

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

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| **Code assigned:** | ***2022.017M*** |  |
| **Short title:** Create a new species in genus *Orthobunyavirus* (*Bunyavirales*: *Peribunyaviridae*) | | |
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**Author(s) and email address(es)**

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| Xia H |

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

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| ICTV *Peribunyaviridae* Study Group |

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

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| Approved. |

**ICTV Study Group votes on proposal**

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| --- | --- | --- | --- |
| **Study Group** | **Number of members** | | |
| **Votes support** | **Votes against** | **No vote** |
| ICTV *Peribunyaviridae* Study Group | 8 | 0 | 1 |

**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)** |
|  |  |  |

**Submission dates**

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| --- | --- |
| Date first submitted to SC Chair | May 27, 2022 |
| 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**

|  |
| --- |
| 2022.017M.N.v1.Orthobunyavirus\_1nsp.xlsx |

**Abstract**

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| The family *Peribunyaviridae* includes four genera: *Herbevirus*, *Orthobunyavirus*, *Pacuvirus*  and *Shangavirus.* Here we propose to create one new species in genus *Orthobunyavirus* for Ebinur Lake virus. |

**Text of proposal**

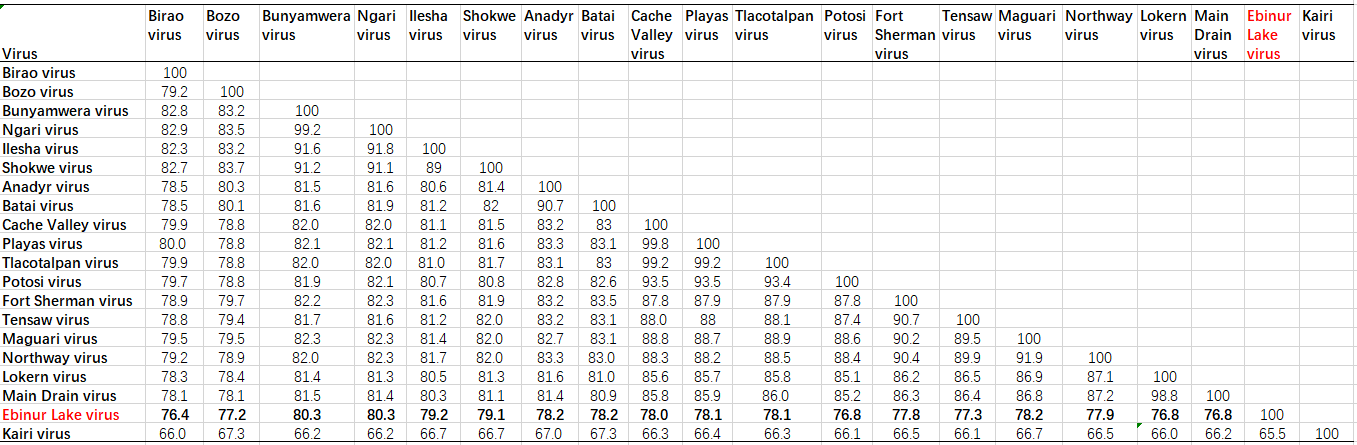
|  |  |  |
| --- | --- | --- |
| |  |  | | --- | --- | | Ebinur Lake virus (EBIV) isolate Cu20-XJ was originally isolated from *Culex modestus* Ficalbi, 1889 mosquitoes in 2013 in Xinjiang Province, China [[1](#_ENREF_1)]. Mature spherical, enveloped virions of approximately 90–100 nm in diameter were detected in pellets generated by ultracentrifugation of EBIV-infected BHK-21 cell culture supernatants, which were structurally similar to those of other members of the genus *Orthobunyavirus*.  The full-length large (L) segment sequence (GenBank #KJ710425) of EBIV is 6,799 nucleotides long encoding a predicted large (L) protein including a RNA-directed RNA polymerase (RdRp) domain of 2,238 amino acids, starting at nucleotide position 47 and including 36 nucleotides of the 3′ noncoding region. The entire medium (M) segment sequence (GenBank #KJ710423) of EBIV is 4,422 nucleotides long encoding a predicted glycoprotein (GP) precursor of 1,435 amino acids. The full-length small (S) segment sequence (GenBank #KJ710424) of EBIV is 973 nucleotides long encoding a predicted nucleoprotein (NP) of 233 amino acids (Table 1).  The phylogenetic results of all three segments demonstrate that EBIV belongs to the peribunyaviral genus *Orthobunyavirus* and clusters with the members of the Bunyamwera serogroup (Figure 1A–C). The nucleotide identity analysis matrix, based on the selected viruses, indicates that the S segment has the highest identity, whereas the M segment has the lowest identity within the Bunyamwera serogroup. The S, M, and L segments of EBIV share the highest sequence similarity with those of Germiston virus (90.7%), Germiston virus (77.3%), and Bunyamwera virus (72.7%), respectively (Figure 1D–F). Amino acid similarity analysis indicated that the amino acid sequences of NP and GP of EBIV have the highest similarity with Germiston virus at 95.7% and 89.0%. In addition, the L segment amino acid identity is less than 96% when compared to other orthobunyaviruses (Table 2).  EBIV can replicated efficiently and cause cytopathic effects (CPEs) in invertebrate and vertebrate cells. EBIV causes severe disease and even death in exposed adult Kunming and BALB/c laboratory mice, and antibodies against EBIV have been detected in local residents, indicating that the virus is a potential animal or human pathogen [[2](#_ENREF_2), [3](#_ENREF_3)].  Based on the morphology of virions, phylogeny, and characteristics of the Infection *in vivo* and *in vitro*, we propose to classify EBIV as a representative of a new orthobunyaviruses species. |  | |

**Supporting evidence**

**Table 1.** Features of the CDSs encoded by Ebinur Lake virus strain Cu20-XJ

|  |  |  |  |  |
| --- | --- | --- | --- | --- |
| Segment | CDS | Start (nt) | Stop (nt) | Length (nt | aa) |
| S | NP | 86 | 787 | 702 | 234 |
| M | GP | 53 | 4360 | 4308 | 1436 |
| L | L | 47 | 6763 | 6717 | 2239 |

**Table 2**. L segment amino acid identity matrix of representative orthobunyaviruses (%).



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**Figure 1.** Maximum likelihood phylogenetic trees (A–C) and pairwise distance (D–F) based on alignments of nucleotide sequences of orthobunyaviruses. The scale bar indicates the evolutionary distance in the number of substitutions per nucleotide substitution/site, and the principal bootstrap support levels are indicated. Branches are color coded according to group. Ebinur Lake virus is indicated by a red square, and Herbert virus (peribunyaviral genus *Herbevirus*) was used as an outgroup in the ML trees.

**References**

1. Liu R, Zhang G, Yang Y, Dang R, Zhao T (2014) Genome sequence of abbey lake virus, a novel orthobunyavirus isolated from china. Genome Announc 2. PMID: 24948753. PMCID: PMC4064019. doi: 10.1128/genomeA.00433-14.

2. Xia H, Liu R, Zhao L, Sun X, Zheng Z, Atoni E, Hu X, Zhang B, Zhang G, Yuan Z (2019) Characterization of Ebinur Lake Virus and Its Human Seroprevalence at the China-Kazakhstan Border. Front Microbiol 10:3111. PMID: 32082268. PMCID: PMC7002386. doi: 10.3389/fmicb.2019.03111.

3. Zhao L, Luo H, Huang D, Yu P, Dong Q, Mwaliko C, Atoni E, Nyaruaba R, Yuan J, Zhang G, Bente D, Yuan Z, Xia H (2020) Pathogenesis and Immune Response of Ebinur Lake Virus: A Newly Identified Orthobunyavirus That Exhibited Strong Virulence in Mice. Front Microbiol 11:625661. PMID: 33597934. PMCID: PMC7882632. doi: 10.3389/fmicb.2020.625661.