

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

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| **Code assigned:** | **2021.011M** |  |
| **Short title:** Create one new genus and three new species (*Mononegavirales*: *Filoviridae*) | | |
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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 *Filoviridae* Study Group |

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

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**Submission dates**

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

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

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

**Name of accompanying Excel module**

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| 2021.011M.R.Filoviridae\_1ngen\_3nsp |

**Abstract**

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| We propose to establish one new filovirid genus, *Oblavirus*, including one new species (*Oblavirus percae*), and two new species in filovirid genus *Thamnovirus* (*Thamnovirus* *percae* and *Thamnovirus* *kanderense*). These three species are proposed to accommodate Oberland virus (OBLV), Fiwi virus (FIWIV), and Kander virus (KNDV), respectively, all of which were discovered by high-throughput sequencing in farmed European perch in Switzerland. |

**Text of proposal**

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| |  | | --- | | We discovered three new viruses in European Perch (*Perca fluviatilis* Linnaeus, 1758) in Switzerland by high-throughput sequencing and bioinformatics analysis (1). We named these viruses Fiwi virus (FIWIV; GenBank #MN510772), after the Centre for Fish and Wildlife Health (FIWI); Oberland virus (OBLV; GenBank #MN510773), after Bernese Oberland; and Kander virus (KNDV; GenBank #MW093492), after the Kander River, which flows through Bernese Oberland. The FIWIV genome sequence is coding-complete, whereas the genomic sequences of OBLV and KNDV are near-complete lacking short sequence stretches at the 5' terminus and at both 3' termini, respectively. However, all three sequences are sufficiently long to consider classification, encoding the canonical proteins found in members of the mononegaviral family *Filoviridae*: nucleoprotein (NP), polymerase cofactor (VP35), glycoprotein (GP1,2), transcriptional activator (VP30), and large protein (L) containing an RNA‑directed RNA polymerase (RdRp) domain, as well as 1–2 novel proteins (2-4) (Figure A).  Phylogenetic comparison of the FIWIV, OBLV, and KNDV genomic sequences (Figure B) and *L* gene sequences with those of representative classified viruses of the family *Filoviridae* (Figure C) confirmed genetic relationships of all three viruses to Huángjiāo virus (HUJV; *Filoviridae*: *Thamnovirus*). The current filovirus sequence-based genus and species demarcation criteria are ≥55% and ≥23% sequence divergence over coding/near-complete genome sequences using PAirwise Sequence Comparison (PASC) (3,5). We found a pairwise divergence of 49% compared to HUJV using the FIWIV genome sequence (Table), indicating that FIWIV is a member of a new thamnovirus species. The available KNDV genome sequence is 49% divergent from HUJV and 37% divergent from FIWIV (Table), suggesting that KNDV represents yet another novel thamnovirus species. In contrast, the OBLV genome sequence is more than 62% divergent from HUVJ, FIWIV, and KNDV.  Based on these results we propose:   1. to establish one new filovirid genus, *Oblavirus*, including one new species (*Oblavirus percae*), to accommodate OBLV; 2. to establish a new species in the filovirid genus *Thamnovirus*: *Thamnovirus percae,* to accommodate FIWIV; and 3. to establish a new species in the filovirid genus *Thamnovirus*: *Thamnovirus kanderense*, to accommodate KNDV.   **References***:*   1. Hierweger MM, Koch MC, Rupp M, Maes P, Di Paola N, Bruggmann R, Kuhn JH, Schmidt-Posthaus H, Seuberlich T. Discovery of the first freshwater fish filoviruses and hantaviruses. Submitted to Emerg Infect Dis. 2021. 2. M, Lin X-D, Chen X, Tian J-H, Chen L-J, Li K, et al. The evolutionary history of vertebrate RNA viruses. Nature. 2018 Apr;556(7700):197-202. 3. Kuhn JH, Amarasinghe GK, Basler CF, Bavari S, Bukreyev A, Chandran K, et al. ICTV virus taxonomy profile: *Filoviridae*. J Gen Virol. 2019 Jun;100(6):911-2. 4. Hume AJ, Mühlberger E. Distinct genome replication and transcription strategies within the growing filovirus family. J Mol Biol. 2019 Oct 4;431(21):4290-320. 5. Bào Y, Amarasinghe GK, Basler CF, Bavari S, Bukreyev A, Chandran K, et al. Implementation of objective PASC-derived taxon demarcation criteria for official classification of filoviruses. Viruses. 2017 May 11;9(5):106.   **Supporting information**  **Figure**  **A**  **G:\ITN\NeuroCenter\Forschung\Clinical_Neurovirology_group\Torsten\2020_Hierweger_NatComm\EID_2nd_prep\Figure_2A.tif**  **B**  **G:\ITN\NeuroCenter\Forschung\Clinical_Neurovirology_group\Torsten\2020_Hierweger_NatComm\EID_2nd_prep\Figure_2B.tif**  **C**  **G:\ITN\NeuroCenter\Forschung\Clinical_Neurovirology_group\Torsten\2020_Hierweger_NatComm\EID_2nd_prep\Figure_2C.tif** | |

**Figure: Three novel filoviruses in European perch.** A)Schematic representation of the genome organization of Fiwi virus (FIWIV), Oberland virus (OBLV), and Kander virus (KNDV) compared to Huángjiāo virus (HUJV): Open reading frames (ORFs) are indicated as colored arrows. ORFs encoding HUJV-like proteins (indicated as percentages) are depicted by the same color. Undetermined ORF starts and ends are shown as stripes. NP, nucleoprotein gene; VP35, polymerase cofactor gene; GP, glycoprotein gene; VP30, transcriptional activator gene; L, large protein gene. B) A maximum likelihood phylogenetic tree of the new filovirus genome sequences (bold blue) using coding-complete and near-complete genome sequences, or only C) L gene sequences, of representative members of the family *Filoviridae*. Numbers near nodes on the trees indicate bootstrap values. Branches are labeled by GenBank accession number, virus name, and virus name abbreviation in parenthesis. The names of unclassified, likely filoviruses are placed in quotation marks and printed without name abbreviations. The scale (bottom left) indicates the number of substitutions per site, reflected by the branch lengths.

**Table**

Pairwise distances of complete or coding-complete genome nucleotide sequences between the newly identified Fiwi virus (FIWIV), Huángjiāo virus (HUJV), and the closest related mammalian filovirus, Bombali virus (BOMV, GenBank #MK340750). Kander virus (KNDV) and Oberland virus (OBLV) near-complete sequences were compared based on the available sequences.

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| **Virus** | **FIWIV** | **OBLV** | **KNDV** | **HUJV** |  |
| **OBLV** | **66%** |  |  |  |  |
| **KNDV** | **37%** | **62%** |  |  |  |
| **HUJV** | **49%** | **64%** | **49%** |  |  |
| **BOMV** | **86%** | **87%** | **87%** | **86%** |  |