

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

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| **Code assigned:** | ***2022.018M*** |  |
| **Short title:** Create 29 new species and abolish 4 species in the genus *Orthobunyavirus* (*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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| 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**

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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)** |
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**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**

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| 2022.0x18M.N.v1.Orthobunyavirus\_29nsp\_abolish4sp.xlsx |

**Abstract**

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| Here we propose 29 new species, following the standardized binomial naming format, and propose the abolition of 4 species of genus *Orthobunyavirus* (*Peribunyaviridae*). |

**Text of proposal**

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| Recent studies, including high-throughput sequencing and discoveries of novel orthobunyaviruses [1-5], have contributed a vast amount of genetic knowledge to the public domain. Given these contributions, the majority of orthobunyaviruses now have fully described genomes allowing for demarcation of species using genetic identity and phylogenetic inference. Historically these viruses were still assigned to species using previous serological criteria. The proposal described herein evaluated the sequences of 150 orthobunyavirus genomes. The genomes of the serological groups Acará, Akabane, Alajuela, Anopheles A, Anopheles B, Bakau, Batama, Bellavista, Bertioga, Bimiti, Bunyamwera, Bushbush, Buttonwillow, Caraparú, Catú, Enseada, Fort Sherman, Gamboa, Koongol, Macauã, Main Drain, Marituba, Minatitlán, M’Poko, Oriboca, Thimiri, Timboteua, Turlock, as well as 14 unclassified orthobunyaviruses were evaluated using the full-length amino acid sequences of the L protein. The sequences were codon aligned in MEGA v7. The percent identities were calculated using the p-distance algorithm of the L protein amino acids with deletion of all missing data. Phylogenies were inferred with maximum likelihood trees using the LG+G+I+F substitution model and bootstrap confidence of 1,000 replicates supported the percent identity demarcations (Figure 1). The current species demarcation criterium for genus *Orthobunyavirus* (*Peribunyaviridae*) is <96% L amino acid sequence identity among member viruses. Application of this criterion (Table 1) confirms the previously recognized 22 species in the genus and indicates the need for 29 new species and abolition of 4 species. |

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**Supporting evidence**

**Table 1. Percent Identities of the genus *Orthobunyavirus***

The sequences of the complete open reading frame of the L segments were codon aligned in MEGA v7. The percent identities were calculated using the p-distance algorithm of the L protein amino acids with deletion of all missing data. Percent identities were calculated in excel (100\*(1-pdist)) and cells highlighted red indicate >96% identity and therefore are viruses within the same species. The Excel sheet is embedded, double-click to open the full spreadsheet. Viruses are labeled by common name and GenBank accession number of the L segment.

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**Figure 1. Phylogenetic inference of the genus *Orthobunyavirus*.** Open reading frames of the complete L segment were codon aligned in MEGA v. 7 using Clustal W. Amino acid sequences were used for maximum likelihood inference using the substitution model LG+G+I+F as determined using model test with removal of missing data. Bootstrap values of 1,000 replicates are indicated on each branch. Scale bar indicates amino acid substitutions per site. Viruses are labeled with common names and GenBank accession number of the L segment. All sequences evaluated in this proposal are labeled with a circle. Black circles = exemplar viruses of a current species. Green circles = exemplar virus representative of proposed new species. Red circles = exemplar virus representatives of proposed abolished species. White circles = non-exemplar virus strains

**References**

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4. Shifman O, Cohen-Gihon I, Beth-Din A, Zvi A, Laskar O, Paran N, Epstein E, Stein D, Dorozko M, Wolf D, Yitzhaki S, Shapira SC, Melamed S, Israeli O (2019) Identification and genetic characterization of a novel *Orthobunyavirus* species by a straightforward high-throughput sequencing-based approach. Sci Rep 9:3398. DOI: 10.1038/s41598-019-40036-4

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