one new species in the genus *Mutorquevirus* ( *Anelloviridae*) | | |
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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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**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)** |  |

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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 | 1st April 2021 |
| Date of this revision (if different to above) | 18th April 2021 |

**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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| 2021.002D.R.Anelloviridae\_1nsp.xlsx |

**Abstract**

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| Here we propose the establishment of a new species to the *Mutorquevirus* genus, name *Mutorquevirus equid2* to accomodate a recently identified virus torque teno equus virus 2 (TTEqV2). The 2,805 nucleotide complete circular genome of TTEqV2 was sequenced from post-mortem lung and liver tissue of a Quarter Horse (*Equus caballus*), assembled and compared to other publically available sequences. It was determined that the closest match was the only other currently publicly available member of *Mutorquevirus*, torque teno equus virus 1 (TTEqV1, accession KR902501.1), with an ORF1 pairwise nucleotide identity of 59.7%. Based on the absence of features highly conserved within *Anelloviridae*, we believe that the untranslated region (UTR) of the TTEqV1 genome is incomplete. This would make TTEqV2 the first complete genome from *Mutorquevirus*. The annotated complete TTVEq2 genome has been uploaded to NCBI with accession MW842984. |

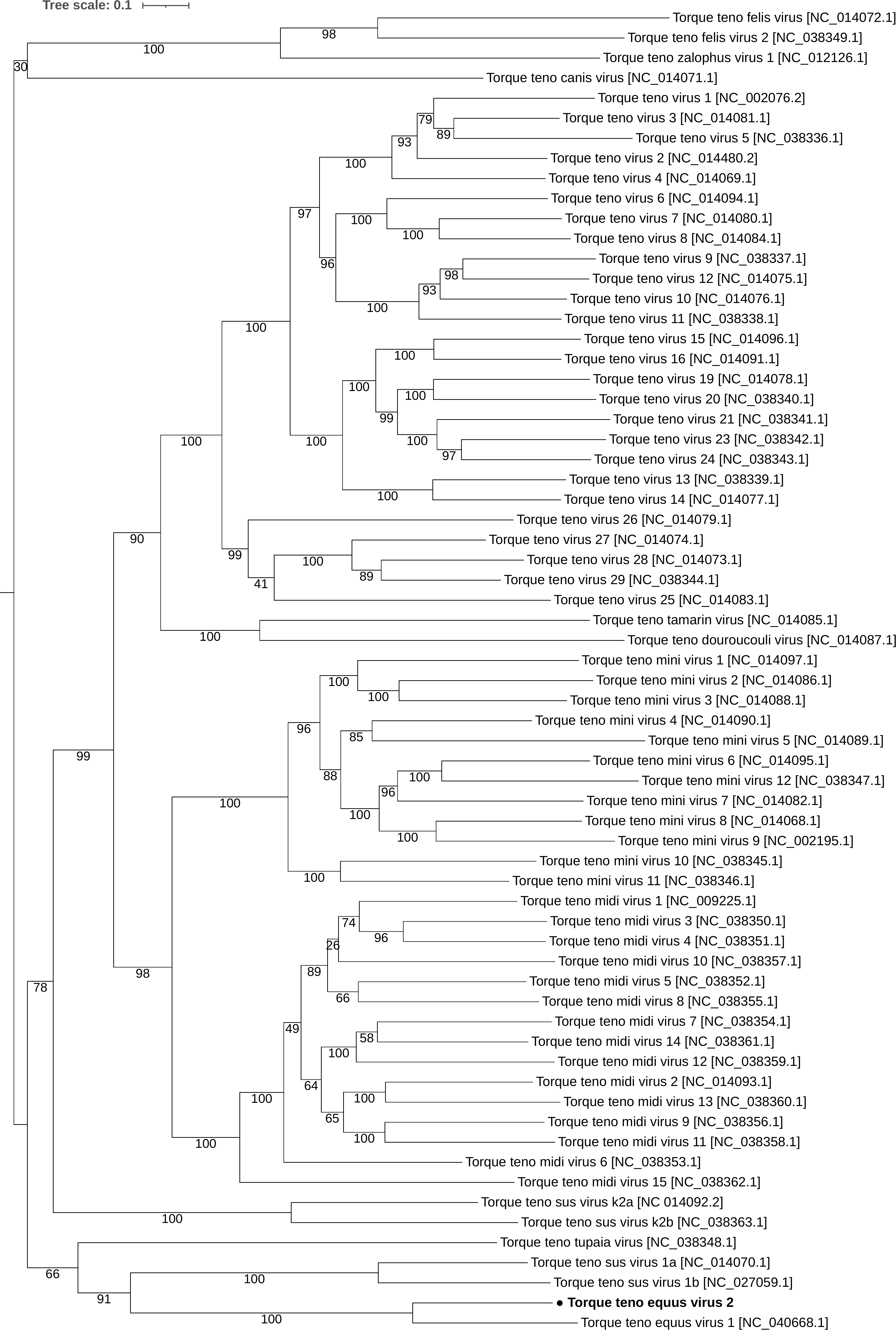
**Text of proposal**

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| |  | | --- | | The 2,805 nucleotide complete circular genome of TTVEqV2 (Table 1) showed the highest degree of nucleotide identity to torque teno equus virus 1 (TTEqV1, accession KR902501.1), which is currently the only publicly available sequence from a member of the *Mutorquevirus* genus. The novel virus named torque teno equus virus 2 (TTEqV2), showed 59.7% genome-wide pairwise nucleotide identity to TTEqV1. When queried against the NCBI nr/nt database no other significant matches with higher percent identity were observed. Anelloviruses are classified into species and genera using respective thresholds of 65% and 44% pairwise nucleotide identity of ORF1 [1, 2]. Based on the nucleotide identity and phylogenetic support presented here (Figure 1), TTEqV2 should be classified as a member of a new species within the genus *Mutorquevirus*.  Comparative genomic analysis of both TTEqV sequences found that several genomic features, which are highly conserved within the untranslated region (UTR) of anelloviruses, were absent in TTEqV1 but present in TTEqV2 (Figure 2). This appears to indicate that the UTR of TTEqV1 is incomplete. The missing features include at least one GC-rich region [3] and the first of two highly conserved 15 nucleotide motifs (CGAATGGCTGAGTTT) [4-7]. Likely as a result of the missing region, TTEqV1 (2,197 nucleotides) is significantly shorter than TTEqV2 (2,805 nucleotides). It is worth noting that ORF1, which is currently used for species demarcation, appears to be complete in TTEqV1. Based on this analysis, TTEqV2 appears to be the first complete genome from the genus *Mutorquevirus*. | |

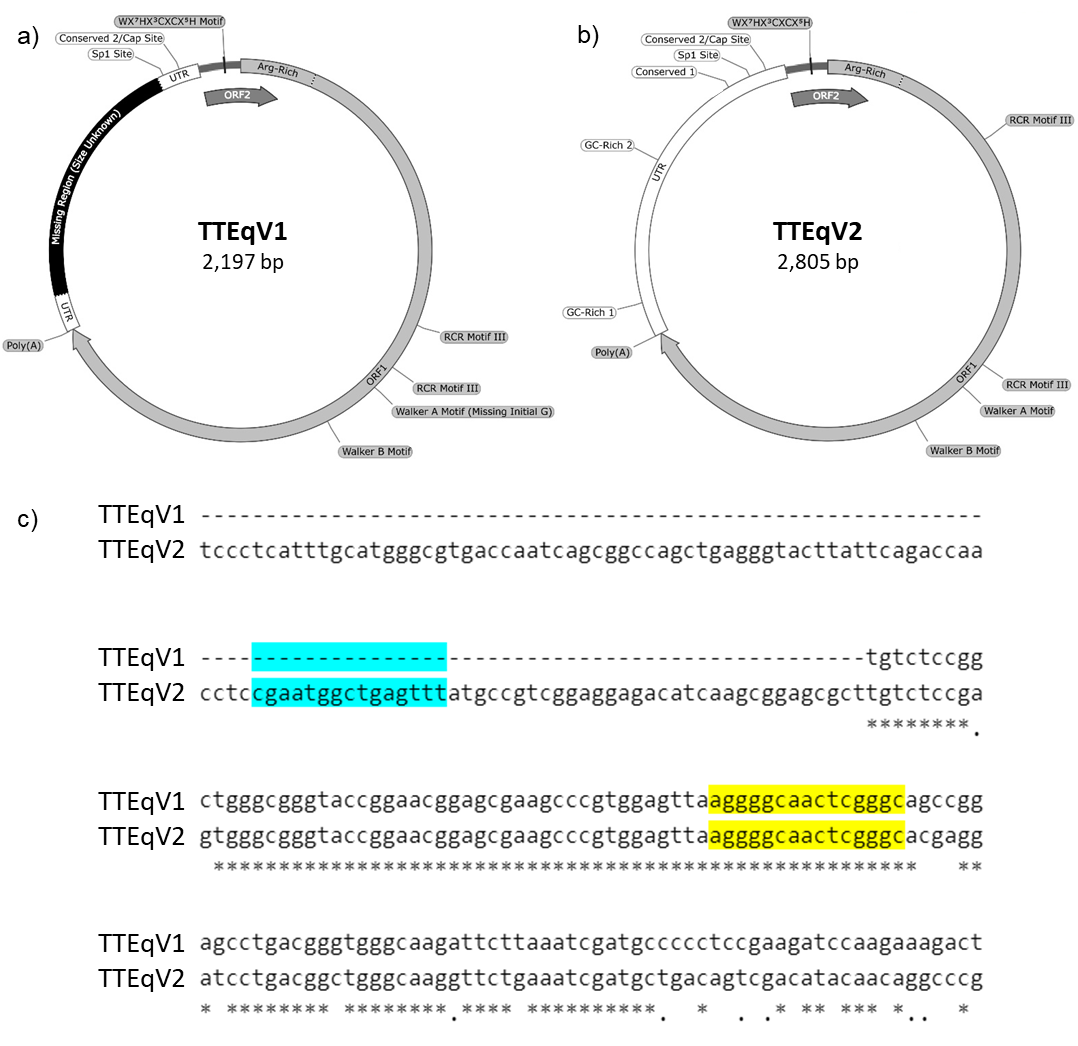
**Supporting evidence**

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| **Species name** | **GenBank accession** | **Virus acronym** | **Isolate ID** | **Country of Isolate** | **Host/isolation source** |
| Mutorquevirus equid2 | MW842984 | TTEqV2 | Alberta/2018 | Canada | Equus caballus |

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



**Figure 1.** Maximum likelihood phylogenetic trees of representative sequences within the family *Anellovirdae*. Sequences were aligned using MAFFT [8], trees generated using IQ-Tree [9] on find best model setting with ModelFinder [10] with 1,000 ultrafast bootstraps [11] and visualized with iTOL [12]. TTEqV2 is indicated in bold text and with “•” before the sequence name. A full mid-point rooted phylogenetic tree generated from representative complete genome nucleotide sequences is shown (model GTR+F+R5).

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**Figure 2.** Circular genome maps including conserved genomic features found in a) TTEqV1 (KR902501.1) and b) TTEqV2 (accession). The suspected missing region within the UTR of TTEqV1 is highlighted in black. ORFs were visualized using SnapGene Viewer v5.0.7 (snapgene.com). c) Alignment of TTEqV sequences in the region surrounding the two 15 nucleotide conserved sequences. The conserved sequence present in both sequences (Conserved 2/Cap Site in above genome maps) is highlighted in yellow, while the one missing from TTEqV1 (Conserved 1 in above genome maps) is highlighted in blue. Sequences were aligned using MAFFT [3].

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