

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 *Orthohantavirus* (*Elliovirales*: *Hantaviridae*): *Orthohantavirus ozarkense* |
| **Code assigned:**  | 2024.011M.N.v1.orthohantavirus\_1nsp.xlsx |

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| **Author(s), affiliation and email address(es):**  |
| **Name**  | **Affiliation**  | **Email address**  | **Corresponding author(s)**  |
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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:** |
| ICTV *Hantaviridae* 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** |
| *Hantaviridae* | 9 | 0 | 0 |

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| **Submission date:** |  12/05/2024 |

**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| W - Withdrawn |  |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:**  |
| 2024.011M.N.v1.orthohantavirus\_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*: *Hantaviridae*: *Orthohantavirus**Description of current taxonomy*: 35 established species*Proposed* *taxonomic change(s):* Addition of 1 new species*Justification*: Using a coding-complete genome sequence comprising all three genomic segments, we demonstrate that a virus discovered in hispid cotton rats (*Sigmodon* (*Sigmodon*) *hispidus* Say and Ord, 1825) sampled in the Ozark Plateau, Arkansas, USA, Ozark virus (OZAV) is a genetically unique orthohantavirus. We propose a novel orthohantavirus species, *Orthohantavirus ozarkense*, for OZAV. |

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| **Text of Taxonomy proposal** |
| *Taxonomic rank(s) affected*: *Hantaviridae*: *Orthohantavirus**Description of current taxonomy*: 35 established species*Proposed* *taxonomic change(s)*: Addition of 1 new species*Demarcation criteria:* Per the ICTV *Hantaviridae* Study Group, “the availability of at least coding-complete sequences of all three genome segments may be sufficient for hantavirid classification in the absence of a cultured isolate. Demarcation of genera is based upon DivErsity pArtitioning by hieRarchical Clustering (DEmARC) analysis) using concatenated deduced S, M, and L segment expression product sequences. DEmARC analysis gave a frequency distribution of Pairwise Evolutionary Distance (PED) values of which the threshold of 0.1 gave an optimal clustering cost of zero and is used as the hantavirid species demarcation criterium. Genera are demarked by a PED-value threshold of 0.95 and subfamilies are demarcated based on their distinct clustering in a Bayesian maximum clade credibility tree and a PED-value threshold of 3.5.” [1]*Justification*: We determined a coding-complete genome sequence comprising all three genomic segments of a new virus discovered in hispid cotton rats (*Sigmodon* (*Sigmodon*) *hispidus* Say and Ord, 1825) sampled in the Ozark Plateau, Arkansas, USA [2]. Phylogenetic analysis of the genome sequence placed this virus, Ozark virus (OZAV), into hantavirid genus *Orthohantavirus*. DEmARC analysis in context of other orthohantavirus sequences revealed a pairwise evolutionary distance value >0.1. The three most closely related orthohantaviruses to OZAV are Black Creek Canal virus (BCCV), bayou virus (BAYV), and Catacamas virus (CATV). The deduced protein sequences of the OZAV S segment are 80.84%, 81.15%, and 80.93% similar to those of BCCV, BAYV, and CATV, respectively; those of the OZAV M segment are 77.91% and 78.11% similar to those of BCCV and BAYV; and those of the OZAV L segment are 80.32%, 80.16%, and 80.01% similar to hose of BCCV, BAYV, and CATV, respectively. Thus, we propose a novel orthohantavirus species, *Orthohantavirus ozarkense*, for OZAV. |

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| **References:**  |
|  1. Bradfute SB, Calisher CH, Klempa B, et al (2024) ICTV Virus Taxonomy Profile: *Hantaviridae* 2024. J Gen Virol. 105. https://doi.org/10.1099/jgv.0.0019752. Mull N, Erdin M, Smura T, et al (2023) Novel Ozark orthohantavirus in hispid cotton rats (*Sigmodon hispidus*), Arkansas, USA. Emerg Infect Dis. 29: 2576**–**2578. https://doi.org/10.3201/eid2912.230549 |

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| **Tables, Figures:**  |

Provided below are the phylogenetic trees of orthohantaviruses based on protein identities for the S (panel A), M (panel B), and L (panel C) segments. Trees use maximum-likelihood and were constructed using IQ-TREE2 using best-fit models GTR+F+I+I+R5 (S), GTR+F+R6 (M), and GTR+F+I+I+R5 (L). Panel D shows the pairwise ORF protein analyses comparing OZAV to other orthohantaviruses. TREE-PUZZLE was used to compare pairwise evolutionary distance using maximum-likelihood approach with a WAG substitution model, with a cutoff value of 0.1 for species recognition [1]. Further details on analyses and products can be gleaned from our published article [2].







 