

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

|  |  |  |
| --- | --- | --- |
| **Code assigned:** | ***2023.025M*** |  |
| **Short title:** Create one new genus including one new species in family *Filoviridae* (*Mononegavirales*) |
|  |

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

|  |  |
| --- | --- |
| Seuberlich T, Kuhn JH, Schmidt-Posthaus H | torsten.seuberlich@unibe.ch; kuhnjens@mail.nih.gov; heike.schmidt@unibe.ch  |

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

|  |
| --- |
| University of Bern, Switzerland [TS, HSP]NIH/NIAID/DCR/Integrated Research Facility at Fort Detrick, USA [JHK] |

**Corresponding author**

|  |
| --- |
| Seuberlich T |

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

|  |
| --- |
| ICTV *Filoviridae* Study Group |

**ICTV Study Group comments and response of proposer**

|  |
| --- |
|  |

**ICTV Study Group votes on proposal**

|  |  |
| --- | --- |
| **Study Group** | **Number of members** |
| **Votes support** | **Votes against** | **No vote** |
| ICTV *Filoviridae* Study Group | 15 | 0 | 0 |

**Authority to use the name of a living person**

|  |  |
| --- | --- |
| **Is any taxon name used here derived from that of a living person (Y/N)**  | N |

|  |  |  |
| --- | --- | --- |
| **Taxon name** | **Person from whom the name is derived** | **Permission attached (Y/N)** |
| N/A | N/A | N/A |

**Submission dates**

|  |  |
| --- | --- |
| Date first submitted to SC Chair | 06/23/2023 |
| Date of this revision (if different to above) |  |

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

|  |
| --- |
|  |

**Part 2:** **NON-TAXONOMIC PROPOSAL**

**Text of proposal**

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

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

**Name of accompanying Excel module**

|  |
| --- |
| 2023.025M.N.v1.Filoviridae\_1ng\_1nsp.xlsx |

**Abstract**

|  |
| --- |
| We have determined the near-complete sequence of a genome of a new virus, Lötschberg virus (LTBV), in European perch (*Perca fluviatilis* Linnaeus, 1758) with sequence similarity to members of mononegaviral family *Filoviridae.* Based on sequence similarity data and the current demarcation criteria for filovirid taxa, we propose to establish a new filovirid genus (“*Loebevirus*”) including a new species (“*Loebevirus percae*”)*.* |

**Text of proposal**

|  |  |
| --- | --- |
|

|  |
| --- |
| By high-throughput sequencing, we obtained a scaffold of 13,584 nt with a GC content of 47.7% and an average depth coverage of 12.8× from RNA extracts of pooled organ samples of European perch (*Perca fluviatilis* Linnaeus, 1758) [1]. The sequence contains seven open reading frames ORFs (> 70 codons), organized similarly to those of filovirid oblaviruses and thamnoviruses, encoding filovirid-typical proteins: nucleoprotein (NP), polymerase co-factor (VP35), glycoprotein (GP1,2), transcriptional activator (VP30), and large protein (L)—plus two new proteins of unknown function. The 3' and 5' termini and the terminal ORFs remained incomplete (Table). We designated this new filovirus as Lötschberg virus (LTBV) [1]. Comparison of LTBV NP, VP35, GP, VP30, and L amino acid sequences with the homologous Fiwi virus, Huángjiāo virus, Kander virus, and Oberland virus proteins revealed 23–48% sequence identity. Pairwise Sequence Comparison (PASC; <https://www.ncbi.nlm.nih.gov/sutils/pasc/viridty.cgi?textpage=overview>) of the near-complete genome sequences indicates that LTBV is most closely related to thamnoviruses (up to 40% PASC similarity), which is also supported by phylogenetic analysis (Figure). Based on the current demarcation criteria for filovirid species (≥23% PASC divergence) and genera (≥55% PASC divergence) [2,3], LTBV represents a member of a new species and a new genus within the family *Filoviridae*. |

 |

**Supporting evidence**

Table: Comparison of the reported genomic sequence lengths and the length of the open reading frames (ORFs) of Lötschberg virus with those of related fish filovirids.

|  |  |  |
| --- | --- | --- |
| **Virus** | **Reported genomic sequence length (nt)** | **Open reading frame (ORF) length (nt)** |
| **ORF 1** | **ORF 2****(NP)** | **ORF 3****(VP35)** | **ORF 4** | **ORF 5****(GP1,2)** | **ORF 6****(VP30)** | **ORF 7****(L)**  |
| Lötschberg virus | 13,584*a* | 336*b* | 1200 | 1680 | 294 | 1800 | 1206 | 6215*b* |
| Oberland virus | 14,682*a* | 466*b* | 1200 | 1968 | 957 | 1263 | 1152 | 6656*b* |
| Kander virus | 13,849*a* | 654*b* | 1206 | 1665 | 279 | 1791 | 1374 | 6373*b* |
| Fiwi virus | 13,764 | 468 | 1203 | 1662 | 276 | 1860 | 1077 | 6435 |
| Huangjao virus | 14,280 | 666 | 1215 | 1686 | 273 | 1881 | 1185 | 6441 |

anear-complete genome sequence

*b*incomplete open reading frame

Figure: Phylogenetic position of Lötschberg virus (LTBV) in the mononegaviral family *Filoviridae*. The neighbor-joining tree was built based on near-complete genome sequences and inferred with the Geneious (Biomatters) consensus tree builder (Jukes-Cantor model; 5,000 bootstraps). GenBank accession numbers are indicated for each sequence at branch tips.



**References**

1 Seuberlich T, Kuhn JH, Schmidt-Posthaus H (2023) Near-complete genome sequence of

Lötschberg virus (*Mononegavirales*: *Filoviridae*) identified in European perch (*Perca fluviatilis* Linnaeus, 1758). Microbiol Resour Announc 12(4):e0002823.

2. Bào Y, Amarasinghe GK, Basler CF, Bavari S, Bukreyev A, Chandran K, Dolnik O,

Dye JM, EbiharaH, Formenty P, Hewson R, KobingerGP, Leroy EM, Mühlberger

E, Netesov SV, Patterson JL, Paweska JT, Smither SJ, Takada A, Towner JS,

Volchkov VE, Wahl-Jensen V, Kuhn JH (2017) Implementation of objective

PASC-derived taxon demarcation criteria for official classification of filoviruses.

Viruses 9:106.

3. Kuhn JH, Amarasinghe GK, Basler CF, Bavari S, Bukreyev A, Chandran K,

Crozier I, Dolnik O, Dye JM, Formenty PBH, Griffiths A, Hewson R, Kobinger

GP, Leroy EM, Mühlberger E, Netesov SV, Palacios G, Pályi B, Pawęska JT,

Smither SJ, Takada A, Towner JS, Wahl V, ICTV Report Consortium (2019) ICTV

virus taxonomy profile: *Filoviridae*. J Gen Virol 100:911–912.