

The International Committee on Taxonomy of Viruses

Taxonomy Proposal Form, 2024

**Part 1a: Details of taxonomy proposals**

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| **Title:** | Create one new species in the genus Mammarenavirus(*Hareavirales*: Arena*viridae*] | |
| **Code assigned:** | 2024.009M.N.v1.Mammarenavirus\_1nsp |

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**Part 1b: Taxonomy Proposal Submission**

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| **ICTV Subcommittee:** | | | |
| Animal DNA Viruses and Retroviruses |  | Bacterial viruses |  |
| Animal minus-strand and dsRNA viruses | **X** | Fungal and protist viruses |  |
| Animal positive-strand RNA viruses |  | Plant viruses |  |
| Archaeal viruses |  | General - |  |

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| **List the ICTV Study Group(s) that have seen or have been involved in creating this proposal:** |
| Arenaviridae Study Group |

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| **Optional – complete only if formally voted on by an ICTV Study Group:** | | | |
| **Study Group** | **Number of members** | | |
| **Votes in support** | **Votes against** | **No vote** |
| ASG | 10 | 0 | 0 |
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| **Submission date:** | 24/05/2024 |

**Part 1c: Feedback from ICTV Executive Committee (EC) meeting**

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| **Executive Committee Meeting Decision code:** | **X** |
| A – Accept |  |
| Ac – Accept subject to revision by relevant subcommittee chair. No further vote required |  |
| U – Accept without revision but with re-evaluation and email vote by the EC |  |
| Uc – Accept subject to revision and re-evaluation and email vote by the EC |  |
| Ud – Deferred to the next EC meeting, with an invitation to revise based on EC comments |  |
| J - Reject |  |
| W - Withdrawn |  |

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| **Comments from the Executive Committee:** |
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**Part 1d: Revised Taxonomy Proposal Submission**

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| **Response of proposer:** |
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| **Revision date:** | DD/MM/YYYY |

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

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| **Name of accompanying Excel module:** |
| 2024.009M.N.v1.Mammarenavirus\_1nsp.xlsx |

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| **Taxonomic changes proposed:** | | | |
| Establish new taxon | **X** | Split taxon |  |
| Abolish taxon |  | Merge taxon |  |
| Move taxon |  | Promote taxon |  |
| Rename taxon |  | Demote taxon |  |
| Move and rename |  |

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| **Is any taxon name used here derived from that of a living person:** | | **N** |
| **Taxon name** | **Person from whom the name is derived** | **Attached X** |
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| **Abstract of Taxonomy Proposal:** |
| *Taxonomic rank(s) affected*: *Hareavirales*: *Arenaviridae*: *Mammarenavirus*  *Description of current taxonomy*: Eleven genomes representing four species of American *Mammarenavirus* clade C were present in public records. An additional 13 clade C Mammarenavirus genomes were added to public records following the sequencing of *Mammarenavirus*-positive rodent samples collected in Argentina from 1990-2020.  *Proposed* *taxonomic change(s):* Establishment of one new species in genus *Mammarenavirus* for a new virus named vello virus, identified following the sequencing of *Mammarenavirus*-positive rodent samples collected in Argentina from 1990-2020.  *Justification*: Two of the L segment sequences of 13 clade C mammarenavirus genomes identified following the sequencing of mammareanvirus-positive rodent samples collected in Argentina from 1990-2020, meet current demarcation species criteria for genus *Mammarenavirus*. We propose the two isolates described by Shedroff and Martin et al. to represent one new virus named *“*vello virus*”* and to assign vello virus to a new species, *Mammarenavirus* vello. |

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| **Text of Taxonomy proposal:** |
| *Proposed* *taxonomic change(s)*: Addition of a new species to genus *Mammarenavirus*  The current *Mammarenavirus* species demarcation thresholds require less than 80% S segment nucleotide identity and less than 76% L segment nucleotide identity [1]. The described vello virus genomes described by Shedroff and Martin et al. exhibit 70.8% L segment nucleotide identity to their closest ancestor, indicating that by L segment diversity, they may be characterized as representing a novel virus belonging to a new species (Table 1-2). Additionally, pairwise sequence comparison (PASC) indicated 69.35% nucleotide identity to Oliveros virus (GenBank accession AY216514), the closest ancestor to vello virus. This relationship is supported by phylogenetic analysis which suggests a distinct clade containing genomes that differ from the *Mammarenavirus oliverosense* clade(Figure 1-2)*.* The proposed species currently satisfies species demarcation criteria for the L segment, however it does not meet the S segment or nucleoprotein demarcation criteria (Table 2) [2]. In previous cases where a virus satisfies criteria for only one segment, the ICTV *Arenaviridae* Study Group (ASG) reports that the L segment dissimilarity has been a deciding factor [3]. We propose the two isolates described by Shedroff and Martin et al. to represent one new virus named *“*vello virus*”* and to assign vello virus to a new species, *Mammarenavirus* vello. The classification of this virus as a member of a novel species is also supported by its association with bolo mice (*Necromys lasiurus*) in the northern provinces of Argentina. Additionally, phylogenetic analysis of American mammarenavirusesreveals strong bootstrap values to support a distinct “vello virus” sister lineage sharing a common ancestor with all other clade C *Mammarenaviruses* (Figure 1). Vello virus originates from Oliveros, Argentina. As the species name *Mammarenavirus oliverosense* is already in use, we propose to name the new species “*Mammarenavirus vello*” for vello virus. The term “vello” describes the fur on a mouse’s tail. Various types of bolo mouse (members of genus *Necromys*) can serve as the natural reservoir for this virus. |

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| **References:** |
| 1. Radoshitzky, S.R., et al., *ICTV Virus Taxonomy Profile: Arenaviridae 2023.* J Gen Virol, 2023. **104**(9), 2.  2. Shedroff, E., et al., *Novel Oliveros-like Clade C Mammarenaviruses from Rodents in Argentina, 1990–2020.* Viruses, 2024. **16**(3): p. 340.  3. Kuhn, J.H., *Personal Communication*. 2023. |

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| **Tables, Figures** |



Figure 1. Inferred phylogenetic relationships generated by maximum likelihood using partial Mammarenavirus L nucleotide segments (1744/7472 bp). Major clades are labeled (A–B through C), and minor clades in Clade C are highlighted, trees are midpoint rooted, and bootstrap support (n = 1000 iterations) is highlighted in red on each node. Black stars indicate mammarenaviruses from the Americas that are known to cause human infections. Three dots indicate sequences generated in this work. Purple highlighting indicates the Pampa/Ura/Oliveros virus clade, green highlighting outlines the Oliveros virus clade, and turquoise highlighting outlines the Vello virus clade.

Figure 2: Inferred nucleotide-based phylogenetic relationships generated by maximum likelihood using all publicly available full-length L segment sequences for Pan-American species of the *Mammarenavirus* genus. Major clades are labeled, trees are midpoint rooted, and bootstrap support (n=1000 iterations) is highlighted in red on each node. Black stars indicate which Mammarenaviruses in the Americas that are known to cause human infections. Three dots indicate sequences generated in this work Three dots indicate sequences generated in this work.

Table 1. Comparison of L segment nucleotide percent identity between full-length and partial clade C Mammarenavirussequences. Red highlighting indicates a percent similarity below the ICTV threshold for *Mammarenavirus* species demarcation.

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|  | AY216514, Oliveros virus | Isolate 18694, Oliveros virus | Isolate 18400, Pampa virus | Isolate 17961, Ura virus | Isolate 18403, vello virus | Isolate 13796, vello virus | EU627612, Latino virus |
| AY216514, Oliveros virus |  |  |  |  |  |  |  |
| Isolate 18694, Oliveros virus | 96.6% |  |  |  |  |  |  |
| Isolate 18400, Pampa virus | 89.4% | 89.2% |  |  |  |  |  |
| Isolate 17961, Ura virus | 83.0% | 82.8% | 83.1% |  |  |  |  |
| Isolate 18403, vello virus | **68.8%** | **68.6%** | **70.8%** | **69.6%** |  |  |  |
| Isolate 13796, vello virus | **70.4%** | **69.8%** | **70.8%** | **70.4%** | 82.9% |  |  |
| EU627612, Latino virus | 67.4% | 64.0% | 64.0% | 64.2% | 64.2% | 64.2% |  |
|  | Full L-segment nucleotide percent identity | | | | | | |

Table 2. Full-length Mammarenavirus species demarcation. Viruses marked with a red diamond indicate proposed virus name. Checkmarks and green highlighting indicate that a genome has satisfied species demarcation criteria. Asterisk indicates that the sequence meets species demarcation against all but one other sequence.

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|  | Isolate 18694 Oliveros virus | Isolate 13796 vello virus✦ | Isolate 18403 vello virus✦ | Isolate 18400 Pampa virus | Isolate 17961 Ura virus✦ |
| Meets S segment criteria  <80% nucleotide identity | no | no | no | no | **Yes\*** |
| Meets NP criteria   <88% amino acid similarity | no | no | no | no | no |
| Meets L segment criteria  <76% nucleotide identity | no | **Yes**  (same species as 18403) | **Yes** (same species as 13796) | no | no |