

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

|  |  |  |
| --- | --- | --- |
| **Code assigned:** | **2021.034M** |  |
| **Short title:** Create four new species in the genus *Quaranjavirus* (*Articulavirales*: *Orthomyxoviridae*) | | |
|  | | |

**Author(s) and email address(es)**

|  |  |
| --- | --- |
| García-Sastre A | [adolfo.garcia-sastre@mssm.edu](mailto:adolfo.garcia-sastre@mssm.edu) |

**Author(s) institutional address(es) (optional)**

|  |
| --- |
| Icahn School of Medicine at Mount Sinai |

**Corresponding author**

|  |
| --- |
| García-Sastre A |

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

|  |
| --- |
| ICTV *Orthomyxoviridae* Study Group |

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

|  |
| --- |
| N/A |

**Submission dates**

|  |  |
| --- | --- |
| Date first submitted to SC Chair | May 28, 2021 |
| Date of this revision (if different to above) | September 17, 2021 |

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

|  |
| --- |
| * I would like to see a simple PB1-based phylogenetic tree, similar to that shown in 2021.024M, although I accept that the table of PB1-relatedness makes a good case for 4 new species.   Response: a simple PB1-based tree was added to this revision.   * The Word document is very poor with much unnecessary information. The RdRP tree should be reference properly if it is used.   Response: the Word document has been drastically shortened and the RdRP tree was removed.   * Most importantly, In the Excel spreadsheet, I request the nucleotide GB accession record numbers for all segments of the exemplar viruses for the 4 new species.   Response: Accession numbers in the Excel sheet were corrected/replaced.   * Could we also please have virus name abbreviations.   Response: Virus abbreviations were added.   * Read the EC-distributed guidance on species naming document, confirm that proposed species names adhere to the guidance, and confirm that you would like to keep the proposed species names as originally proposed.   Response: Read, confirmed, and confirmed. |

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

**Name of accompanying Excel module**

|  |
| --- |
| 2021.034M.R.Quaranjavirus\_4nsp |

**Abstract**

|  |
| --- |
| Genus *Quaranjavirus,* included in family *Orthomyxoviridae,* harbors two distinct viruses classified into separate species: Johnston Atoll virus and Quaranfil virus. These viruses have genomes consisting of ≥ 6 single-stranded negative-sense RNA genomes and infect arthropods and birds. In the last years the complete (7-segment) genome sequences of these viruses have been generated, enabling the identification of additional, closely related viruses, including Araguari virus, Tyulek (Tjuloc) virus, Wellfleet Bay virus, Lake Chad virus. Here, these four viruses are proposed to be assigned to new quaranjavirus species. |

**Text of proposal**

|  |  |
| --- | --- |
| |  | | --- | | Complete seven segment coding sequences for Johnston Atoll virus (JAV) are available in GenBank: MN585121-7. Taxonomy ID: 688437  Complete six segment coding sequences for Quaranfil virus (QRFV) are also available in GenBank: Taxonomy ID: 1559362  Unclassified, putative quaranjaviruses included in the taxonomy of GenBank include:  Guadeloupe mosquito quaranja-like virus 1  Guadeloupe mosquito quaranja-like virus 2  Guadeloupe mosquito quaranja-like virus 3  Jingshan fly virus  Jiujie fly Virus  Longchuang virus  Sanxia water strider virus 3  Shayang spider virus 3  Shuangao insect virus 4  Soybean thrips quaranja-like virus 1  Soybean thrips quaranja-like virus 2  Soybean thrips quaranja-like virus 3  Soybean thrips quaranja-like virus 4  Wellfleet Bay virus (WFBV)  Wuhan louse fly virus 3  Wuhan louse fly virus 4  Wuhan mosquito virus 3  Wuhan mosquito virus 4  Wuhan mosquito virus 5  Wuhan mosquito virus 6  Wuhan mosquito virus 7  Wuhan mothfly virus  Zambezi tick virus 1  Additional viruses include:  Araguari virus (ARAV)  Culex orthomyxo-like virus  Cygnet River virus  Lake Chad virus (LKCV)  Tyulek (Tjuloc) virus (TLKV)  Of all new unclassified quaranjavirus-like viruses, complete (7-segment genome sequences are available for only Araguari virus, Lake Chad virus, Tyulek (Tjuloc) virus, and Wellfleet Bay virus. These viruses are closely related but significantly different from each other and from the already classified two quaranjaviruses, justifying the establishment of four novel quaranjavirus species.  The proposed names for these four new species are:  Araguari virus: *Quaranjavirus araguariense* (after the Araguari River, Brazil)  Lake Chad virus: *Quaranjavirus chadense* (after Lake Chad, Central Africa)  Tyulek (Tjuloc) virus: *Quaranjavirus tyulekense* (after Tyulek, Kyrgyzstan)  Wellfleet Bay virus: *Quaranjavirus wellfleetense* (after Wellfleet Bay, USA) | |

**Supporting evidence**

**Table of amino acid identity/coverage of PB1 segments of novel quaranjaviruses (red), the two classified quaranjaviruses (black), and the two more distantly related thogotoviruses (black)**

**ARAV**

**JAV**

**QRFV**

**THOV**

**DHOV**

**JAV**

**THOV**

**DHOV**

100

100

100

100

***Thogotovirus***

***Quaranjavirus***

***Orthomyxoviridae***

83

83

62

62

**LKCV**

**WFBV**

**TLKV**

**ARAV**

**LKCV**

**WFBV**

**TLKV**

25

25

25

25

25

25

25

25

71

82

84

70

100

72

72

100

100

100

73

73

71

71

71

71

71

26

26

28

28

86

86

84

84

70

70

84

26

26

26

26

84

84

82

71

71

25

25

70

26

26

70

70

24

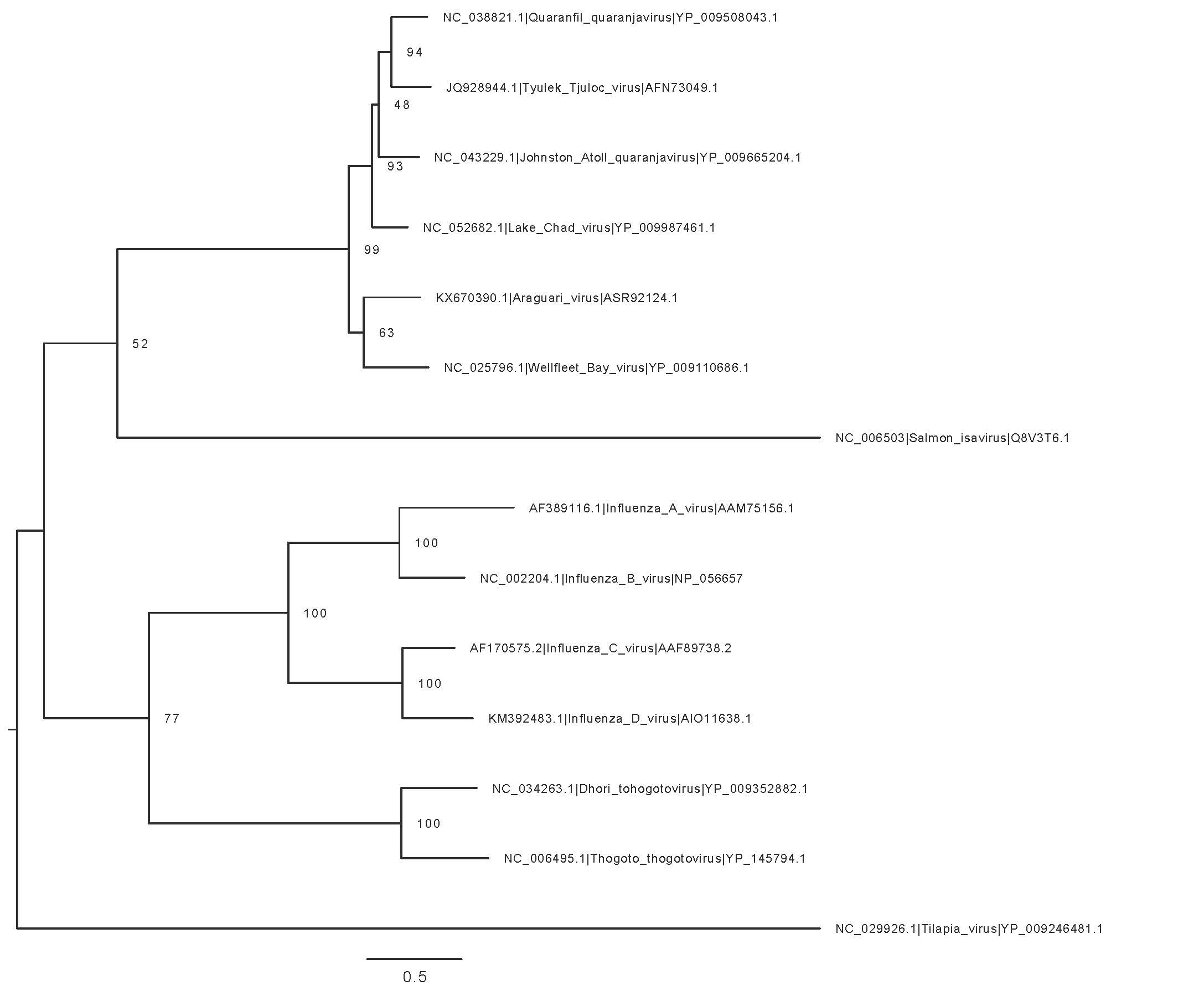
24

24

24

**QRFV**

**Phylogenetic tree of PB1 segments of novel quaranjaviruses, the two classified quarajanviruses, and the rest of the different members of class *Insthoviricetes***

****