

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 species in the genus *Avastrovirus* (*Stellavirales*: *Astroviridae*) |
| **Code assigned:**  | 2025.001S.Ac.v3.Avastrovirus\_1nsp |

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|  | **Author(s), affiliation and email address(es):**  |
| **Given name (+middle initial(s))** | **Surname** | **Affiliation**  | **Email address**  | **Corresponding author(s)** X |
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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 |  | 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:**  |
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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** |
| ICTV *Astroviridae* Study Group | 4 | 0 | 0 |
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| **Submission date:** |  19/06/2025 |

**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| W - Withdrawn |  |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:** |
| Correct species name to correct Latin; make text clearer; ensure separation of virus vs species throughout. |

**Part 1d: Revised Taxonomy Proposal Submission**

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| **Response of proposer:**  |
| Done. |

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| **Revision date:** | 09/19/2025 |

**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** |
| *Avastrovirus marecae* | Named after the host genus name (falcated ducks (*Mareca falcata* (Georgi, 1775))). |
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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*: Species*Description of current taxonomy*: The current taxonomy of *Astroviridae* includes three avastrovirus species.*Proposed* *taxonomic change(s):* We propose the establishment of a new species in the *Avastrovirus* genus, which would include the recently sequenced duck astrovirus M (DAstV-M). We suggest the species name *Avastrovirus marecae* in line with the new binomial species nomenclature. The complete genome (6,566 nt) was sequenced from fecal swab samples collected from the host falcated duck (*Mareca falcata* (Georgi, 1775))). The resulting assembled contig was compared to publicly available sequences. *Justification*:It was found that the closest match was a avastrovirus 3 isolate MPJ1364 RdRp gene, partial cds (390bp, JX985709), which had the highest nucleotide identity (93.08%) and amino acid identity (98.46%).The nucleotide identity and amino acid identity between new species and other members of the *Avastrovirus* genus are much lower. The p-distance of ORF2 between new species and each avastrovirus species was met with ICTV classification criteria, which requires the average p-distances within 0.576 to 0.742. The results of ORF2 phylogenetic analysis and genetic distance analysis indicate that DAstV-M should be classified in a fourth species in the *Avastrovirus* genus (1). |

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| * **Text of Taxonomy proposal:**
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| The 9th ICTV Report proposal in 2010 describes species classification criteria within the genus *Avastrovirus*. A phylogenetic analysis of *Astroviridae* based on the amino acid sequence of the full-length ORF2 is a prerequisite and mean amino acid genetic distances range between 0.576-0.742, and 0.204-0.284 between and within groups, respectively (https://ictv.global/ictv/proposals/2010.017a-cV.A.v3.Avastrovirus.pdf). According to the newly revised guidelines in the 2023 proposal, all virus species should be named using the binomial nomenclature system (https://ictv.global/ictv/proposals/2023.004S.Astroviridae\_22sprenamed.zip).This proposal presents the analysis of a first complete genome of a new avastrovirus, duck astrovirus M (DAstV-M), from a falcated duck (*Mareca falcata*(Georgi, 1775)) fecal sample collected in 2022 in the Hong Kong Mai Po Wetland (Table 1). The 6,566-nt genome showed the greatest degree of similarity (93.08% nucleotide identity and 98.46% amino acid identity) to avastrovirus 3 isolate MPJ1364 RdRp gene (JX985709) according to the BLAST match, which only is 390 nt long (Table 2). When queried against the NCBI nr/nt database, no other complete genome matches with a higher percent identity were found. Overall nucleotide identity (31.14-34.26%) and amino acid identity (ORF1a: 16.93-18.12%; ORF1b: 37.84-44.20%; ORF2: 17.81-20.87%) between new species and other members of the *Avastrovirus* genus with the complete genome are much lower (Table 2). Additionally, the p-distance results between new species and the other three members of *Avastrovirus* genus (0.697 to 0.722) met the ICTV classification criteria, which require the average p-distances between sub-clades to be within 0.576 to 0.742. Phylogenetic analysis was also conducted based on full genome sequences, ORF1a, ORF1b, and ORF2 region (Figure 1). These results also showed confirmed the need for a new species, which we propose to be named *Avastrovirus marecae*, as a new genetic lineage closely related to *Avastrovirus* and distinct from *Mamastrovirus* (Figure 1).Comparative genomic analysis of the complete genome of *Avastrovirus marecae* revealed conserved motifs present within other astrovirids: a transmembrane domain (TM), a serine protease (PRO), a viral genome-linked protein (VPg), a nuclear localization signal (NLS), and a hepta-nucleotide ribosomal frameshift signal and TEEEY-like motif (Figure 2). |

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| **References:**  |
|  1. Ng DYM, Sun W, Sit THC, Brackman CJ, Tse ACN, Bui CHT, Tang AWY, Wong ANC, Tsang ATL, Koo JCT, Cheng SMS, Peiris M, Chin AWH, Poon LLM. Genetic diversity of astroviruses detected in wild aquatic birds in Hong Kong. Virol J. 2024 Jul 7;21(1):153.
2. Nguyen LT, Schmidt HA, von Haeseler A, Minh BQ. IQ-TREE: a fast and effective stochastic algorithm for estimating maximum-likelihood phylogenies. Mol Biol Evol. 2015;32(1):268-74.
3. Guindon S, Dufayard JF, Lefort V, Anisimova M, Hordijk W, Gascuel O. New algorithms and methods to estimate maximum-likelihood phylogenies: assessing the performance of PhyML 3.0. Syst Biol. 2010;59(3):307-21.
4. Kalyaanamoorthy S, Minh BQ, Wong TKF, von Haeseler A, Jermiin LS. ModelFinder: fast model selection for accurate phylogenetic estimates. Nat Methods. 2017;14(6):587-9.
5. Hoang DT, Chernomor O, von Haeseler A, Minh BQ, Vinh LS. UFBoot2: Improving the Ultrafast Bootstrap Approximation. Mol Biol Evol. 2018;35(2):518-22.
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| **Accompanying files:**  |
| **Filename** | **Description of contents** |
| 2025.001S.Ac.v3.Avastrovirus\_1nsp | Excel module |
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| **Tables, Figures:**  |

**Table 1:** Summary of details regarding the proposed novel *Avastrovirus* species

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| **Species name** | **GenBank accession** | **Virus acronym** | **Isolate** | **Country**  | **Host** | **Isolation source** |
| *Avastrovirus marecae* | PP623814 | DAstV-M | MP22-196 | China: Hong Kong | Falcated duck (*Mareca falcata* (Georgi, 1775)) | Fecal swab samples |

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| **Table 2.** Percentage nucleotide and amino acid identity and genetic distances between *Avastrovirus marecae* and genus *Avastrovirus* references. |
|  |  |  | **Percentage identity (%)** | **p-distance** |
| **Species** | **Viruses** | **Accession No.** | **Nt** | **ORF1a (aa)** | **ORF1b (aa)** | **ORF2 (aa)** | **ORF2** **(aa)** |
| *Avastrovirus meleagridis**(*avastrovirus 1) | turkey astrovirus | NC\_002470 | 34.26 | 17.96 | 41.01 | 20.47 | 0.702 |
| *Avastrovirus galli**(*avastrovirus 2) | avastrovirus 2 | MH453801 | 32.88 | 16.93 | 41.02 | 20.81 | 0.697 |
| avian nephritis virus 2 | MH028405 | 31.14 | 17.29 | 41.25 | 19.53 | 0.722 |
| avian nephritis virus | MN732559 | 31.85 | 17.48 | 41.05 | 19.78 | 0.712 |
| chicken astrovirus | NC\_003790 | 31.65 | 17.22 | 40.63 | 20.87 | 0.714 |
| feral pigeon astrovirus | FR727146 | 32.65 | NAa | 43.45 | 18.47 | 0.712 |
| wood pigeon astrovirus | FR727149 | 32.09 | NA | 44.20 | 19.73 | 0.699 |
| *Avastrovirus intestini**(*avastrovirus 3) | chicken astrovirus | JF414802 | 31.65 | 17.22 | 38.92 | 20.87 | 0.714 |
| duck astrovirus | NC\_012437 | 32.08 | 16.47 | 37.84 | 18.37 | 0.707 |
| goose astrovirus | NC\_034567 | 33.32 | 17.57 | 39.73 | 19.12 | 0.714 |
| turkey astrovirus 2 | NC\_005790 | 33.16 | 18.12 | 38.83 | 17.81 | 0.704 |
| Unclassified*(*avastrovirus 4)b | avastrovirus 3 MPJ0552 | JX985682 | 67.72 | NA | 66.14 | NA | NA |
|  | avastrovirus 3 MPJ1332 | JX985700 | 76.34 | NA | 80.65 | NA | NA |
|  | avastrovirus 3 MPJ1348 | JX985704 | 77.6 | NA | 82.03 | NA | NA |
|  | avastrovirus 3 MPJ1364 | JX985709 | 93.08 | NA | 98.46 | NA | NA |
|  | avastrovirus 3 MPJ1433 | JX985714 | 72.85 | NA | 70.97 | NA | NA |
|  | avastrovirus 3 MPJ1442 | JX985715 | 73.12 | NA | 70.97 | NA | NA |
|  | avastrovirus 3 Sweden 701 | KY320411 | 75 | NA | 82.4 | NA | NA |
| a No sequences available of specific ORF region in the public databaseb The reference sequence identified as avastrovirus 4 only consists of an RdRp region (Located in ORF1b) |

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**Figure 1.** Maximum likelihood phylogenetic analysis of DAstV-M(red) and representative astrovirus strains of each species based on (A) complete genome sequences, (B) ORF1a, (C) ORF1b, and (D) ORF2 region using IQ‐TREE v1.6.12 (2). The best-fit model of sequence evolution was selected based on the Bayesian information criterion (BIC) score calculated by ModelFinder, GTR+I+G substitution model was selected (3,4). Node support was estimated by ultrafast bootstrap with 1,000 replicates each (5). The trees are rooted with mamastroviruses. Representative astrovirid references (n=41) of different species with GenBank accession numbers are shown. According to the ICTV taxonomic classification, 19 sequences related to the *Mamastrovirus* genus were selected as references. It is worth noting that some references are only partial sequences, so they are not included in some phylogenetic trees.



**Figure 2.** Schematic representation of the complete genome organization of DAstV-M. The line at the upper indicated the nucleotide (nt) length and the dashed line stated the location of 5' UTR, 3' UTR, and the starting and final nucleotide for ORF. The total nucleotide length (upper rectangles), different conserved domain hits with nucleotide location, accession number (Cdd), and E-value (below rectangles) are shown in each ORF. TEEEY-like motif and ribosomal frame-shift heptameric signal are stated at ORF1a. Putative sgRNA promoter is indicated between the end of ORF1b and the start of >