

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

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| **Code assigned:** | **2021.022M** |  |
| **Short title:** Create one new genus (*Mykissvirus*) including one species (*Mykissvirus tructae*) (*Articulavirales*: *Orthomyxoviridae*) | | |
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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 *Orthomyxoviridae* Study Group |

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

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| N/A |

**Submission dates**

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| Date first submitted to SC Chair | 05/28/2021 |
| Date of this revision (if different to above) | 09/17/2021 |

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

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| * It would be good to see a PB1- based phylogenetic analysis of the *Orthomyxoviridae*. Actually, this tree is found in 2021.024M and strengthens the argument for 2021.022M.   Response: the tree from TP 2021.022M was added to this revision.   * 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**

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| 2021.022M.A.v1.Orthomyxoviridae\_1ngen\_1nsp\_Mykiss |

**Abstract**

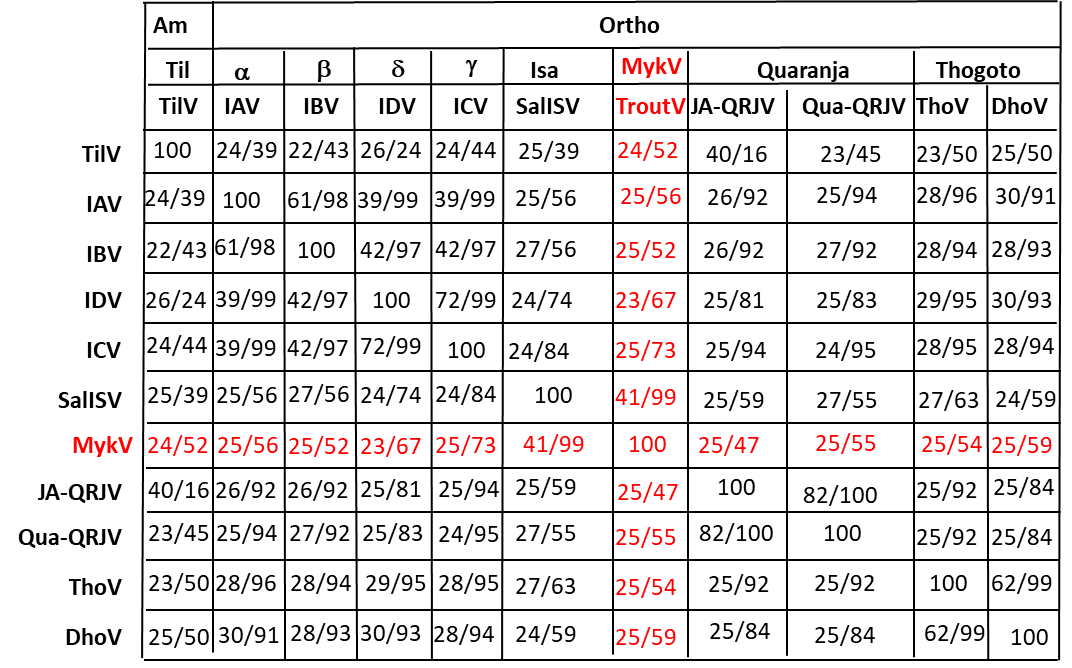
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| Two isolates of rainbow trout orthomyxovirus (RbtOV) were obtained from samples of rainbow trout (*Oncorhynchus mykiss*) at a commercial trout farm in Hagerman Valley, Idaho. The isolates were discovered in 1997 and again in 2000 (RbtOV-1 and RbtOV-2). In 2014, another virus, steelhead trout orthomyxovirus (SttOV-1), was isolated from a steelhead trout (*O. mykiss*) collected in the Kewaunee River near Green Bay, Wisconsin. RbtOV-1 and SttOV-1 viral genes and phylogenetic relationships were described by Batts *et al*. These viruses are very similar, have 8 RNA segments of negative polarity with the same genome segment order and the closest pairwise amino acid sequence identities of 16–42% with Infectious salmon anemia virus (ISAV: *Orthomyxoviridae*: *Isavirus*). RbtOV-1 appears to be a member of a novel virus species that, although most like ISAV, is sufficiently distinct to merit consideration as a member of a new orthmyxovirus genus, proposed to be named *Mykissvirus.* |

**Text of proposal**

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| |  | | --- | | Two isolates of rainbow trout orthomyxovirus (RbtOV) were obtained from samples of early life stage rainbow trout (*Oncorhynchus mykiss*) approximately 60 days old at a commercial trout farm in Hagerman Valley, Idaho. The isolates were discovered in 1997 and again in 2000. In 2014, the LaCrosse Fish Health Center (U.S. Fish and Wildlife Service) in Wisconsin isolated another virus, from an ovarian fluid sample of spawning steelhead trout (*Oncorhynchus mykiss*) collected at a weir in the Kewaunee River near Green Bay, Wisconsin. This steelhead orthomyxovirus isolate was subsequently designated steelhead trout orthomyxovirus (SttOV-1). The complete nucleotide sequences of the coding regions of the 8 viral RNA segments of RbtOV-1 ave been deposited in GenBank under accession numbers KX882061 to KX882068. The complete nucleotide sequences of the coding regions of the 8 viral RNA segments of the SttOV-1 isolate have been deposited in GenBank under accession numbers KX882069 to KX882076. The partial sequence of the PB1 gene of the RbtOV-2 isolate has been deposited in GenBank under accession number KX880091.  The following is the summary of the BLAST analysis of the 10 proteins encoded by the 8 genes of RbtOV-1  PB1 gene (the RNA-directed RNA polymerase)  Rainbow trout orthomyxovirus-1, strain Rainbow/Idaho/347/1997, putative polymerase basic 1 (PB1) gene, complete cds: 2,184 bp linear cRNA; encoding a protein of 701 aa  Accession AQM37674  *Very close relatives:*  PB1 of steelhead trout orthomyxovirus-1. Complete PB1 sequence. 99.14% identity over 100% amino acids  PB1 of rainbow trout orthomyxovirus-2. Partial (55%) PB1 sequence. 99.75% identity over this partial sequence  *Next relatives:*  PB1 of Wuhan carp isavirus 1 AVM87639.1 43.12% identity over 99% sequence  PB1 of Wuhan carp isavirus 2 AVM87640.1 43.26% identity over 96% sequence  PB1 of Salmon isavirus, ABG65761.1 42.14% identity over 99% sequence  Based on 99% identity in PB1 between rainbow trout and steelhead trout orthomyxoviruses, they should belong to the same species.  However, because PB1 is far away from the closest classified relative isavirus, this justify to create a new genus for the rainbow trout orthomyxovirus, named *Mykissvirus*, as proposed by Batts *et al.* who named it based on the species of the host of isolation, *Oncorhynchus mykiss,* and who also proposed the species of *Mykissvirus tructae.*(the species epithet is the singular genitive of Latin tructa (trout), the host of the virus).  The remaining 7 genes:  Segment 8, encoding M1 and M2  Putative M1, accession AQM37681.1, 207 aa  Closest relative: Putative M1 of steelhead trout orthomyxovirus-1. 98% identity over 99%  No other close relative, not even isaviruses  Putative M2, accession AQM37682.1, 235 aa  Closest relative: Putative M2 of steelhead trout orthomyxovirus-1. 94% identity over 100%  No other close relative, not even isaviruses  Segment 7, encoding NS1 and NEP  Putative NS1, accession AQM37679.1, 306 aa  Closest relative: Putative NS1 of steelhead trout orthomyxovirus-1. 98% identity over 42% (truncated NS1?)  No other close relative, not even isaviruses  Putative NEP, accession AQM37680.1, 143 aa  Closest relative: Putative NEP of steelhead trout orthomyxovirus-1. 96% identity over 100%  No other close relative, not even isaviruses  Segment 6, encoding HA  Putative HA, accession AQM37678.1, 464 aa  Closest relative: Putative HA of steelhead trout orthomyxovirus-1. 88% identity over 98%  No other close relative, not even isaviruses  Segment 5, encoding NA  NA, accession AQM37677, 480 aa  Closest relative: Putative NA of steelhead trout orthomyxovirus-1. 98% identity over 100%  Next relative: NA of influenza A/pintail/Primorie/625/76(H2N3), 25% identity over 62%  Segment 4, encoding PA  PA, accession AQM37676.1, 588 aa  Closest relative: PA of steelhead trout orthomyxovirus-1. 99% identity over 97%  Next relatives: PA of salmon isavirus, 32% identity over 99%  PA of pilchard orthomyxovirus, 29% identity over 99%  Segment 3, encoding NP  NP, accession AQM37675.1, 638 aa  Closest relative: NP of steelhead trout orthomyxovirus-1. 99% identity over 94%  Next relative: NP of salmon isavirus, 27% identity over 66%  No other close relative  Segment 1, encoding PB2  PB2, accession AQM37673, 727 aa  Closest relative: PB2 of steelhead trout orthomyxovirus-1. 99% identity over 99%  Next relative: PB2 of salmon isavirus, 32% of 99%  PA of pilchard orthomyxovirus, 32% identity over 97%  In summary, these two negative segmented RNA viruses, with 8 segments, fully sequenced, described as rainbow trout orthomyxovirus 1 and steelhead trout orthomyxovirus, are related to isaviruses, but far away enough to justify the establishment of a new orthomyxovirus genus.  The closest PB1 comes from Wuhan carp isavirus 1 and 02, but these viruses are not fully sequenced. | |

**Supporting evidence**

**Table of amino acid identity/coverage between PB1 segments of MykV with the different members of class *Insthoviricetes***

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Sequences used:

Tilapia virus: YP\_009246481.1

Influenza A virus: AAM75156.1

Influenza B virus: NP\_056657

Influenza D virus: AIO11638.1

Influenza C virus: AAF89738.2

Infectious salmon anemia virus: Q8V3T6.1

Johnston Atoll virus: YP\_009665204.1

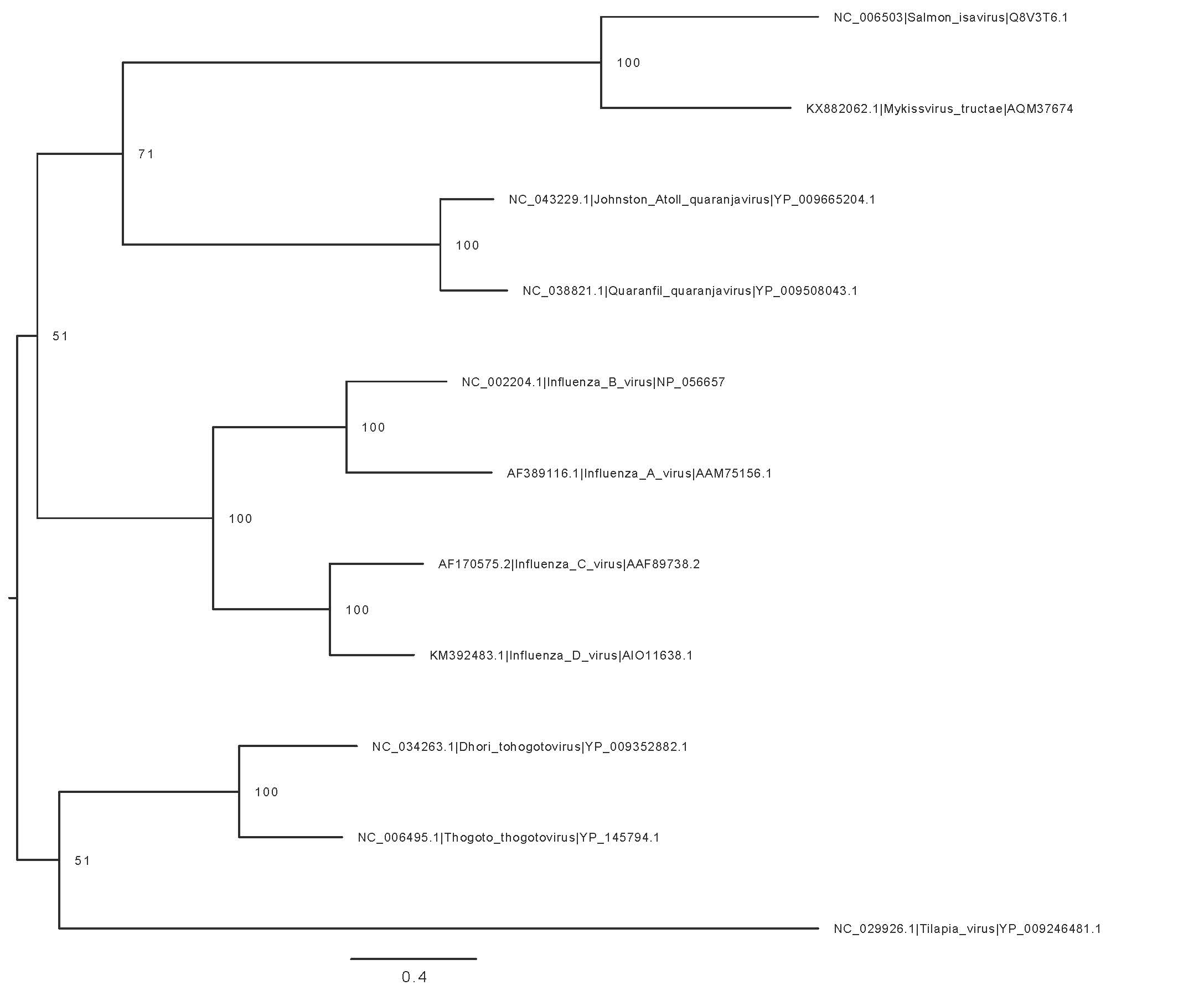
Quaranfil virus: YP\_009508043.1

Thogoto virus: YP\_145794.1

Dhori tvirus: YP\_009352882.1

Rainbow trout orthomyxovirus: AQM37674

**Figure 1. Phylogenetic tree of PB1 segments of MykV with the different members of class *Insthoviricetes***

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**References**

Batts WN, LaPatra SE, Katona R, Leis E, Ng TFF, Brieuc MSO, Breyta RB, Purcell MK, Conway CM, Waltzek TB, Delwart E, Winton JR (2017) Molecular characterization of a novel orthomyxovirus from rainbow and steelhead trout (*Oncorhynchus mykiss*). Virus Res 230: 38−49

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<https://doi.org/10.1016/j.virusres.2017.01.005>