

The International Committee on Taxonomy of Viruses

Taxonomy Proposal Form, 2025

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

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| **Title:** | Create one new virus species in genus *Paslahepevirus*, family *Hepeviridae* (*Hepelivirales*) |
| **Code assigned:** | 2025.003S.N.v1.Paslahepevirus\_1nsp | |

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| **Author(s), affiliation and email address(es):** | | | | |
| **Given name (+middle initial(s))** | **Surname** | **Affiliation** | **Email address** | **Corr. author(s)** |
| Viola C. | Haring | Institute of Novel and Emerging Infectious Diseases, Friedrich-Loeffler-Institut, 17493 Greifswald – Isle of Riems, Germany | Viola.Haring@fli.de |  |
| Rainer G. | Ulrich | Institute of Novel and Emerging Infectious Diseases, Friedrich-Loeffler-Institut, 17493 Greifswald – Isle of Riems, Germany | Rainer.Ulrich@fli.de |  |
| Florian | Pfaff | Institute of Diagnostic Virology, Friedrich-Loeffler-Institut, 17493 Greifswald – Isle of Riems, Germany | Florian.Pfaff@fli.de | X |

**Part 1b: Taxonomy Proposal Submission**

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| **ICTV Subcommittee:** | | | |
| Animal DNA Viruses and Retroviruses |  | Bacterial viruses |  |
| Animal minus-strand and dsRNA viruses |  | Fungal and protist viruses |  |
| Animal positive-strand RNA viruses | **x** | 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:** |
| N/A |

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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** |
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| **Submission date:** | 20/06/2025 |

**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:** |  |

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

<https://ictv.global/taxonomy/templates>

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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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| **Etymology (origin) of proposed taxonomic names:** | |
| **Taxon name** | **Etymology of the term** |
| *Paslahepevirus crocidurae* | “*crocidurae*” from the shrew genus *Crocidura*, a genus of white-toothed shrews (subfamily Crocidurinae, family Soricidae) |

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| **Permission for use of names derived from a living person:** | | |
| **Taxon name** | **Full name of person from whom the name is derived** | **Attached** |

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| **Abstract of Taxonomy Proposal:** |
| *Taxonomic rank(s) affected*: *Paslahepevirus*  *Description of current taxonomy*:  *Riboviria* › *Orthornavirae* › *Kitrinoviricota* › *Alsuviricetes* › *Hepelivirales* › *Hepeviridae* › *Orthohepevirinae* (4 genera) › *Paslahepevirus* (2 species)  *Proposed* *taxonomic change(s):*  Add one (1) new species to genus *Paslahepevirus* (“*Paslahepevirus crocidurae”*).  *Justification*:  The proposed new species is based on two newly released genome sequences in GenBank (OR713884, OR713885) that meet the current hepevirid species demarcation criteria. |

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| **Text of Taxonomy proposal:** |
| *Taxonomic rank(s) affected*: *Paslahepevirus*  *Description of current taxonomy*:  Within the family *Hepeviridae*, two subfamilies with five genera and ten species are differentiated. Their viruses are faecal-orally transmitted and form small, quasi-enveloped particles [1]. They possess linear, positive-sensed, single-stranded RNA genomes with poly(A) tail at the 3’-ends.  Members of the subfamily *Orthohepevirinae* can infect mammals and birds and some even have zoonotic potential, causing acute, self-limiting to chronic hepatitis in humans [2] .  As of June 2025, two (2) species are included in genus *Paslahepevirus*:   * *Paslahepevirus alci* * *Paslahepevirus balayani*   *Proposed* *taxonomic change(s)*:  We propose to create one (1) new species within the genus *Paslahepevirus* that is based on two complete viral genome sequences that have recently been determined during metagenomic sequencing of greater white‑toothed shrews (*Crocidura russula* (Hermann, 1780)) [3].  In detail, greater white-toothed shrew hepatitis E virus genome (shrewHEV; OR713884 and OR713885) was assembled from metagenomic RNA sequencing datasets of tissue pools from two greater white-toothed shrews trapped in North-Rhine Westphalia and Thuringia, Germany.  Based on the genomic organization, amino acid (aa) sequence similarity, phylogenetic analysis and host range, we propose the establishment of a new species within the genus *Paslahepevirus* and propose the following species name:  greater white-toothed shrew hepatitis E virus (shrewHEV; OR713884 and OR713885) → “*Paslahepevirus crocidurae”*  *Etymology:*  *Paslahepevirus crocidurae: “*crocidurae” from the shrew genus *Crocidura*, a genus of white-toothed shrews (subfamily Crocidurinae, family Soricidae).  *Demarcation criteria:*  Members of different species in the genus *Paslahepevirus* are phylogenetically distinct based upon analysis of ORF1 codon positions 1−450 (methyltransferase), ORF1 codon positions 971–1692 (RNA-directed RNA polymerase) and ORF2 codon positions 121−473 (capsid protein not including the region encoded by the overlapping ORF3). Members of different species may also have different host ranges.  *Justification*:  We *de novo* assembled the closely related complete genome sequences of shrewHEV from two greater white-toothed shrew samples using metagenomic RNA sequencing data from tissue pools. A specific RT-qPCR confirmed the presence of the virus RNA in different organ tissues of these animals. The highest viral RNA loads were detected in the liver, kidney and intestinal tissue, suggesting faecal-oral transmission [3].  **Genomic organization**  The genomic structure of shrewHEV resembles other paslahepeviruses with an overlapping region of ORF2/3 and the absence of ORF 4 (**Figure 1**). ORF 4 was previously only identified in rat hepatitis E virus (*Rocahepevirus ratti*) and related members of the genus *Rocahepevirus* [4]. The length of the genome is around 7,040 nucleotides and the typical poly(A) tail at the 3’-end was confirmed by “Rapid Amplification of cDNA Ends” (RACE) [3].  **Phylogenetic analysis**  A phylogenetic analysis for three genomic regions, based on the ICTV demarcation criteria (aa similarity of ORF1 aa 1-450; ORF1 aa 971-16972; ORF2 aa 121-473), put shrewHEV on a unique branch that is basal to viruses from the genus *Paslahepevirus* but clearly separated from viruses of the other hepevirid genera (**Figure 2**).  **Amino acid sequence similarity**  A comparison of the aa sequence similarity of shrewHEV to representative members of hepevirid genera was conducted, with the lowest results obtained for the genus *Chirohepevirus*. The sequence similarity for ORF1 1-450 aa was found to be 47.4%, for ORF1 971-1692 aa it was 46.9%, and for ORF2 121-473 aa it was 64%. The highest sequence similarity was observed to members of the genus *Paslahepevirus*. The sequence similarity for ORF1 1-450 aa was found to be between 55.6% and 61.4%, for ORF1 971-1692 aa it was between 59% and 60.3%, and for ORF2 121-473 aa it was between 67.4% and 72%. These analyses support that the novel shrewHEV is a unique virus. The highest aa sequence similarity with members of the genus *Paslahepevirus* indicated that it should be classified within that genus (**Figure 3**). |

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| **References:** |
| References  1. Purdy MA, Drexler JF, Meng X-J et al. (2022) ICTV Virus Taxonomy Profile: Hepeviridae 2022. Journal of General Virology 103. https://doi.org/10.1099/jgv.0.001778  2. Velavan TP, Pallerla SR, Johne R et al. (2021) Hepatitis E: An update on One Health and clinical medicine. Liver Int 41:1462–1473. https://doi.org/10.1111/liv.14912  3. Haring VC, Litz B, Jacob J et al. (2024) Detection of novel orthoparamyxoviruses, orthonairoviruses and an orthohepevirus in European white-toothed shrews. Microb Genom 10. https://doi.org/10.1099/mgen.0.001275  4. Johne R, Heckel G, Plenge-Bönig A et al. (2010) Novel hepatitis E virus genotype in Norway rats, Germany. Emerg Infect Dis 16:1452–1455. https://doi.org/10.3201/eid1609.100444 |

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| **Accompanying files:** | |
| **Filename** | **Description of contents** |
| 2025.003S.N.v1.Paslahepevirus\_1nsp.xlsx | Excel module |

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| **Tables, Figures:** |

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**Figure 1**: Genome structure of the novel greater white-toothed shrew hepatitis E virus (member of proposed species: “*Paslahepevirus crocidurae”*). Modified from Haring et al., 2024 [3].

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**Figure 2**: For the phylogenetic analysis of the novel greater white-toothed shrew hepatitis E virus (shrewHEV), 34 representative genomes of the subfamily *Orthohepevirinae* were selected as references. **(a)** The first 450 amino acids of ORF1-encoded non-structural polyprotein were aligned and a phylogenetic tree was calculated (IQ-TREE2; version 2.4.0). **(b)** Phylogenetic analysis of the alignment of the 971 -1692 aa sequence of ORF1-encoded protein is depicted. **(c)** The phylogeny of the ORF2-encoded capsid protein aa 121-473 excluding the overlapping region with ORF3 is shown. ICTV accepted species are indicated by different tip colours, while not yet classified viruses are indicated by black tip circles. The novel shrewHEV sequences are indicated in red. Statistical support is shown using % ultrafast-bootstrap.



**Figure 3:** Heatmap representing the amino acid (aa) sequence similarity for all three genomic regions used for species demarcation (ORF1 1-450 aa; ORF1 971-1692 aa; ORF2 121-473 aa) for representative members of the genera *Paslahepevirus*, *Rocahepevirus*, *Avihepevirus* and *Chirohepevirus* in comparison to the novel greater white-toothed shrew hepatitis E virus (OR713854 and OR713855).