

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

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| **Code assigned:** | ***2023.031M*** |  |
| **Short title:** Create five new species in genus *Orthobunyavirus (Bunyavirales: Peribunyavirdae),* and create one new peribunyavirid genus, *Gryffinivirus,* including two species | | |
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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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**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 | 9 | 0 | 0 |

**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 |

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

**Submission dates**

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| Date first submitted to SC Chair | June 23, 2023 |
| Date of this revision (if different to above) |  |

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

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

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| N/A |

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

**Name of accompanying Excel module**

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| 2023.031M.N.v1.Peribunyaviridae\_1ng\_7nsp.xlsx |

**Abstract**

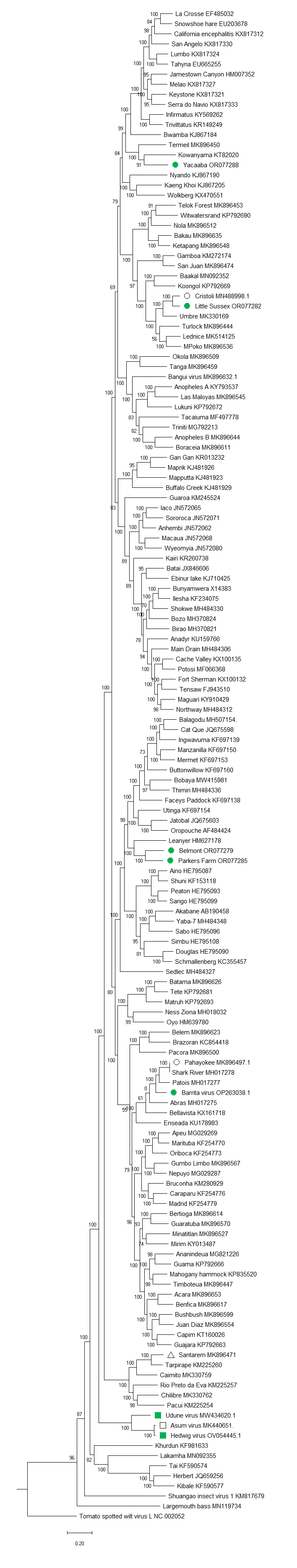
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| We propose the creation of five new species in the genus *Orthobunyavirus,* and the creation of genus *Gryffinivirus* including two species, within family *Peribunyaviridae.* |

**Text of proposal**

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| |  | | --- | | The genomes of several historical peribunyavirus isolates were recently sequenced, in addition to the description of newly recognized viruses. This proposal evaluated the taxonomic positions of Belmont, Little Sussex, Yacaaba, Barrita, Pahayokee, Parker’s Farm, and Cristoli viruses (genus *Orthobunyavirus*) (Table 1); Santarém virus (genus *Pacuvirus*) (Table 2); and Hedwig, Asum, and Udune viruses (Table 3). Here we propose the creation of five new species in genus *Orthobunyavirus,* and the creation of a new genus with two species in family *Peribunyaviridae* (Figure 1).  In genus *Orthobunyavirus,* Belmont [3], Parker’s Farm [4], Little Sussex [4], Yacaaba [7], and Barrita [5] viruses have less than 96% pairwise identity of the L protein amino acid sequence to any known orthobunyavirid (Table 1). These viruses are representatives of the proposed species:   * *Orthobunyavirus belmontense,* proposed for Belmont virus (BELV). Named after Belmont, Australia where the exemplar virus was isolated in 1968 from a pool of common banded mosquitoes (culicid *Culex annulirostris* Skuse, 1889). * *Orthobunyavirus parkeri,* proposed for Parker’s Farm virus (PFV). Named after the farm in Queensland, Australia where the exemplar virus was isolated in 1976 from a pool of common banded mosquitoes (culicid *Culex annulirostris* Skuse, 1889). * *Orthobunyavirus sussexense*, proposed for Little Sussex virus (LTLSV). Named after Sussex inlet, Australia, isolated in 1976 from a pool of (culicid *Culex annulirostris* Skuse, 1889). Cristoli virus was isolated in 2018 from a fatal case of encephalitis in France [9]. This virus was found to have less than 96% pairwise amino acid identity to Little Sussex virus L protein and is considered an LTLSV isolate. * *Orthobunyavirus yacaabaense*,proposed for Yacaaba virus (YACV). Named after Mount Yacaaba in New South Wales, Australia, near where the exemplar virus was isolated in 1970 from a pool of mosquitoes (culicid *Ochlerotatus vigilax* (Skuse, 1889). * *Orthobunyavirus barritaense*, proposed for Barrita virus (BITV). Named after Barrita de Pajón in Mexico where the exemplar virus was isolated from a pool of mosquitoes (culicid *Psorophora varipes* (Coquillett, 1904)) in 2007 [5].   Pahayokee virus (PAHV) was isolated in 1967 from a pool of *Culex* mosquitoes in Florida, USA [6]. The PAHV L protein was found to have greater than 96% pairwise amino acid identity to Shark River virus (species *Orthobunyavirus squalofluvii)* L protein and hence is an isolate of Shark River virus*.*  Santarém virus (STMV) (genus *Pacuvirus*) was isolated from *Oryzomys* rodents in 1973 near Santarém, Brazil. The virus has also been isolated from sandflies (psychodid *Lutzomyia (Nyssomyia) carrerai,* (França, 1924)) [2]. The concatenated genomes of pacuviruses were compared to STMV (Table 2). STMV has less than 0.1 pairwise evolutionary distance (PED) to Tapirapé virus (species *Pacuvirus tapirapeense*) and hence is considered a isolate of Tapirapé virus*.*  Genus *Gryffinivirus* is proposed with two representative species. Hedwig virus (HEDV) was isolated in 2018 from a captive snowy owl (strigid *Bubo scandiacus* (Linnaeus, 1758)) in Germany [10]. HEDV shares similar genetic characteristics with peribunyavirids, including the tripartite genome with small (S), medium (M), and large (L) segments of negative-sense RNA. The S segment encodes a putative nonstructural protein (NSs) upstream of the nucleoprotein (NP) gene. The M segment encodes another nonstructural protein (NSm) and the glycoproteins Gn and Gc, and the L segment encodes a large protein (L) with N terminal endonuclease and central RNA-directed RNA polymerase (RdRp) domains. However similar, the HEDV M segment does not encode the conserved Gn C terminus (VAKI306) found in other orthobunyaviruses and pacuviruses and is unique compared to herbeviruses and shangaviruses. Additionally, the Gc C-terminal protein contains a 26–35 amino-acid-residue insertion. Asum virus, was identified using high-throughput sequencing. L segment sequences were described from a pool of mosquitoes (culicid *Culex pipiens*,Linnaeus, 1758) sampled in Kristianstand, Sweden in 2006 [8]. Although Asum virus sequences have been identified in several pools of *Culex* mosquitoes, no viral isolates nor complete coding sequences from a single source have been described. Udune virus (UDNV) is the representative of the second proposed species in this new genus. UDNV was identified using high-throughput sequencing in a single mosquito (*Culex pipiens*,Linnaeus, 1758)sampled in 2017 California, USA [1]. Phylogenetic inference of HEDV, Asum, and UDNV show a distinct new branch basal to viruses of the genus *Pacuvirus* (Figure 1). Pairwise percent identities were calculated for the L segment amino acid sequences aligned with Clustal W (Table 3), showing high divergence between UDNV and HEDV, with Asum virus closely related to HEDV. We propose a new genus be created including two species, using the demarcation criteria of <90% amino acid pairwise percent identity of the L segment.  Genus *Gryffinivirus,* including two species:  Name inspired by the fictional character Gryffindor.  *Gryffinivirus hedwigae* is proposed for Hedwig virus (HEDV).  Named for the exemplar virus Hedwig virus isolated from a snowy owl and named inspired by the fictional owl Hedwig. Asum virus is now considered an isolate of HEDV.  *Gryffinivirus alamedaense* is proposed for Udune virus (UDNV).  Named after Alameda, California, USA, where the virus was discovered. | |

**Supporting evidence**

**Figure 1. Maximum likelihood tree depicting the relationships of the L segment of peribunyavirids.** Species-representative viruses are listed by virus name and GenBank accession number. Viruses included in this proposal are labeled with a shape by the taxon name, solid green shapes are proposed new species, open shapes are new strains of species. Orthobunyaviruses are labeled with circles, pacuviruses are labeled with triangles, and those of the proposed new genus *Gryffinivirus* are labeled with squares.

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**Table 1. Percent identity of the L protein amino acid sequences of orthobunyaviruses.** L amino acid sequences were aligned with Clustal W in Mega X and p-distances were calculated with pairwise deletion. Sequences with greater than 96% pairwise identity are highlighted red and considered representatives of the same species. The percent identity matrix is embedded, please double-click to open entire sheet.

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**Table 2. Pairwise evolutionary distances of concatenated pacuvirus genome segment sequences.** The L, M, and S segment coding regions were concatenated and codon aligned with Clustal W. Pairwise evolutionary distances (PED) were calculated for the amino acid sequences using the WAG model. PED values of less the 0.1 are highlighted red and indicate representatives of the same species. The PED matrix is presented in an embedded excel file, please double-click to open entire sheet.

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**Table 3. Percent identity of the L protein amino acids of viruses of the proposed genus *Gryffinivirus.*** The L segment amino acid sequences were aligned with Clustal W in Mega X. Pairwise p-distances were calculated. Viruses with greater than 90% identity are highlighted in red and proposed to be representatives of the same species.

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