

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

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| **Code assigned:** | **2021.027M** |  |
| **Short title:** Create three new genera (*Khurdivirus*, *Lakivirus* and *Lambavirus*) including three new species (*Bunyavirales*: *Peribunyaviridae*) | | |
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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 *Peribunyaviridae* Study Group |

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

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| N/A |

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

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

**Submission dates**

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| Date first submitted to SC Chair | 5/28/2021 |
| Date of this revision (if different to above) | 9/17/2021 |

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

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| * would like for the rationale/demarcation criteria for defining new genera/species to be more clearly spelled out in the proposal—a sentence or two.   Response: Species demarcation cannot yet be established as all three proposed genera are currently monospecific (only one virus is assigned to each. A paragraph on genus demarcation criteria has been added to the text as requested.   * in the word file the name of accompanying excel is 026, not 027   Response: The Excel file names was corrected.   * 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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| 2021.027M.R.Peribunyaviridae\_3ngen\_3nsp |

**Abstract**

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| We propose three new genera (*Khurdivirus, Lakivirus*, and *Lambavirus*) to be included in the family *Peribunyaviridae.* Viruses proposed to be classified in these new genera have unique hosts, genome features, and phylogenetic placements. |

**Text of proposal**

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| |  | | --- | | Genus *Khurdivirus*, including one species, *Khurdivirus volgaense*,is proposed for Khurdun virus (KHURV) isolated in 2001 from a Eurasian coot (*Fulica atra* Linnaeus, 1758) in Astrakhan Oblast, Russia. The virus was named after the Khurdun (Хурдун) distributary within the Volga River delta [1]. KHURV has a tripartite genome consistent with the genomic organization of peribunyavirids. The proteins expressed form the KHURV genome included the large (L) protein with its RNA-directed RNA polymerase (RdRp), glycoprotein N (GN) and glycoprotein C (GC), and the nucleoprotein (NP). Although the KHURV genome has complementary terminal ends identical to those found in orthobunyavirus genomes, KHURV does not encode the non-structural M (NSm) protein that is encoded by all known orthobunyaviruses. Additionally, phylogenetic inference using the L sequence (Figure 1) places KHURV basal to the viruses of genera *Orthobunyavirus* and *Pacuivirus.* This phylogenetic inference is similar to one previously reported using KURV’s M and S segment sequences [2].  Etymologies of proposed taxa:   * *Khurdivirus*: derived from Khurdun virus * *Khurdivirus volgaense*: singular genitive of Volga, a reference to the Volga River delta.   Genus *Lakivirus*,including one species, *Lakivirus lakamhaense* is proposed for Lakamha virus (LAKV) identified in a *Wyeomyia complosa* (Dyar, 1928)mosquito from Palenque, Mexico. The virus was named after Lakamha, the historical name of Palenque [2]. LAKV has a tripartite genome consistent with the genomic organization of peribunyavirids. LAKV does not encode the non-structural proteins NSs or NSm, and has a truncated M open-reading frame, similar to ORFs found in peribunyavirid herbeviruses. However, the LAKV genomic termini are similar to those of orthobunyavirus genomes. Phylogenetic inference using the LAKV L segment sequence (Figure 1) places LAKV basal to the viruses of genus *Herbivirus,* similar to previous reports [2].  Etymologies of proposed taxa:   * *Lakivirus*: derived from Lakamha virus * *Lakivirus lakamhaense*: singular genitive of Lakhama.   Genus *Lambavirus*, including one species, *Lambavirus wisconsinense*,is proposed for largemouth bass bunyavirus (LBBV). LBBV is the first virus with peribunyavirid features to be isolated from a fish. It was detected in largemouth bass (*Micropterus salmoides* (Lacépède, 1802)) sampled in the upper Mississippi River near Prairie du Chien, Wisconsin, USA [3]. LBBV has a tripartite genome consistent with the genomic organization of peribunyavirids, but the LBBV complementary genomic termini are unique. Each genomic segment has features similar to those of peribunyavirids,including the RdRp motifs, GN and GC, and a NP. LBBV does not encode NSs or NSm, similar to herbiviruses. Phylogenetic inference using the L sequence (Figure 1) places LBBV basal to all described peribunyavirids with strong bootstrap support, while distinguishing the virus from viruses of other bunyaviral families*.*  Etymologies of proposed taxa:   * *Lambavirus*: derived from Largemouth bass bunyavirus * *Lambavirus wisconsinense:* the singular genitive referring to Wisconsin.   Genus demarcation criteria:  Presently, genus inclusion criteria include forming a phylogenetic clade with viruses within an established genus and presence of genetic features (e.g., presence or absence of NSm). The viruses of the proposed genera, *Khurdivirus* and *Lambavirus*, form paraphyletic clades with the viruses of established genera, suggesting these new viruses represent new genera. The proposed genus *Lakivirus*, forms a clade with genus *Herbevirus*; however, the viruses of the proposed genus share genetic features with viruses of both genera *Herbevirus* and *Orthobunyavirus.* LAKV shares less amino acid identity to genus *Herbevirus* (35.9%),than the orthobunyaviruses share with pacuviruses (47%) (Table), suggesting LAKV virus is genetically distinct from established genera. | |

**Supporting evidence**

**Figure 1. Maximum likelihood phylogenetic inference of proposed new peribunyavirid genera compared to representative bunyavirals.** The deduced amino acid sequences of L segment open reading frames were aligned using ClustalW in MEGA v7. Phylogenies were inferred using IQ-Tree with the JTT+I+G F4 model, which was determined by model selection in IQ-Tree, and bootstrapping support of 5,000 replicates. The viruses representing proposed new genera are indicated with black circles. Branches are labeled with virus names and GenBank accession numbers. Branch lengths are drawn to scale with the scale bar indicating amino acid substitutions.

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**Table. Average percent identity between established genera and proposed genera of the family *Peribunyaviridae.*** The deduced amino acid sequences from the L segment of viruses within each genuswere aligned using ClustalW, and precent identities were calculated. Viruses were assigned to groups based on the respective genus, and between group p-distances were computed after deletion of missing data using MEGA v7. The analysis included 74 viruses comprising *Orthobunyavirus,* 3 viruses from *Herbevirus,* 5 viruses from *Pacuivirus,* and single virus representatives from *Shangavirus,* and the proposed *Lambavirus, Lakivirus, and Khurdivirus.*

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|  | *Lambavirus* | *Khurdivirus* | *Lakivirus* | *Shangavirus* | *Herbevirus* | *Pacuvirus* |
| *Lambavirus* |  |  |  |  |  |  |
| *Khurdivirus* | 25.34 |  |  |  |  |  |
| *Lakivirus* | 22.86 | 32.11 |  |  |  |  |
| *Shangavirus* | 20.06 | 25.71 | 24.37 |  |  |  |
| *Herbevirus* | 24.67 | 32.44 | 35.92 | 23.56 |  |  |
| *Pacuvirus* | 23.02 | 33.41 | 29.41 | 24.28 | 28.68 |  |
| *Orthobunyavirus* | 23.03 | 33.41 | 29.58 | 24.85 | 28.72 | 47.09 |

**References**

1. Альховский СВ, Щетинин АМ, Львов ДК, Щелканов МЮ, Дерябин ПГ, Львов ДН, Самохвалов ЕИ, Гительман АК, Ботиков АГ (2013) Вирус Хурдун (KHURV): новый вирус рода *Orthobunyavirus* (*Bunyaviridae*). Вопр вирусолог 58:10-13

2. Kopp A, Hübner A, Zirkel F, Hobelsberger D, Estrada A, Jordan I, Gillespie TR, Drosten C, Junglen S (2019) Detection of two highly diverse peribunyaviruses in mosquitoes from Palenque, Mexico. Viruses 11:832

3. Waltzek TB, Subramaniam K, Leis E, Katona R, Ng TFF, Delwart E, Barbknecht M, Rock K, Hoffman MA (2019) Characterization of a peribunyavirus isolated from largemouth bass (*Micropterus salmoides*). Virus Res 273:197761