

The International Committee on Taxonomy of Viruses

Taxonomy Proposal Form, 2024

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

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| **Title:**  | Creating 55 new species in family *Parvoviridae*  |
| **Code assigned:**  | 2024.008D.N.v1.1.Parvoviridae\_55nsp |

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**Part 1b: Taxonomy Proposal Submission**

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| **ICTV Subcommittee:**  |
| Animal DNA Viruses and Retroviruses | **X** | Bacterial viruses |  |
| Animal minus-strand and dsRNA viruses |  | 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:**  |
| *Parvoviridae* 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** |
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| **Submission date:** |  08/06/2024 |

**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| W - Withdrawn |  |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:**  |
| 2024.008D.N.v1.1.Parvoviridae\_55nsp.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:**  |  **Y/N** |
| **Taxon name** | **Person from whom the name is derived** | **Attached X** |
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| **Abstract of Taxonomy Proposal:**  |
| *Taxonomic rank(s) affected*: Subfamily *Densovirinae*, genera *Blattambidensovirus, Scindoambidensovirus, Protoambidensovirus, Aquambidensovirus*.Subfamily *Parvovirinae*, genera *Aveparvovirus, Bocaparvovirus, Dependoparvovirus, Protoparvovirus**Description of current taxonomy*: The family currently includes:* Subfamily *Densovirinae* with 11 genera and 38 species
* Subfamily *Parvovirinae* with 11 genera and 107 species
* Subfamily *Hamaparvovirinae* with 5 genera and 42 species
* Unassigned genus *Metalloincertoparvovirus* with 1 species

*Proposed* *taxonomic change(s):* This TP describes the creation of 26 new species in the subfamily *Densovirinae* and of 29 new species in the subfamily *Parvovirinae*. Additionally, we modified the virus definition to allow for the classification of sequences derived from cDNA-based metatranscriptomes if specific circumstances are met. *Justification*:Several novel viruses have been described in the literature that fulfill the criteria to be classified as separate species. Additionally, various complete coding genomes derived from metatranscriptomic experiments have been published and we changed the virus definition to allow the classification of these viruses if there are reasons to believe that the sequences originate from viral DNA, i.e the sample preparation did not involve a DNase treatment step.  |

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| * **Text of Taxonomy proposal:**
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| *Taxonomic rank(s) affected*: Two of the three subfamilies and 9 of the 28 genera in the *Parvoviridae* are affected by this TP. In the subfamily *Densovirinae*, affected genera are *Blattambidensovirus, Scindoambidensovirus, Protoambidensovirus,* and *Aquambidensovirus*. In the subfamily *Parvovirinae*, affected genera are *Aveparvovirus, Bocaparvovirus, Dependoparvovirus,* and *Protoparvovirus.**Description of current taxonomy*: The family currently includes:* Subfamily *Densovirinae* with 11 genera and 38 species
* Subfamily *Parvovirinae* with 11 genera and 107 species
* Subfamily *Hamaparvovirinae* with 5 genera and 42 species
* Unassigned genus *Metalloincertoparvovirus* with 1 species

We propose to assign 26 new species to the subfamily *Densovirinae*, bringing the total number of species in this subfamily to 64, and 29 new species in the subfamily *Parvovirinae*, bringing the total number of species in this subfamily to 136. *Proposed* *taxonomic change(s)*: 1. Create twenty-six new species within the subfamily *Densovirinae* (Figure 1)

Create a new species in genus ***Blattambidensovirus*** 1. Assign ParvoviridaeDogfe393C1 to the species Blattambidensovirus incertum5
* Shares 75.6% identity on 100% coverage with *Blattambidensovirus incertum3* (MN099038) NS1 protein, and harbors an ambisense genome.Detected in canine feces (1). As viruses of this subfamily infect inveretebrate hosts exclusively, we believe the source organism of this virus is not the true host.

Create a new species in genus ***Scindoambidensovirus***1. Assign Burswood densovirus isolate mosComB to the species Scindoambidensovirus dipteran1
* Shares 69.5% identity on 100% coverage with *Scindoambidensovirus incertum2* (MT734805) NS1 protein, and harbors an ambisense genome.Detected in mosquitoes (2).

Create four new species in genus ***Protoambidensovirus***1. Assign ParvoviridaeDogfe426C1 to the species Protoambidensovirus incertum2
* Shares 44.7% identity on 100% coverage with *Protoambidensovirus lepidopteran1* NS1 protein, and harbors an ambisense genome.Detected in canine feces (1).
1. Assign Ambidensovirus sp. strain NGR\_2017\_NHP\_ADV to the species Protoambidensovirus incertum3
* Shares 71.8% identity on 100% coverage with *Protoambidensovirus lepidopteran1* (L32896) NS1 protein, and harbors an ambisense genome. The virus was found in the stool of a drill monkey from Nigeria (3).
1. Assign ParvoviridaeDogfe420C1 to the species Protoambidensovirus incertum4
* Shares 68.2% identity on 100% coverage with *Protoambidensovirus incertum1* (MW306771) NS1 protein, and harbors an ambisense genome.Detected in canine feces (1).
1. Assign Densovirinae sp. isolate ltt163par2 to the species Protoambidensovirus incertum5
* Shares 54.4% identity on 100% coverage with *Protoambidensovirus dipteran1* (FJ810126) NS1 protein, and harbors an ambisense genome.Detected in bird feces (4).

Create twenty new species in genus***Aquambidensovirus***All of them harbor an ambisense genome and were detected in sea stars (invertebrates, Asteroidea) (5).1. Assign Uncultured densovirus clone EtaDV1 to the species Aquambidensovirus asteroid3
* Shares 50.8% identity on 100% coverage with Uncultured densovirus clone EtaDV2 NS1 protein.
1. Assign Uncultured densovirus clone EtaDV2 to the species Aquambidensovirus asteroid4
* Shares 67.9% identity on 100% coverage with Aquambidensovirus asteroid2 (MN190158) NS1 protein.
1. Assign Uncultured densovirus clone EtaDV3 to the species Aquambidensovirus asteroid5
* Shares 70.6% identity on 100% coverage with Uncultured densovirus clone LaaDV2 NS1 protein.
1. Assign Uncultured densovirus clone LaaDV1 to the species Aquambidensovirus asteroid6
* Shares 76.6% identity on 100% coverage with Uncultured densovirus clone PoaDV2 NS1 protein.
1. Assign Uncultured densovirus clone LaaDV2 to the species Aquambidensovirus asteroid7
* Shares 70.6% identity on 100% coverage with Uncultured densovirus clone EtaDV3 NS1 protein.
1. Assign Uncultured densovirus clone LaaDV3 to the species Aquambidensovirus asteroid8
* Shares 46.0% identity on 100% coverage with Uncultured densovirus clone NgaDV3 NS1 protein.
1. Assign Uncultured densovirus clone LmaDV1 to the species Aquambidensovirus asteroid9
* Shares 71.1% identity on 100% coverage with Aquambidensovirus ostreid1 (KY548840) NS1 protein.
1. Assign Uncultured densovirus clone NgaDV1 to the species Aquambidensovirus asteroid10
* Shares 64.0% identity on 100% coverage with Aquambidensovirus asteroid2 NS1 protein.
1. Assign Uncultured densovirus clone NgaDV3 to the species Aquambidensovirus asteroid11
* Shares 64.5% identity on 100% coverage with Uncultured densovirus clone EtaDV3 NS1 protein.
1. Assign Uncultured densovirus clone NgaDV4 to the species Aquambidensovirus asteroid12
* Shares 61.2% identity on 100% coverage with Uncultured densovirus clone PhaDV4 NS1 protein.
1. Assign Uncultured densovirus clone PhaDV4 to the species Aquambidensovirus asteroid13
* Shares 61.2% identity on 100% coverage with Uncultured densovirus clone NgaDV4 NS1 protein.
1. Assign Uncultured densovirus clone PoaDV2 to the species Aquambidensovirus asteroid14
* Shares 84.9% identity on 100% coverage with Uncultured densovirus clone PoaDV6 NS1 protein.
1. Assign Uncultured densovirus clone PoaDV3 to Aquambidensovirus asteroid15
* Shares 77.3% identity on 100% coverage with Uncultured densovirus clone PoaDV2 NS1 protein.
1. Assign Uncultured densovirus clone PoaDV4 to the species Aquambidensovirus asteroid16
* Shares 76.1% identity on 100% coverage with Uncultured densovirus clone PoaDV2 NS1 protein.
1. Assign Uncultured densovirus clone PoaDV5 to the species Aquambidensovirus asteroid17
* Shares 56.4% identity on 100% coverage with Aquambidensovirus asteroid2 NS1 protein.
1. Assign Uncultured densovirus clone PoaDV6 to Aquambidensovirus asteroid18
* Shares 84.9% identity on 100% coverage with Uncultured densovirus clone PoaDV2 NS1 protein.
1. the species
* Shares 50.5% identity on 100% coverage with Uncultured densovirus clone NgaDV4 NS1 protein.
1. Assign Uncultured densovirus clone PoaDV8 to the species Aquambidensovirus asteroid20
* Shares 43.4% identity on 100% coverage with Uncultured densovirus clone PoaDV7 NS1 protein.
1. Assign Uncultured densovirus clone PoaDV13 to the species Aquambidensovirus asteroid21
* Shares 79.5% identity on 100% coverage with Uncultured densovirus clone PoaDV2 NS1 protein.
1. Assign Uncultured densovirus clone PoaDV11 to the species Aquambidensovirus asteroid22
* Shares 39.5% identity on 100% coverage with Uncultured densovirus clone NgaDV4 NS1 protein.
1. Create Twenty-nine new species within the subfamily *Parvovirinae* (Figure 2)

Create 7 new species in genus ***Aveparvovirus***1. Aveparvovirus psittacine1. This species includes Ara ararauna aveparvovirus and similar viral strains identified in fecal samples of Chinese psittacides. Its NS1 protein shares 78% identity with that of Parvovirus par081par1 to be classified in the species Aveparvovirus psittacine2 (4,6).
2. Aveparvovirus avian1. Bird parvovirus Bir-01-1 was originally identified in pooled fecal samples from galliformes and gruiformes, but the virus was also detected in samples from peacocks, pheasants, cockatoo, and crane. Its NS1 protein shares 61.6% identity with the closest classified relative in the species *Aveparvovirus columbid1* (4,7)*.*
3. Aveparvovirus psittacine2. Parvovirus par081par1 was detected in fecal samples from Chinese Southern mealy amazon. Its NS1 protein shares 78% identity with the closest to be classified relative in the species Aveparvovirus psittacine1 (4).
4. Aveparvovirus galliform2. Parvovirus gps215par1 was detected in fecal samples of Golden pheasants. Its NS1 protein shares approximately 75% identity with members of the species *Aveparvovirus galliform1* (4).
5. Aveparvovirus passeriform2. Aveparvovirus bfb009ave01 and similar strains were found in fecal samples of buntings and flycatchers. Its NS1 protein shares 66% identity with the closest classified relative in the species *Aveparvovirus passeriform1* (4).
6. Aveparvovirus passeriform3. Parvoviridae sp. wwb174par01 found in Radde's warbler from China. Its NS1 protein is less than 55% identical to the closest relatives in the genus (4).
7. Aveparvovirus anseriform1. Mute swan feces associated aveparvovirus was found in fecal samples from UK swans and, according to sequences found in GeneBank, from Chinese geese. Its NS1 protein is less than 50% identical to the closest relatives in the genus (8).

Create 5 new species in genus ***Bocaparvovirus***1. Bocaparvovirus chiropteran6. Bat bocavirus BtBoV/CMR/2014 was identified in pooled fecal samples from bats of the species Eidolon helvum from Cameroon. Its NS1 protein is less than 50% identical to the closest relatives in the genus (9).
2. Bocaparvovirus ungulate10. Equine bocaparvovirus was identified in the spleen and intestine content of a foal with interstitial pneumonia. Its NS1 protein shares 54% identity with the closest classified relative in the species *Bocaparvovirus ungulate7* (10).
3. Bocaparvovirus incertum2. ParvoviridaeDogfe322C1 was found in fecal samples from Chinese dogs, but there is a highly identical GenBank sequence obtained from a yak. Its NS1 protein shares 56-57% identity with the closest classified relatives in the species *Bocaparvovirus ungulate1* and *Bocaparvovirus ungulate6* (1).
4. Bocaparvovirus incertum3. ParvoviridaeDogfe373C3 was found in fecal samples from Chinese dogs, but there is a highly identical GenBank sequence from Sagus Kul lizard. Its NS1 protein shares 53% identity with the closest classified relative in the species *Bocaparvovirus rodent2* (1).
5. Bocaparvovirus incertum4. ParvoviridaeDogfe362C9 was found in fecal samples from Chinese dogs. Its NS1 protein shares 58.7% identity with the closest classified relative in the species Bocaparvovirus rodent2 (1).

Create 13 new species in genus ***Dependoparvovirus***1. Dependoparvovirus anseriform2. Anser anser dependoparvovirus was found in fecal samples from Greylag geese. Its NS1 protein shares 66.7% identity with the closest classified relative in the species *Dependoparvovirus rodent1* (6).
2. Dependoparvovirus anseriform3. Dependoparvovirus zftwig01adas1 was found in fecal samples of Chinese Bar-headed geese. Its NS1 protein shares 66% identity with the closest to be classified relative in the species Dependoparvovirus carnivoran4 (4).
3. Dependoparvovirus passeriform1. Dependoparvovirus swa134par4 was found in fecal samples from swallows. Its NS1 protein shares 68.8% identity with the closest related member of the genus, hence it is to be classified relative in the species Dependoparvovirus carnivoran4 (4).
4. Dependoparvovirus anseriform5. Dependoparvovirus zftwig05par3 was found in fecal samples from a Bar-headed goose. Its NS1 protein shares 73% identity with the closest to be classified relative in the species Dependoparvovirus passeriform3 (4).
5. Dependoparvovirus passeriform2. Dependoparvovirus plw155par1 and similar strains were found in fecal samples of warblers and tits. Its NS1 protein shares 73% identity with the closest to be classified relative in the species Dependoparvovirus anseriform5 (4).
6. Dependoparvovirus anseriform4. Adeno-associated\_virus\_MHH-05-2015 was isolated from a Muscovy ducks from China that was also positive for duck adenovirus type 3. Later on, it was detected in greater white-fronted geese. Its NS1 protein shares 62% identity with the closest classified relative in the species *Dependoparvovirus avian1* (4,11).
7. Dependoparvovirus carnivoran2. ParvoviridaeDogfe340C1 was identified in fecal samples from Chinese dogs. Its NS1 protein shares 53.3% identity with the closest classified relative in the species *Dependoparvovirus mammalian1* (1).
8. Dependoparvovirus carnivoran3. ParvoviridaeDogfe380C5 was identified in fecal samples from Chinese dogs. Its NS1 protein shares 68% identity with the closest to be classified relative in the species Dependoparvovirus carnivoran5(1).
9. Dependoparvovirus carnivoran4. ParvoviridaeDogfe346C1 was identified in fecal samples from Chinese dogs. Its NS1 protein shares 74.5% identity with the closest to be classified relative in the species Dependoparvovirus carnivoran5(1).
10. Dependoparvovirus carnivoran5. ParvoviridaeDogfe385C1 was identified in fecal samples from Chinese dogs. Its NS1 protein shares 83% identity with the closest to be classified relative in the species Dependoparvovirus carnivoran6(1).
11. Dependoparvovirus carnivoran6. ParvoviridaeDogfe383C2 was identified in fecal samples from Chinese dogs. Its NS1 protein shares 83% identity with the closest to be classified relative in the species Dependoparvovirus carnivoran5(1).
12. Dependoparvovirus rodent3. Myodes glareolus adeno-associated virus 1 was identified in plasma samples from Ukrainian bank voles. Its NS1 protein shares 81.7% identity with the closest to be classified relative in the species Dependoparvovirus rodent4 (12).
13. Dependoparvovirus rodent4. Myodes glareolus adeno-associated virus 2 was identified in plasma samples from Ukrainian bank voles. Its NS1 protein shares 81.7% identity with the closest to be classified relative in the species Dependoparvovirus rodent3 (12).

Create 4 new species in genus ***Protoparvovirus***1. Protoparvovirus chiropteran2. Bat parvovirus BtPk-PV/Switzerland/2019 was identified in organ samples (liver and spleen) of Plecotus auritus bats in Switzerland. Similar viruses were also found in fecal and organ samples of other species of bats (Pipistrellus pipistrellus, Plecotus auritus, Nyctalus noctula, Pipistrellus nathusii, and Pipistrellus kuhlii) from the same area and of Nyctalus velutinus from China. While these viruses likely constitute one species, Bat parvovirus BtPk-PV/Switzerland/2019 is the only virus whose coding sequence has been fully obtained. The NS1 of viruses within this species share approximately 85% amino acid identity with their closest relative to be classified in the species Protoparvovirus carnivoran8 (13,14).
2. Protoparvovirus carnivoran6. ParvoviridaeDogfe372C6 was identified in fecal samples from Chinese dogs. Its NS1 protein shares 80.5% identity with the closest classified relative in the species *Protoparvovirus carnivoran4* (1).
3. Protoparvovirus carnivoran7. ParvoviridaeDogfe373C1 was identified in fecal samples from Chinese dogs. Its NS1 protein shares about 70% identity with members of the closest classified species in the species *Protoparvovirus carnivoran3* (1).
4. Protoparvovirus carnivoran8. ParvoviridaeDogfe342C1 was identified in fecal samples from Chinese dogs. Its NS1 protein shares less than 60% identity with other members of the genus (1).

*Demarcation criteria:*We modified the virus definition to allow for the classification of sequences derived from cDNA-based metatranscriptomes if specific circumstances are met (see sentence in **bold**).Virus definition:In order for an agent to be classified in the family *Parvoviridae*, it must be judged to be an authentic parvovirus on the basis of having been sequenced from tissues, secretions, or excretions of its possible host or, failing this, from an additional biological source when the true viral host identity remains unknown. All such sequences must be reported in a credible peer-reviewed publication, in which insights into their host and biology, such as genome annotation, transcription strategy, epidemiology, serology, structure, trafficking, replication and evolution, are strongly encouraged. The sequence must contain the complete coding region of the large nonstructural protein (NS1), which must possess an SF3 helicase domain in its protein sequence, as well as the virus particle (VP) coding regions. If the genome is multipartite, evidence must be presented to confirm that these are indeed multiple genome segments of the same viral genome (e.g., corresponding termini, experimental evidence of concurrent replication). The sequence must also meet the size constraints and motif patterns typical of the family**. Sequences derived from cDNA-based metatranscriptomes can be accepted only if a DNase treatment was not performed prior to reverse transcription and it is presumed that sequences originated from viral DNA, i.e the nucleic acid was derived from a metazoan animal or from its associated excretions or secretions. As the former is difficult to verify in case of environmental samples (e.g. marine water, soil, air, fresh water), parvovirus-related metatranscriptome sequences from these sources are not eligible for classification.** In case a presumed host cannot be assigned, the ambiguous host assignment must be indicated in species level nomenclature. This definition is designed to allow the inclusion of viruses identified by virus discovery approaches, including those with an unknown host, which typically lack reliable sequences from the telomeric hairpins, while avoiding viral sequence fragments integrated into the host genomes.Demarcation criteria and nomenclature:Species: two parvoviruses can be potentially classified in one species if their NS1 proteins share at least 85% protein sequence identity. Species must be designated under a binomial name, consisting of the genus name, within which given virus is classified, and a specific epithet. The epithet must mirror the order level affiliation of the virus host, or in case of multiple host involvement, the lowest taxonomy unit encompassing the affected host species. Failing this, if the exact host spectrum is unknown, the epithet will be indicated as “incertum”. A number in simple Arabic numeric may be added if more species are to share the same epithet within a given genus, e.g., *Copiparvovirus ungulate2*.Genus: two parvoviruses can be potentially classified in one genus if they cluster as a robust monophyletic lineage based on their complete NS1 protein sequence in case of subfamily-level phylogeny and also based on their SF3 helicase domains in case of family-wide phylogenetic inference. Additionally, their NS1 proteins should share 35-40% protein sequence identity and display a coverage of at least 80% between two members of the genus in question. Flexibility in these numbers may apply. Failing the sequence-identity-based criteria, common genus affiliation can also be justified by similar genome organization, i.e., presence or absence of certain auxiliary protein encoding genes, genome length and/or transcription strategy, provided the criterion of the well-supported monophyly is still satisfied.*Justification*: Several novel viruses have been described in the literature that fulfill the criteria to be classified as separate species. Additionally, various complete coding genomes derived from metatranscriptomic experiments have been published, and we changed the virus definition to allow the classification of these viruses if a DNase treatment was not performed prior to reverse transcription. The virus definition already accommodated viruses from metagenomic experiments encompassing the simultaneous sequencing of RNA and DNA viruses. If a DNase treatment is not performed before the reverse transcriptase, metatranscriptomic experiment can produce complete genomes of parvoviruses, similarly to metagenomics. The new virus definition will allow the classification of several novel species, more realistically reflecting the diversity within this family.  |

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| **References:**  |
|  1. Jiang X, Liu J, Xi Y, Zhang Q, Wang Y, Zhao M, et al. Virome of high-altitude canine digestive tract and genetic characterization of novel viruses potentially threatening human health. mSphere. 2023 Sep 19;8(5):e00345-23. 2. Lamichhane B, Brockway C, Evasco K, Nicholson J, Neville PJ, Levy A, et al. Metatranscriptomic Sequencing of Medically Important Mosquitoes Reveals Extensive Diversity of RNA Viruses and Other Microbial Communities in Western Australia. Pathogens. 2024 Feb;13(2):107. 3. George U, Simsek C, Faleye TOC, Arowolo O, Oragwa A, Adewumi OM, et al. Genome Sequences of Novel Members of Previously Described DNA and RNA Virus Families, Isolated from Feces of a Drill Monkey in Nigeria. Microbiol Resour Announc. 2020 Apr 23;9(17):e00092-20. 4. Shan T, Yang S, Wang H, Wang H, Zhang J, Gong G, et al. Virome in the cloaca of wild and breeding birds revealed a diversity of significant viruses. Microbiome. 2022 Apr 12;10(1):60. 5. Jackson EW, Wilhelm RC, Johnson MR, Lutz HL, Danforth I, Gaydos JK, et al. Diversity of Sea Star-Associated Densoviruses and Transcribed Endogenous Viral Elements of Densovirus Origin. J Virol. 2020 Dec 9;95(1):e01594-20. 6. Dai Z, Wang H, Wu H, Zhang Q, Ji L, Wang X, et al. Parvovirus dark matter in the cloaca of wild birds. GigaScience. 2023 Jan 1;12:giad001. 7. Wang Y, Sun Y, Li X, Chen R, Li W, Ji L, et al. Molecular detection and characterization of three novel parvoviruses belonging to two different subfamilies in zoo birds. Arch Virol. 2023 May 17;168(6):163. 8. Hill SC, François S, Thézé J, Smith AL, Simmonds P, Perrins CM, et al. Impact of host age on viral and bacterial communities in a waterbird population. ISME J. 2023 Feb 1;17(2):215–26. 9. Yinda CK, Ghogomu SM, Conceição-Neto N, Beller L, Deboutte W, Vanhulle E, et al. Cameroonian fruit bats harbor divergent viruses, including rotavirus H, bastroviruses, and picobirnaviruses using an alternative genetic code. Virus Evol. 2018 Jan 1;4(1):vey008. 10. Altan E, Hui A, Li Y, Pesavento P, Asín J, Crossley B, et al. New Parvoviruses and Picornavirus in Tissues and Feces of Foals with Interstitial Pneumonia. Viruses. 2021 Aug;13(8):1612. 11. Su XN, Liu JJ, Zhou QF, Zhang XH, Zhao LC, Xie QM, et al. Isolation and genetic characterization of a novel adeno-associated virus from Muscovy ducks in China. Poult Sci. 2017 Nov 1;96(11):3867–71. 12. Kesäniemi J, Lavrinienko A, Tukalenko E, Mappes T, Watts PC, Jurvansuu J. Infection Load and Prevalence of Novel Viruses Identified from the Bank Vole Do Not Associate with Exposure to Environmental Radioactivity. Viruses. 2019 Dec 30;12(1):44. 13. Hardmeier I, Aeberhard N, Qi W, Schoenbaechler K, Kraettli H, Hatt JM, et al. Metagenomic analysis of fecal and tissue samples from 18 endemic bat species in Switzerland revealed a diverse virus composition including potentially zoonotic viruses. PLOS ONE. 2021 giu;16(6):e0252534. 14. Wu Z, Yang L, Ren X, He G, Zhang J, Yang J, et al. Deciphering the bat virome catalog to better understand the ecological diversity of bat viruses and the bat origin of emerging infectious diseases. ISME J. 2016 Mar;10(3):609–20.   |

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| **Tables, Figures:**  |

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**Figure 1.** Maximum likelihood phylogenetic inference of the subfamily *Densovirinae*, based on the homologous regions of the NS1 protein-derived amino acid sequences (291 aa), and rooted by two members of the subfamily *Parvovirinae*. The reliability of the tree topology is indicated by bootstrap values, shown as node labels. The calculations were carried out by RAxMLv8 under the LG+GAMMA substitution model. Each species is indicated after the GenBank accession number. New species to be classified in this proposal are indicated in red.

**Figure 2.** Maximum likelihood phylogenetic inference of the subfamily *Parvoviridae*, based on the homologous regions of the NS1 protein-derived amino acid sequences (573 aa), and rooted at midpoint. The reliability of the tree topology is indicated by ultrafast bootstrap and SH-aLRT values, shown as node labels. The calculations were carried out by IQTREE2 under the Q.pfam+F+R8 substitution model. Each virus name is indicated after the GenBank accession number and species names are indicated on the right. New species to be classified in this proposal are indicated in red, and genera in which no new species are classified are collapsed, while those affected by this TP are indicated in red on the left.