

**Part 1:** **TITLE, AUTHORS, APPROVALS, etc**

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| **Code assigned:** | **2022.005D** |  |
| **Short title:** *Parvoviridae*: introduction of the binomial nomenclature, establishment of two new genera and the classification eligibility of parvoviruses derived from ambiguous host origin | | |
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**List the ICTV Study Group(s) that have seen this proposal**

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| *Parvoviridae* Study Group |

**ICTV Study Group comments and response of proposer**

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| We have voted within the Study Group on the best nomenclature, and this one presented was preferred. |

**ICTV Study Group votes on proposal**

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| **Study Group** | **Number of members** | | |
| **Votes support** | **Votes against** | **No vote** |
| *Parvoviridae* | 8 |  | 3 |

**Authority to use the name of a living person**

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| **Is any taxon name used here derived from that of a living person (Y/N)** | N |

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| **Taxon name** | **Person from whom the name is derived** | **Permission attached (Y/N)** |
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**Submission dates**

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| Date first submitted to SC Chair | 05/17/2022 |
| Date of this revision (if different to above) | 05/18/2022 |

**ICTV-EC comments and response of the proposer**

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**Part 2:** **NON-TAXONOMIC PROPOSAL**

**Text of proposal**

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

**Name of accompanying Excel module**

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| 2022.005D.N.v2.Parvoviridae\_2ngen\_49nsp\_125rensp.xlxs |

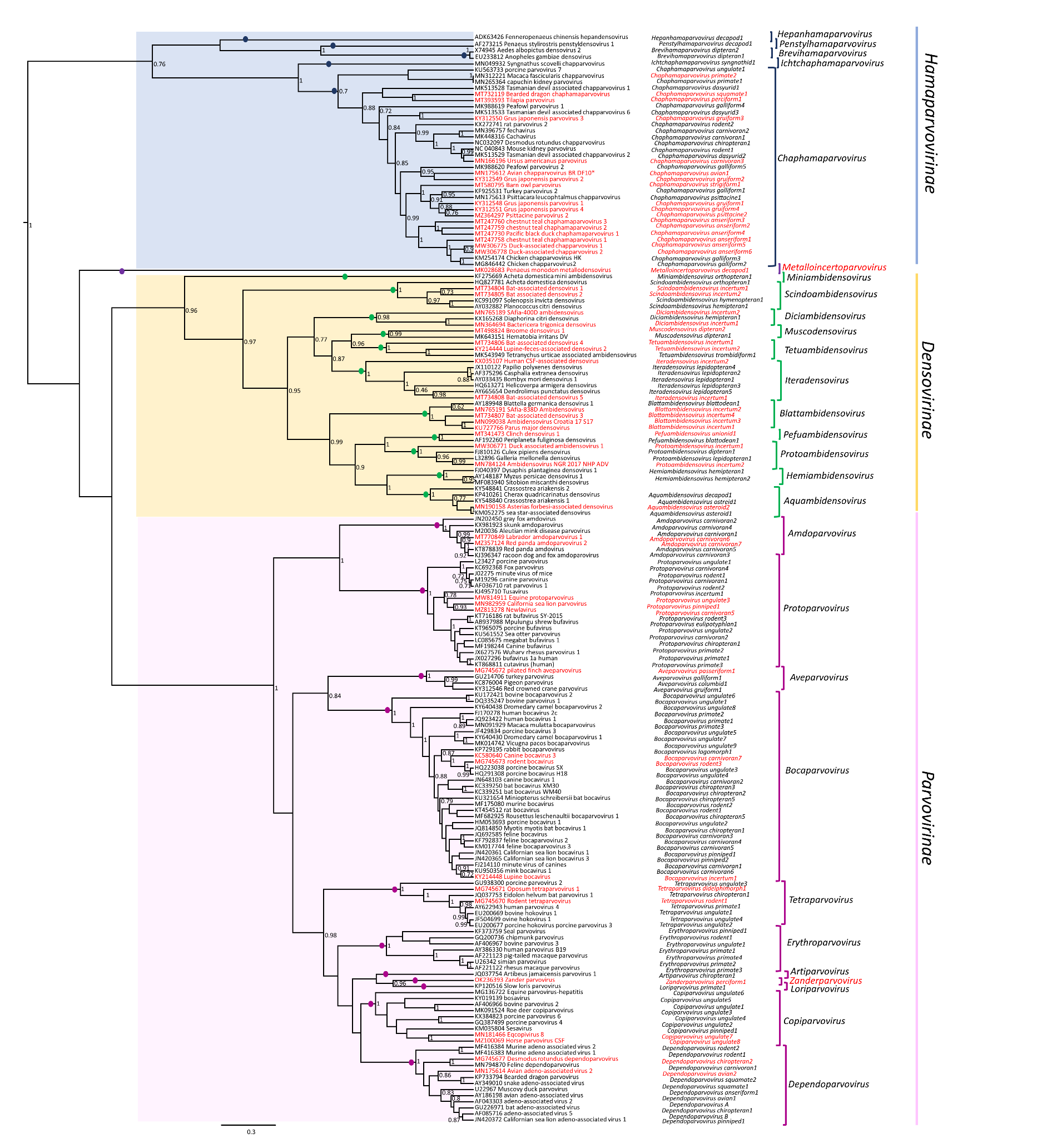
**Abstract**

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| The *Parvoviridae* study group (SG) decided to revise which genomes of parvoviruses can be classified in the *Parvoviridae* family, in order to make it more inclusive. With this revision, parvovirus sequences become eligible for classification even if their natural host spectrum has not been determined. Newly proposed viruses, however, are still required to fulfill the other criteria established by the *Parvoviridae* SG. Owing to the definition change, along with the rapidly accumulating number of potential new parvoviruses, the SG proposes the introduction of 46 new species, out of which 44 can be classified under already established genera. For the classification of the two new viruses, the introduction of further two new genera is necessary. In this proposal we also want to introduce a new binomial species nomenclature system, which will be applied for all newly, as well as previously, classified parvovirus species. |

**Text of proposal**

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| |  | | --- | | **1. Demarcation criteria, definition of a parvovirus suitable for classification**  The number of fully sequenced parvoviral genomes that were derived from metagenomic or environmental sources, as well as from hosts falling outside of the known host spectrum of a given subfamily, has increased significantly in the last couple of years. These genomes, due to their complete nature, contribute significantly to the known parvoviral diversity, hence their potential eligibility for classification requires the attention of the *Parvoviridae* study group (SG). The SG is determined to base its classification criteria on the broadest spectrum of information available to accurately assess parvovirus evolution, an essential approach to establish a robust and functional family-wide taxonomy system. Taken together, the SG decided to revise the virus definition of the *Parvoviridae* family, which, if ratified, would provide an opportunity to classify the above-mentioned potential family members. Furthermore, the SG has now revised the species-level nomenclature of the family, in order to conform with the latest ICTV guidelines, explicitly requiring a binomial naming system. As a result, the virus definition and demarcation criteria are now as follows:  I, Classification eligibility of potential genomes:  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 or evolution, are strongly encouraged. The sequence must be in one piece, containing 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. The sequence must also meet the size constraints and motif patterns typical of the family. 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 host genomes as well as sequences derived from cDNA-based metatranscriptomes.  II, Demarcation criteria and nomenclature:  *Species:* two parvoviruses can potentially be 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 the 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.  **2. Objectives and aims of the current proposal**  As a result of the modification of the definitions and the nomenclature, several novel parvoviruses are now eligible for classification, many of which were deposited into the GenBank several years ago. This indicates and justifies the inclusion of the above-mentioned relaxations, essential to maintain a robust classification system. The introduction of the new binomial nomenclature requires the species-level renaming of all previously classified members of the *Parvoviridae*. In this taxonomy proposal we aim to:   * Rename 130 hitherto classified parvovirus species * Establish a new genus within *Parvoviridae* of a currently unknown subfamily affiliation and establish a new species within this genus * Establish a new genus within the *Parvovirinae* subfamily with one new species * Introduce 15 new species to the genus *Chaphamaparvovirus* within the subfamily *Hamaparvovirinae* * Introduce a new species to the genus *Aquambidensovirus* within the subfamily *Densovirinae* * Introduce four new species to the genus *Blattambidensovirus* within the subfamily *Densovirinae* * Introduce two new species to the genus *Diciambidensovirus* within the subfamily *Densovirinae* * Introduce two new species to the genus *Iteradensovirus* within the subfamily *Densovirinae* * Introduce a new species to the genus *Muscodensovirus* within the subfamily *Densovirinae* * Introduce a new species to the genus *Pefuambidensovirus* within the subfamily *Densovirinae* * Introduce two new species to the genus *Protoambidensovirus* within the subfamily *Densovirinae* * Introduce two new species to the genus *Scindoambidensovirus* of the subfamily *Densovirinae* * Introduce two new species to the genus *Tetuambidensovirus* of the subfamily *Densovirinae* * Introduce two new species to the genus *Amdoparvovirus* of the subfamily *Parvovirinae* * Introduce a new species to the genus *Aveparvovirus* within the subfamily *Parvovirinae* * Introduce three new species to the genus *Bocaparvovirus* of the subfamily *Parvovirinae* * Introduce two new species to the genus *Copiparvovirus* within the subfamily *Parvovirinae* * Introduce a new species to the genus *Dependoparvovirus* of the subfamily *Parvovirinae* * Introduce three new species to the genus *Protoparvovirus* within the subfamily *Parvovirinae* * Introduce two new species to the genus *Tetraparvovirus* of the subfamily *Parvovirinae*   **3. Renaming 130 already-classified parvoviruses**  As a consequence of the introduction of a compulsory binomial species naming system throughout the whole ICTV, the *Parvoviridae* SG decided to re-classify its existing species under a binomial species naming formula as follows: *Genus-name old-species-epithet*. This means that all established *Parvoviridae* species names have been transformed as demonstrated by the examples below by each of the subfamily type species:   * Minute virus of mice * Former: Rodent protoparvovirus 1 * New binomial: *Protoparvovirus rodent1* * Galleria mellonella densovirus * Former: Lepidopteran protoambidensovirus 1 * New binomial: *Protoambidensovirus lepidopteran1* * Aedes albopictus densovirus 2 * Former: Dipteran hamabreviparvovirus 1 * New binomial: *Hamabreviparvovirus dipteran1*   There are, however, some exceptions from this rule, which affects:   * Parvoviruses of carnivores, which now receive the “carnivoran” epithet instead of the former carnivore, as shown here through the example of minute virus of canines; * Former: Carnivore bocaparvovirus 1 * New binomial: *Bocaparvovirus carnivoran1* * Two species of dependoparvoviruses, encompassing all primate adeno-associated viruses (AAVs) and other closely related AAVs, infecting primates and bovid ungulates. The SG decided to uniformize these species names with the rest of the species names within the family, as follows: * Adeno-associated dependoparvovirus A, with a host spectrum exclusively of primates is now *Dependoparvovirus primate1* * Adeno-associated dependoparvovirus B, with a host spectrum encompassing primates and bovid ungulates is now known as *Dependoparvovirus mammalian1* * Tusavirus, the only member of the former sepcies Primate protoparvovirus 4, which has been shown to be present in ungulates, with a strong suspicion that these are it original hosts and humans, as previously belived [1]. As at this point the real host affiliation of tusavirus is ambiguous, we propose to re-classify it as species *Protoparvovirus incertum1*.   All the other species names follow the general formula, detailed above, and are summarized in the Excel module attached to this taxonomy proposal (TP).  **4. Establishing a new genus within *Parvoviridae* of currently unknown subfamily affiliation with one new species**  Penaeus monodon metallodensovirus (PmMDV) was derived from a mass mortality event affecting the widely farmed giant tiger prawn (*Penaeus monodon*) [2]. PmMDV has a small ssDNA genome of just over 4.3 kb in length, flanked by rather large, Y-shaped, partially double-stranded hairpins, organized into inverted terminal repeats (ITRs). Although the PmMDV *NS* and *VP* genes lack any significant similarity to those of any members of the *Parvoviridae*, the PmMDV NS1 protein still harbors the SF3 helicase domain. Furthermore, its capsid structure displays T=1 icosahedral symmetry, consistent with all members of the *Parvoviridae* thus far. As PmMDV fulfills all criteria to be classified as a parvovirus, albeit fails to cluster within any of the currently established subfamilies, the SG decided not to classify it under any of the currently existing subfamilies (Fig. 1). Although PmMDV displays a close phylogenetic relationship with endogenous parvovirus-like elements and transcripts derived from other crustaceans, the existence of one classification-eligible viral entry does not yet validate the establishment of a fourth subfamily. Therefore, we would like to classify PmMDV in its own genus under the name *Metalloincertoparvovirus* and into the new species *Metalloincertoparvovirus decapod1*.  **5. Introducing 15 new species to the genus *Chaphamaparvovirus* within the subfamily *Hamaparvovirinae***  All of the following viruses clustered robustly within the genus *Chaphamaparvovirus*, based on both the SF3 helicase domain (Fig. 1) and the complete NS1-derived aa sequence (Fig. 2). According to these criteria, we would like to assign them as follows:  I, Six new chaphamaparvoviruses, associated with various duck hosts, to six new species within the genus *Chaphamaparvovirus*:   * Chestnut teal chaphamaparvovirus 1, 2 and 3 to species *Chaphamaparvovirus anseriform1*, *Chaphamaparvovirus anseriform2* and *Chaphamaparvovirus anseriform 3*, respectively. All three viruses were derived from the chestnut teal (*Anas castanea*) during a metagenomic study concerning the yearly virome changes of Australian wild ducks [3]. Based on the obtained complete coding sequences of all three viruses, the derived NS1 aa sequence displays at least 80% coverage with almost all chaphamaparvoviruses classified to date, yet with no higher identity than 78.7% to each other or to other chaphamaparvoviruses. * Pacific black duck chaphamaparvovirus to *Chaphamaparvovirus anseriform4*. Detected in the same study in the Pacific black duck (*Anas superciliosa*) [3], the NS1 of this virus displays 46.53% identity at aa level to that of chicken chapparvovirus 1, the highest with any hitherto classified member of the genus. * Duck-associated chapparvovirus 1 and 2 to *Chaphamaparvovirus anseriform5* and *Chaphamaparvovirus anseriform6*, respectively. The complete genome sequence of both viruses was derived from various duck species, including the American black duck (*Anas rubripes*), the common mallard (*A. platyrhynchos*) and the northern pintail (*A. acuta*) with a rather high prevalence of 5.7% [4]. The NS1 derived aa sequence is 82% identical within these two viruses, yet only 65.4% identical to their closest relative of chestnut teal chaphamaparvovirus 1.   II, Four new chaphamaparvoviruses of the red-crowned crane (*Grus japonensis*) to four new species within the genus *Chaphamaparvovirus*:   * Grus japonensis-associated parvovirus 1 to 4 were detected in the fecal virome of wild and captive red crowned cranes and were the only four such viruses of the study with their complete genome sequence obtained [5]. All four viruses display ~46% NS1 protein sequence identity to peafowl parvovirus 1 of the species *Chaphamaparvovirus galliform4* and 46-72% identity to one another, based on their NS1 derived aa sequence. According to these criteria, they are to be classified as species *Chaphamaparvovirus gruiform1*, *Chaphamaparvovirus gruiform2*, *Chaphamaparvovirus gruiform3*, *Chaphamaparvovirus gruiform4*, respectively.   III, Assigning a new chaphamaparvovirus, barn owl parvovirus, to the species *Chaphamaparvovirus strigiform1*:   * Barn owl parvovirus was detected in fecal specimens from barn owl (*Tyro alba*), captured in Hungary [6]. Barn owl parvovirus shares 45.4% identity at the NS1 aa level with peafowl parvovirus 2 of species *Chaphamaparvovirus galliform5*, which is its closest relative.   IV, Assigning a new chaphamaparvovirus, psittaciform chaphamaparvovirus 2 to the species *Chaphamaparvovirus psittacine2*:   * Psittaciform chaphamaparvovirus 2 was derived from Australian Neophema parrots during a metagenomics study [7] and displays the closest NS1-based identity (48.5%) with another avian chaphamaparvovirus, peafowl parvovirus 2.   V, Assigning a new chaphamaparvovirus, tilapia parvovirus, to the new species *Chaphamaparvovirus perciform1*   * Tilapia parvovirus, with its complete coding sequence determined, displays 89-99% NS1 aa identity to various fish parvoviruses disclosed under the names of Ichtyic parvovirus [8] [9]. Interestingly, the same virus could be identified in the fecal virome of crocodiles, which were fed on the same marine fish species. Tilapia parvovirus is closest related to bearded dragon chaphamaparvovirus, (NS1 identity of 45.5%) which was derived from the metatranscriptome of bearded dragons (*Pogona vitticeps*), deceased during a mass mortality event in Australia [10](Fig. 2).   VI, Assigning Macaca fascicularis parvovirus to the new species, *Chaphamaparvovirus primate2*   * Macaca fascicularis parvovirus was detected from cynomolgus macaques (*Macaca fascicularis*) captured in Thailand and screened for the diversity of virus sequences in their fecal virome [11]. This parvovirus is closest related to porcine parvovirus 7 of species *Chaphamaparvovirus ungulate1* (48% identity, NS1 aa) and clusters to a divergent branch of genus *Chaphamaparvovirus*, with no close relation to the other primate chaphamaparvovirus, capuchin kidney parvovirus *of Chaphamaparvovirus primate1* (Fig. 2).   VII, Assigning Ursus americanus parvovirus to the new species, *Chaphamaparvovirus carnivoran3*   * Ursus americanus parvovirus was detected in one American black bear (*Ursus americanus*) individual’s spleen, lymph node and liver samples, in co-infection with a novel circovirus of the same host species [12]. The complete genome of this virus is among the smallest parvoviruses thus far, at only 3.7 kb. Its closest relative is mouse kidney parvovirus of species *Chaphamaparvovirus rodent1*, with an NS1-based aa identity of 73.4%.   **6. Introducing 16 new species to the subfamily *Densovirinae***  I, Establishing the new species *Aquambidensovirus asteroid1* within the genus *Aquambidensovirus*   * Asterias forbesi-associated densovirus was detected in sea stars from the North American Atlantic coast, among sea star samples collected in order to investigate sea star wasting syndrome [13]. Asterias forbesi-associated densovirus, though closely related to sea star-associated densovirus, comprises its own species as the two are only 85% identical at the NS1 aa level. Both clusters robustly within genus *Aquambidensovirus*, along with several recently discovered sea star densoviruses from metatranscriptomes of various species, providing insights into echinoderm aquambidensovirus diversity [14] (Fig. 3).   II, Establishing four new species within the genus *Blattambidensovirus*  All of the following viruses cluster robustly within the genus *Blattambidensovirus*, which was previously perceived as a monotypic genus comprising only Blattella germanica densovirus (Fig. 3).   * Parus major densovirus was detected in the lung tissue of a great tit (*Parus major*), with the capability of causing cytopathic effects (CPE) in feline kidney cells [15]. Based on phylogenetic calculations and the fact that this virus shares 59% identity at the NS1 aa level with that of Blattella germanica densovirus, it becomes clear that Parus major densovirus is probably of arthropod host origin. Due to its ambiguous host origin, we would like to assign this virus to the new species *Blattambidensovirus incertum1*. * Ambidensovirus Croatia 17-S17 was detected in the viral metagenome of guano and oral swabs, derived from Croatian bats captured for a large-scale viral ecology study [16]. As this virus displays the highest identity with the Blattella germanica densovirus NS1 protein, it will be classified to the new species *Blattambidensovirus incertum2*. * Bat-associated densovirus 3 was shown to be a commonly present densovirus in bat roosts found in Northern California [17] and displays 65.5% NS1 aa identity with that of its closest relative, Blattella germanica densovirus. Bat-associated densovirus is to be assigned to species *Blattambidensovirus incertum3*. * SAfia-838D ambidensovirus was identified in a metagenomic study of the blood virosphere of Tanzanian children along with several other ambisense densovirus sequences [18]. It shares the highest NS1-related aa identity with that of Blattella germanica densovirus (64.85%) and is to be assigned to the species *Blattambidensovirus incertum4*.   III, Establishing two new species within the genus *Diciambidensovirus*  Both of these sequences cluster with a strong monophyly into this previously monotypic genus (Fig. 3)   * Bactericera trigonica densovirus was detected to infect the carrot psyllid (*Bactericera trigonica*), responsible for spreading various viral pathogens of carrots [19]. Its NS1 protein aa sequence harbors 54.76% identity to that of Diaphorina citri densovirus, the type virus of the genus *Diciambidensovirus*. Bactericera trigonica densovirus is to be classified to the new species *Diciambidensovirus hemipteran2*. * SAfia-400D ambidensovirus is another one of the ambisense densoviruses detected in and fully-sequenced from the blood virome of Tanzanian children [18], harboring 37% identity of its NS1 protein with that of Diaphorina citri densovirus, hence it is to be classified as species *Diciambidensovirus incertum1.*   IV, Establishing two new species within the genus *Iteradensovirus*   * Bat-associated densovirus 5 was derived from the same Californian study of bat roost viromes as bat associated densoviruses 1 to 4 [17]. Apart from clustering among iteradensoviruses (Fig. 1 and 3), it also possesses a monosense genome, similarly to all members of genus *Iteradensovirus* thus far. Its NS1 protein sequence displays 36% similarity with that of Helicoverpa armigera densovirus. Based on these, bat-associated densovirus is to be assigned to the species *Iteradensovirus incertum1*. * Human CSF-associated densovirus also harbors a monosense genome and clusters among iteradensoviruses (Fig. 1 and 3). This virus was derived from the cerebrospinal fluid of a human patient displaying signs of encephalitis, yet no other viral infectious agents could be revealed [20]. The NS1 protein sequence of human CSF-associated densovirus displays over 90% coverage and 35.4% sequence identity with the same protein of Dendrolimus punctatus densovirus, hence it is to be classified as a new species within genus *Iteradensovirus*, as species *Iteradensovirus incertum2*.   V, Establishing a new species within the genus *Muscodensovirus*   * Broome densovirus was detected in Western Australia during the metagenomic analysis of the Skuse mosquito (*Culex annulirostris*) virome, an important vector of various arboviruses [21]. Although the NS1 protein of Broome densovirus displays 85% coverage with that of Hematobia irritans densovirus, the sole hitherto member of genus *Muscodensovirus*, the identity they share is only 28.04%. Despite of this, Broome densovirus forms a strong monophyletic clade with Hematobia irritans densovirus (Fig. 1 and 3) and both are derived from dipteran hosts. Moreover, both possess a similarly sized monosense genome, unlike most members of the *Densovirinae* subfamily (with members of genus *Iteradensovirus* being the other exception, possibly evolved independently). Considering the striking differences in the degree of conversation within the *Densovirinae* genera, the SG decided to give more weight to the results of the phylogenetic calculations, general genome organization as well as high protein coverage, as opposed to sheer NS1 aa sequence identity. According to this, Broome densovirus will be assigned to genus *Muscodensovirus*, as a new species *Muscodensovirus dipteran2*.   VI, Establishing a new species within the genus *Pefuambidensovirus*   * Clinch densovirus was detected in association with a mass mortality event occurring in freshwater mussels (*Actinonaias pectorosa*) living in the Clinch River from the state of Tennessee to Virginia [22]. Despite of its aquatic origins, Clinch densovirus clusters within genus *Pefuambidensovirus* (Fig. 1 and 3), together with a starfish-derived densovirus, detected from the metatranscriptome study already detailed above [14]. The NS1-based pairwise aa sequence identity between Clinch densovirus and Periplaneta fuliginosa densovirus is 63.74%, hence it will be classified under the new species *Pefuambidensovirus unionid1*.   VII, Establishing a new species within the genus *Protoambidensovirus*   * Duck associated ambidensovirus 1 and its closely related counterparts were detected and described in the same study as duck-associated chapparvovirus 1 and 2 [4]. This virus was revealed to be highly prevalent in the North American ducks. All duck-associated ambidensoviruses detected within the aforementioned study are members of the same species (~95% identical at NS1 aa level) and we propose to classify them as *Protoambidensovirus incertum1*. This classification is supported by the phylogenetic position of duck-associated ambidensovirus 1 as well as by its NS1 protein aa coverage of 98%, disclosing 38.3% identity to that of Diatraea saccharalis densovirus, a member of the species *Protoambidensovirus lepidoptean1*.   VIII, Establishing two new species within the genus *Scindoambidensovirus*   * Bat-associated densovirus 1 and 2 are to be assigned to two new species within genus *Scindoambidensovirus*, under species names *Scindoambidensovirus incertum1* and *Scindoambidensovirus incertum2*, respectively. Both densoviruses were detected during the Californian bat virome study [17]. At the NS1 aa sequence level, the two viruses display 49% similarity, while this value is ~50% with their closest relative, Solenopsis invicta densovirus of species *Scindoambidensovirus hymenopteran1*.   IX, Establishing two new species within the genus *Tetuambidensovirus*   * Bat-associated densovirus 4, also from the aforementioned study [17], clusters within a robust monophyletic clade that includes Tetranychus urticae-associated densovirus, the sole hitherto classified member of genus *Tetuambidensovirus* (Fig. 1 and 3). These two viruses share NS1 protein sequences of 90% pairwise coverage as well as of 34.71% similarity. Based on these, we would like to classify Bat-associated densovirus 5 as a member of genus *Tetuambidensovirus*, under the species name of *Tetuambidensovirus incertum1*. * Lupin feces-associated densovirus 2 harbors 38% aa identity with 93% coverage when its NS1 is compared to that of its closest relative, Tetranychus urticae-associated densovirus. This virus was derived from the fecal matter of free-ranging wolfs (*Canis lupus*) with ongoing diarrhea in Portugal [23] and is to be classified within the genus *Tetuambidensovirus* under new species *Tetuambidensovirus incertum2*.   **7. Introducing 14 new species to the subfamily *Parvovirinae***  I, Introduction of two new species to genus *Amdoparvovirus*   * *Amdoparvovirus carnivoran6*. We propose to assign the Labrador amdoparvovirus 1 (LaAV-1) to this new species within the genus *Amdoparvovirus*. This virus was discovered in spleen samples from animals from Labrador (Canada) and was found to circulate among foxes (3.5%) and martens (3.4%). Carnivory is suspected to be involved in its cross-species transmission [24]. The complete coding sequence of this virus exists, and it fulfills the requirements for its classification as a parvovirus. In the phylogenetic analysis based on the NS1 of all members of the subfamily *Parvovirinae* (Fig. 4), LaAV-1 clusters within a highly supported clade corresponding to the genus *Amdoparvovirus*, but its NS1 is approximately 80% identical to the NS1 of its closest relatives [24], fulfilling the requirements to be classified as a new species. * *Amdoparvovirus carnivoran7*. We propose to assign the red panda amdoparvovirus 2 (RpAV-2) to this new species within the genus *Amdoparvovirus*. This virus was found in various tissue samples of 32 captive Chinese red pandas circulating with a prevalence of 56.4% [25]. The complete coding sequence of this virus exists, and it fulfills the requirements for its classification as a parvovirus. RpAV-2 is a close relative of viruses within the genus *Amdoparvovirus* (Fig. 4) but its NS1 diverges by at least ~20% from other amdoparvoviruses (2), fulfilling the requirements to be classified as a new species.   II, Introduction of a new species to the genus *Aveparvovirus*   * *Aveparvovirus passeriform1*. We propose to assign the pileated finch aveparvovirus (PfPV) to this new species within the genus *Aveparvovirus*. This virus was found in pooled cloacal swabs of grey pileated finches in Brazil [26]. The complete coding sequence of this virus has been sequenced and it fulfills the requirements for its classification as a parvovirus. The NS1 of this virus clusters within a highly supported clade corresponding to the genus *Aveparvovirus* (Fig.4) but it is approximately 65% identical to its closest aveparvoviral relative, fulfilling the requirements to be classified as a new species within this genus.   III, Introduction of three new species to the genus *Bocaparvovirus*   * *Bocaparvovirus carnivoran7*. We propose to assign canine bocavirus 3 (CnBoV3) to this new species within the genus *Bocaparvovirus*. This virus was found in the liver of a dog with severe hemorrhagic gastroenteritis, necrotizing vasculitis, granulomatous lymphadenitis and anuric renal failure [27]. However, the link between this virus and disease has not been established. The complete genome of this virus exists, and it fulfills the requirements for its classification as a parvovirus, including the NP1 ORF typical of bocaparvoviruses. The NS1 of this virus is included in a highly supported clade uniting all other members of the *Bocaparvovirus* (Fig. 4) but shares only ~60% identity with its closest bocaparvoviral relative, fulfilling the requirements to be classified in a new species. * *Bocaparvovirus incertum1*. We propose to assign the lupine bocavirus (LuBoV) and the rabbit bocavirus (RBoV) to this new species within the genus *Bocaparvovirus*. LuBoV was discovered in 2017 in fecal material of Portuguese wolves and screening revealed a viral prevalence of 36.6% in the wolf population [23]. RBoV was identified in 2020 in oral swabs, skin, blood, and fecal samples of laboratory rabbits with a prevalence of 59.7% [28]. The complete coding sequence of these viruses show all characteristics typical of bocaviruses, including the NP1 ORF. The NS1 proteins of these two viruses share less than 50% identity with other bocaparvoviruses but are 99% identical to each-other and belong, therefore, to the same species. Phylogenetically, these two viruses cluster within the *Bocaparvovirus* genus clade (Fig. 4), fulfilling the requirements to be classified as a new species. Since, at this time, the host distribution of these viruses is still unclear, we propose the name *Bocaparvovirus incertum1* for this species. * *Bocaparvovirus rodent3*. We propose to assign the rodent bocavirus (RoBoV) to this new species within the genus *Bocaparvovirus*. This virus was found in pooled blood samples of hairy-tailed bolo mice in Brazil [26]. The complete coding sequence of this virus has been sequenced and it fulfills the requirements for its classification as a parvovirus, including the NP1 ORF typical of bocaparvoviruses. The NS1 of this virus clusters within a highly supported clade corresponding to the genus *Bocaparvovirus* (Fig. 4) but it is approximately 77% identical to its closest bocaparvoviral relative, fulfilling the requirements to be classified as a new species within this genus.   IV, Introduction of two new species to the genus *Copiparvovirus*   * *Copiparvovirus ungulate7*. We propose to assign the Eqcopivirus (EqCoPV) to this new species within the genus *Copiparvovirus*. This virus was discovered in plasma from horses with respiratory signs and it was later detected also in respiratory swabs of the same animals, indicating that this virus could be a respiratory pathogen. However, since there was no statistically significant difference in viral prevalence in plasma from animals with respiratory signs and those from healthy animals, its role as a pathogen remains unclear [29]. The complete coding sequence of this virus exists, and it fulfills the requirements for its classification as a parvovirus. The NS1 of this virus is included in a highly supported clade corresponding to the genus *Copiparvovirus* (Fig. 4) but it shares only ~40% identity with its closest copiparvoviral relative, fulfilling the requirements to be classified as a new species within this genus. * *Copiparvovirus ungulate8*. We propose to assign Horse parvovirus CSF (EqPV-CSF) to this new species within the genus *Copiparvovirus*. This virus was discovered, but only partially sequenced, in 2015 in one cerebrospinal fluid sample from a horse with neurological signs and lymphocytic pleocytosis [30]. Several follow-up studies confirmed the presence of this virus in sera, plasma, cerebrospinal fluid and respiratory swabs collected from various horse populations [29, 31, 32], but its role as a pathogen is still unclear. The complete coding sequence of this virus is now available, and it fulfills the requirements for its classification as a parvovirus. The NS1 of this virus is included in the *Copiparvovirus* clade (Fig. 4) but shares only ~40% identity with its closest copiparvoviral relative, fulfilling the requirements to be classified as a new species within this genus.   V, Introduction of a new species to the genus *Dependoparvovirus*   * *Dependoparvovirus chiropteran2*. We propose to assign the Desmodus rotundus dependoparvovirus (DrAAV) to this new species within the genus *Dependoparvovirus*. This virus was found in pooled kidney samples collected from vampire bats in Brazil [26]. The complete coding sequence of this virus has been sequenced and it fulfills the requirements for its classification as a parvovirus. The NS1 of this virus clusters within a highly supported clade corresponding to the genus *Dependoparvovirus* (Fig. 4) but it is approximately 50% identical to its closest dependoparvoviral relative, fulfilling the requirements to be classified as a new species within this genus.   VI, Introduction of three new species to the genus *Protoparvovirus*   * *Protoparvovirus pinniped1*. We propose to assign the California sea lion parvovirus Hanchett (CslPV) to this new species within the genus *Protoparvovirus*. This virus was discovered in a mesenteric lymph node collected from a stranded emaciated sea lion with polyserositis and steatitis [33]. However, a link between this virus and disease has not been established. The complete coding sequence of this virus has been sequenced and it fulfills the requirements for its classification as a parvovirus. The NS1 of this virus clusters within a highly supported clade corresponding to the genus *Protoparvovirus* (Fig. 4) but it is less than 60% identical to its closest protoparvoviral relative, fulfilling the requirements to be classified as a new species within this genus. * *Protoparvovirus carnivoran5*. We propose to assign the parvovirus newlavirus (NLPV) to this new species within the genus *Protoparvovirus*. This virus was discovered in foxes from the Canadian Province Newfoundland and Labrador and found to circulate in fox populations with high prevalence (39.4-44%). Thirteen different genotypes were described, and the virus was not detected in other sympatric carnivorans [34]. The complete coding sequence of this virus has been sequenced and it fulfills the requirements for its classification as a parvovirus. The NS1 of this virus clusters within a highly supported clade corresponding to the genus *Protoparvovirus* (Fig. 4) but it is less than 60% identical to its closest protoparvoviral relative, fulfilling the requirements to be classified as a new species within this genus. * *Protoparvovirus ungulate3*. We propose to assign the Equine protoparvovirus (EqPV) to this new species within the genus *Protoparvovirus*. This virus was found in tissues of foals with interstitial pneumonia, but the causative link between this virus and the disease has not been established [35]. The complete coding sequence of this virus has been sequenced and it fulfills the requirements for its classification as a parvovirus. The NS1 of this virus clusters within the *Protoparvovirus* clade (Fig. 4) but it is ~50% identical to its closest protoparvoviral relative, fulfilling the requirements to be classified as a new species within this genus.   VII, Introduction of two new species to the genus *Tetraparvovirus*   * *Tetraparvovirus didelphimorph1*. We propose to assign the opossum tetraparvovirus (OpPARV4) to this new species within the genus *Tetraparvovirus*. This virus was discovered in a sample of pooled sera collected from opossums in Brazil [26]. The complete coding sequence of this virus has been sequenced and it fulfills the requirements for its classification as a parvovirus. The NS1 of this virus clusters within a highly supported clade corresponding to the genus *Tetraparvovirus* (Fig. 4) but it is less than 50% identical to its closest tetraparvoviral relative, fulfilling the requirements to be classified as a new species within this genus. * *Tetraparvovirus rodent1*. We propose to assign the rodent tetraparvovirus (RoPARV4) to this new species within the genus *Tetraparvovirus*. This virus was discovered in two samples of pooled blood collected from mice in Brazil [26]. The complete coding sequence of this virus has been sequenced and it fulfills the requirements for its classification as a parvovirus. The NS1 of this virus clusters within a highly supported clade corresponding to the genus *Tetraparvovirus* (Fig. 4) but it is approximately 51% identical to its closest tetraparvoviral relative, fulfilling the requirements to be classified as a new species within this genus.   **8. Creating a new genus and one new species within the subfamily *Parvovirinae*.**  I, Establishing the new genus *Sandeparvovirus*   * The zander parvovirus (ZPV) was recently discovered in fecal samples from pike-perch fish (*Sander lucioperca*) in Hungary. Screening 62 fecal specimens collected from 13 freshwater fish species, demonstrated that only this fish species was positive for this virus with three out of the seven specimens from this species (42.8%) being ZPV-positive [36]. The complete coding sequence of this virus was obtained, and it showed all the characteristics for the virus to be classified as a parvovirus, including the two ORFs coding for the NS1 and VP1/VP2 proteins and the helicase and RCR motifs in the predicted NS1. However, the virus lacked the PLA2 domain in VP1, as also previously reported for other parvoviruses. ZPV contains an additional ORF downstream the ORF for the structural proteins coding for a hypothetical protein with unknown function. Since the NS1 protein of this virus is not included in a highly supported clade and it does not disclose NS1 protein pairwise sequence identity higher than 33% (H1 parvovirus of genus *Protoparvovirus*), we would like to establish a new genus, Sandeparvovirus, to accommodate the new species *Sandeparvovirus perciform1*. | |

**Supporting evidence**



**Figure 1** Bayesian inference of the entire *Parvoviridae* family, based on the SF3 helicase domain (155-aa-long) of the NS1 protein (by the BEAST v.1.10 suite using the LG+I+G substitution model, with a lognormal relaxed clock and Yule speciation model through 100 million generations). The posterior probability values are shown as node labels, if significant (>0.7). The nodes of each genus are labelled with a spot, color coded based on subfamily affiliation. Taxa and viruses introduced in this proposal are highlighted in red. Proposed taxa and viruses in the TP by Duarte et al. (Create 1 new species in the genus *Chaphamaparvovirus*, and 1 new species in the genus *Dependoparvovirus*, in the family *Parvoviridae*) are marked with a star (\*).

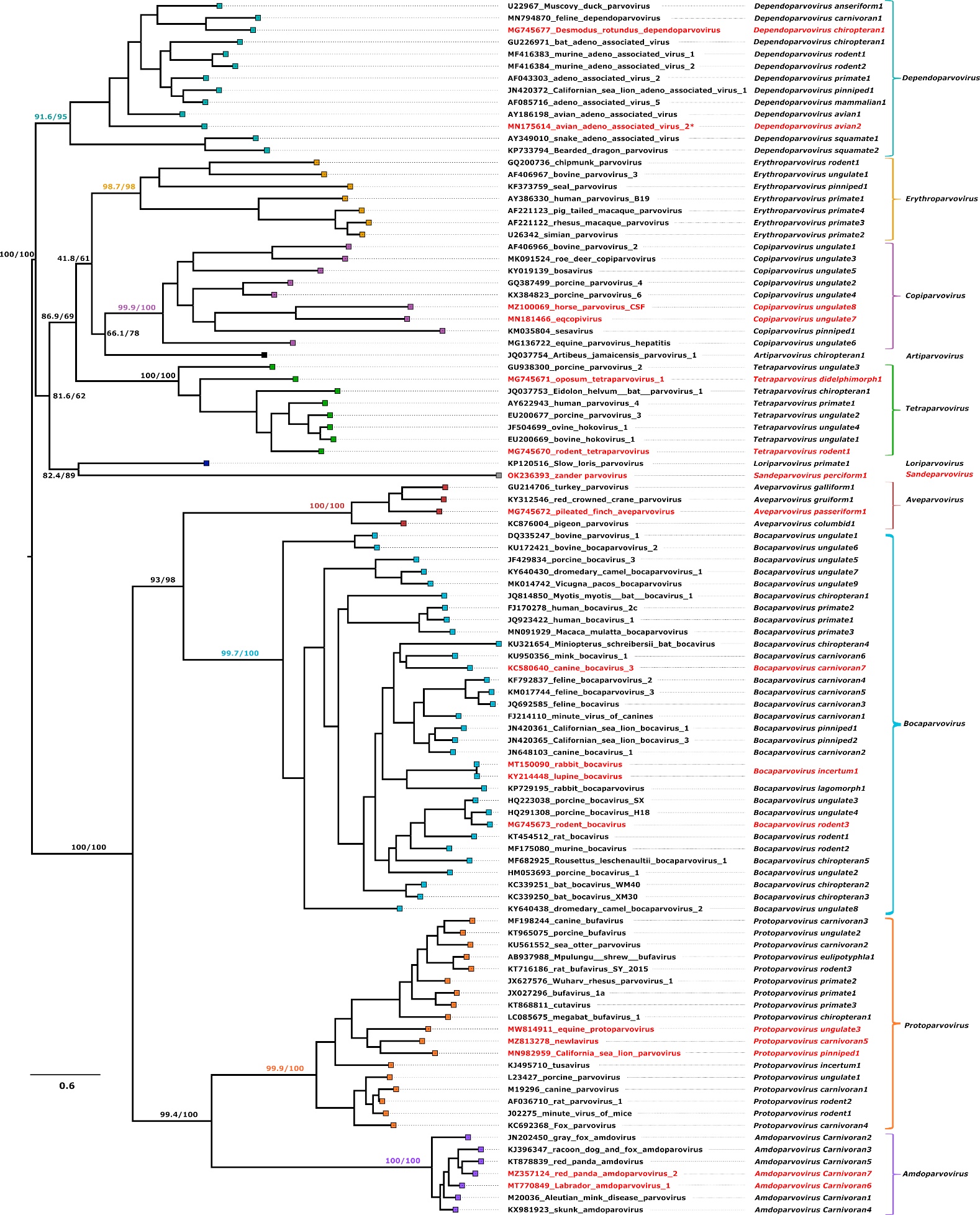
Diagram

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**Figure 2** Bayesian inference of the subfamily *Hamaparvovirinae*, based on the 475-aa-long homologous region of the NS1 protein (by the BEAST v.1.10 suite using the LG+I+G substitution model, with a lognormal relaxed clock and Yule speciation model through 30 million generations). The posterior probability values are shown as node labels, if significant (>0.7). The nodes of each genus are labelled with a dark blue circle. Taxa and viruses introduced in this proposal are highlighted in red. The proposed virus in the TP by Duarte et al. (Create 1 new species in the genus *Chaphamaparvovirus*, and 1 new species in the genus *Dependoparvovirus*, in the family *Parvoviridae*) is marked with a star (\*). Viruses for which the complete coding sequence has been determined albeit are not eligible for classification, are indicated in blue and included for more reliable phylogenetic inference.



**Figure 3** Maximum likelihood inference of the subfamily *Densovirinae*, based on the 552-aa-long homologous regions of the NS1 protein (by PhyML v3.3 using the LG+G+I substitution model). The reliability of the topology was tested by aLRT-sh-like test and bootstrapping of 1000 replicates, shown as percentage on node labels, if significant (>70). The nodes of each genus are labelled with a green circle. Taxa and viruses introduced in this proposal are highlighted in red. Viruses for which the complete coding sequence has been determined, yet are not eligible for classification, are indicated in blue and included for a more reliable phylogenetic inference.



**Figure 4** Maximum likelihood inference of subfamily *Parvovirinae*, based on a 582-aa-long alignments encompassing the homologous regions of the NS1 protein (by IQ-TREE 2 using the LG+F+R7 substitution model). The reliability of the topology was tested by SH-aLRT test and bootstrapping of 1000 replicates and results are shown for all main nodes. Sequences in each genus are labelled with a colored square that is unique for each genus. The proposed virus in the TP by Duarte et al. (Create 1 new species in the genus Dependoparvovirus, in the family Parvoviridae) is marked with a star (\*).

**References**

1. Reuter G, Pankovics P, László Z, Gáspár G, Hui A, Delwart E, Boros Á (2022) Human-stool-associated tusavirus (Parvoviridae) in domestic goats and sheep. Arch Virol 167:1307-1310, 10.1007/s00705-022-05424-8:10.1007/s00705-022-05424-8, PMC9038789, PMID: 35355143

2. Pénzes JJ, Pham HT, Chipman P, Bhattacharya N, McKenna R, Agbandje-McKenna M, Tijssen P (2020) Molecular biology and structure of a novel penaeid shrimp densovirus elucidate convergent parvoviral host capsid evolution. Proc Natl Acad Sci U S A 117:20211-20222, 10.1073/pnas.2008191117:10.1073/pnas.2008191117, PMC7443866, PMID: 32747554

3. Vibin J, Chamings A, Klaassen M, Bhatta TR, Alexandersen S (2020) Metagenomic characterisation of avian parvoviruses and picornaviruses from Australian wild ducks. Sci Rep 10:12800, 10.1038/s41598-020-69557-z:10.1038/s41598-020-69557-z, PMC7393117, PMID: 32733035

4. Canuti M, Verhoeven JTP, Munro HJ, Roul S, Ojkic D, Robertson GJ, Whitney HG, Dufour SC, Lang AS (2021) Investigating the Diversity and Host Range of Novel Parvoviruses from North American Ducks Using Epidemiology, Phylogenetics, Genome Structure, and Codon Usage Analysis. Viruses 13, 10.3390/v13020193:10.3390/v13020193, PMC7912424, PMID: 33525386

5. Wang Y, Yang S, Liu D, Zhou C, Li W, Lin Y, Wang X, Shen Q, Wang H, Li C, Zong M, Ding Y, Song Q, Deng X, Qi D, Zhang W, Delwart E (2019) The fecal virome of red-crowned cranes. Arch Virol 164:3-16, 10.1007/s00705-018-4037-x:10.1007/s00705-018-4037-x, PMC7086969, PMID: 30225519

6. Hargitai R, Boros Á, Pankovics P, Mátics R, Altan E, Delwart E, Reuter G (2021) Detection and genetic characterization of a novel parvovirus (family Parvoviridae) in barn owls (Tyto alba) in Hungary. Arch Virol 166:231-236, 10.1007/s00705-020-04862-6:10.1007/s00705-020-04862-6, PMID: 33136208

7. Sarker S (2021) Molecular and Phylogenetic Characterisation of a Highly Divergent Novel Parvovirus (Psittaciform Chaphamaparvovirus 2) in Australian Neophema Parrots. Pathogens 10, 10.3390/pathogens10121559:10.3390/pathogens10121559, PMC8706300, PMID: 34959514

8. Liu W, Zhang Y, Ma J, Jiang N, Fan Y, Zhou Y, Cain K, Yi M, Jia K, Wen H, Guan W, Zeng L (2020) Determination of a novel parvovirus pathogen associated with massive mortality in adult tilapia. PLoS Pathog 16:e1008765, 10.1371/journal.ppat.1008765:10.1371/journal.ppat.1008765, PMC7588064, PMID: 32970777

9. Du J, Wang W, Chan JF, Wang G, Huang Y, Yi Y, Zhu Z, Peng R, Hu X, Wu Y, Zeng J, Zheng J, Cui X, Niu L, Zhao W, Lu G, Yuen KY, Yin F (2019) Identification of a Novel Ichthyic Parvovirus in Marine Species in Hainan Island, China. Front Microbiol 10:2815, 10.3389/fmicb.2019.02815:10.3389/fmicb.2019.02815, PMC6907010, PMID: 31866980

10. Chang WS, Li CX, Hall J, Eden JS, Hyndman TH, Holmes EC, Rose K (2020) Meta-Transcriptomic Discovery of a Divergent Circovirus and a Chaphamaparvovirus in Captive Reptiles with Proliferative Respiratory Syndrome. Viruses 12, 10.3390/v12101073:10.3390/v12101073, PMC7600432, PMID: 32992674

11. Sawaswong V, Fahsbender E, Altan E, Kemthong T, Deng X, Malaivijitnond S, Payungporn S, Delwart E (2019) High Diversity and Novel Enteric Viruses in Fecal Viromes of Healthy Wild and Captive Thai Cynomolgus Macaques (Macaca fascicularis). Viruses 11, 10.3390/v11100971:10.3390/v11100971, PMC6832579, PMID: 31652508

12. Alex CE, Fahsbender E, Altan E, Bildfell R, Wolff P, Jin L, Black W, Jackson K, Woods L, Munk B, Tse T, Delwart E, Pesavento PA (2020) Viruses in unexplained encephalitis cases in American black bears (Ursus americanus). PLoS One 15:e0244056, 10.1371/journal.pone.0244056:10.1371/journal.pone.0244056, PMC7745964, PMID: 33332429

13. Jackson EW, Pepe-Ranney C, Johnson MR, Distel DL, Hewson I (2020) A Highly Prevalent and Pervasive Densovirus Discovered among Sea Stars from the North American Atlantic Coast. Appl Environ Microbiol 86, 10.1128/aem.02723-19:10.1128/aem.02723-19, PMC7054102, PMID: 31924612

14. Jackson EW, Wilhelm RC, Johnson MR, Lutz HL, Danforth I, Gaydos JK, Hart MW, Hewson I (2020) Diversity of Sea Star-Associated Densoviruses and Transcribed Endogenous Viral Elements of Densovirus Origin. J Virol 95, 10.1128/jvi.01594-20:10.1128/jvi.01594-20, PMC7737747, PMID: 32967964

15. Yang WT, Shi SH, Jiang YL, Zhao L, Chen HL, Huang KY, Yang GL, Wang CF (2016) Genetic characterization of a densovirus isolated from great tit (Parus major) in China. Infect Genet Evol 41:107-112, 10.1016/j.meegid.2016.03.035:10.1016/j.meegid.2016.03.035, PMID: 27051046

16. Šimić I, Zorec TM, Lojkić I, Krešić N, Poljak M, Cliquet F, Picard-Meyer E, Wasniewski M, Zrnčić V, Ćukušić A, Bedeković T (2020) Viral Metagenomic Profiling of Croatian Bat Population Reveals Sample and Habitat Dependent Diversity. Viruses 12, 10.3390/v12080891:10.3390/v12080891, PMC7472731, PMID: 32824037

17. Li Y, Altan E, Reyes G, Halstead B, Deng X, Delwart E (2021) Virome of Bat Guano from Nine Northern California Roosts. J Virol 95, 10.1128/jvi.01713-20:10.1128/jvi.01713-20, PMC7925108, PMID: 33115864

18. Cordey S, Laubscher F, Hartley MA, Junier T, Keitel K, Docquier M, Guex N, Iseli C, Vieille G, Le Mercier P, Gleizes A, Samaka J, Mlaganile T, Kagoro F, Masimba J, Said Z, Temba H, Elbanna GH, Tapparel C, Zanella MC, Xenarios I, Fellay J, D'Acremont V, Kaiser L (2021) Blood virosphere in febrile Tanzanian children. Emerg Microbes Infect 10:982-993, 10.1080/22221751.2021.1925161:10.1080/22221751.2021.1925161, PMC8171259, PMID: 33929935

19. Ghosh S, Sela N, Ghanim M (2019) Complete Genome Sequence of a Putative Densovirus Infecting the Carrot Psyllid Bactericera trigonica. Microbiol Resour Announc 8, 10.1128/mra.01103-19:10.1128/mra.01103-19, PMC6883104, PMID: 31776217

20. Phan TG, Messacar K, Dominguez SR, da Costa AC, Deng X, Delwart E (2016) A new densovirus in cerebrospinal fluid from a case of anti-NMDA-receptor encephalitis. Arch Virol 161:3231-3235, 10.1007/s00705-016-3002-9:10.1007/s00705-016-3002-9, PMC6550996, PMID: 27522586

21. Williams SH, Levy A, Yates RA, Somaweera N, Neville PJ, Nicholson J, Lindsay MDA, Mackenzie JS, Jain K, Imrie A, Smith DW, Lipkin WI (2020) The Diversity and Distribution of Viruses Associated with Culex annulirostris Mosquitoes from the Kimberley Region of Western Australia. Viruses 12, 10.3390/v12070717:10.3390/v12070717, PMC7411826, PMID: 32630711

22. Richard JC, Leis E, Dunn CD, Agbalog R, Waller D, Knowles S, Putnam J, Goldberg TL (2020) Mass mortality in freshwater mussels (Actinonaias pectorosa) in the Clinch River, USA, linked to a novel densovirus. Sci Rep 10:14498, 10.1038/s41598-020-71459-z:10.1038/s41598-020-71459-z, PMC7468154, PMID: 32879395

23. Conceição-Neto N, Godinho R, Álvares F, Yinda CK, Deboutte W, Zeller M, Laenen L, Heylen E, Roque S, Petrucci-Fonseca F, Santos N, Van Ranst M, Mesquita JR, Matthijnssens J (2017) Viral gut metagenomics of sympatric wild and domestic canids, and monitoring of viruses: Insights from an endangered wolf population. Ecol Evol 7:4135-4146, 10.1002/ece3.2991:10.1002/ece3.2991, PMC5478050, PMID: 28649326

24. Canuti M, Todd M, Monteiro P, Van Osch K, Weir R, Schwantje H, Britton AP, Lang AS (2020) Ecology and Infection Dynamics of Multi-Host Amdoparvoviral and Protoparvoviral Carnivore Pathogens. Pathogens 9, 10.3390/pathogens9020124:10.3390/pathogens9020124, PMC7168296, PMID: 32075256

25. Zhao M, Yue C, Yang Z, Li Y, Zhang D, Zhang J, Yang S, Shen Q, Su X, Qi D, Ma R, Xiao Y, Hou R, Yan X, Li L, Zhou Y, Liu J, Wang X, Wu W, Zhang W, Shan T, Liu S (2022) Viral metagenomics unveiled extensive communications of viruses within giant pandas and their associated organisms in the same ecosystem. Sci Total Environ 820:153317, 10.1016/j.scitotenv.2022.153317:10.1016/j.scitotenv.2022.153317, PMID: 35066043

26. de Souza WM, Dennis T, Fumagalli MJ, Araujo J, Sabino-Santos G, Maia FGM, Acrani GO, Carrasco AOT, Romeiro MF, Modha S, Vieira LC, Ometto T, Queiroz LH, Durigon EL, Nunes MRT, Figueiredo LTM, Gifford RJ (2018) Novel Parvoviruses from Wild and Domestic Animals in Brazil Provide New Insights into Parvovirus Distribution and Diversity. Viruses 10, 10.3390/v10040143:10.3390/v10040143, PMC5923437, PMID: 29565808

27. Li L, Pesavento PA, Leutenegger CM, Estrada M, Coffey LL, Naccache SN, Samayoa E, Chiu C, Qiu J, Wang C, Deng X, Delwart E (2013) A novel bocavirus in canine liver. Virol J 10:54, 10.1186/1743-422x-10-54:10.1186/1743-422x-10-54, PMC3577433, PMID: 23402347

28. Xiao Y, Wang H, Feng L, Pan J, Chen Z, Yang S, Shen Q, Wang X, Shan T, Zhang W (2020) Fecal, oral, blood and skin virome of laboratory rabbits. Arch Virol 165:2847-2856, 10.1007/s00705-020-04808-y:10.1007/s00705-020-04808-y, PMC7546134, PMID: 33034764

29. Altan E, Li Y, Sabino-Santos G, Jr., Sawaswong V, Barnum S, Pusterla N, Deng X, Delwart E (2019) Viruses in Horses with Neurologic and Respiratory Diseases. Viruses 11, 10.3390/v11100942:10.3390/v11100942, PMC6832430, PMID: 31614994

30. Li L, Giannitti F, Low J, Keyes C, Ullmann LS, Deng X, Aleman M, Pesavento PA, Pusterla N, Delwart E (2015) Exploring the virome of diseased horses. J Gen Virol 96:2721-2733, 10.1099/vir.0.000199:10.1099/vir.0.000199, PMC4635498, PMID: 26044792

31. Xie J, Tong P, Zhang A, Song X, Zhang L, Shaya N, Kuang L (2020) An emerging equine parvovirus circulates in thoroughbred horses in north Xinjiang, China, 2018. Transbound Emerg Dis 67:1052-1056, 10.1111/tbed.13443:10.1111/tbed.13443, PMID: 31793239

32. Yoon J, Park T, Kim A, Song H, Park BJ, Ahn HS, Go HJ, Kim DH, Lee JB, Park SY, Song CS, Lee SW, Choi IS (2021) First Detection and Genetic Characterization of New Equine Parvovirus Species Circulating among Horses in Korea. Vet Sci 8, 10.3390/vetsci8110268:10.3390/vetsci8110268, PMC8621016, PMID: 34822641

33. Altan E, Delaney MA, Colegrove KM, Spraker TR, Wheeler EA, Deng X, Li Y, Gulland FMD, Delwart E (2020) Complex Virome in a Mesenteric Lymph Node from a Californian Sea Lion (Zalophus Californianus) with Polyserositis and Steatitis. Viruses 12, 10.3390/v12080793:10.3390/v12080793, PMC7472147, PMID: 32718049

34. Canuti M, Bouchard É, Rodrigues B, Whitney HG, Hopson M, Gilroy C, Stenson G, Dufour SC, Lang AS, Verhoeven JTP (2021) Newlavirus, a Novel, Highly Prevalent, and Highly Diverse Protoparvovirus of Foxes (Vulpes spp.). Viruses 13, 10.3390/v13101969:10.3390/v13101969, PMC8537079, PMID: 34696399

35. Altan E, Hui A, Li Y, Pesavento P, Asín J, Crossley B, Deng X, Uzal FA, Delwart E (2021) New Parvoviruses and Picornavirus in Tissues and Feces of Foals with Interstitial Pneumonia. Viruses 13, 10.3390/v13081612:10.3390/v13081612, PMC8402702, PMID: 34452477

36. Reuter G, Boros Á, Mátics R, Altan E, Delwart E, Pankovics P (2022) A novel parvovirus (family Parvoviridae) in a freshwater fish, zander (Sander lucioperca). Arch Virol 167:1163-1167, 10.1007/s00705-022-05419-5:10.1007/s00705-022-05419-5, PMC8964545, PMID: 35278130