This Word module should be used for all taxonomic proposals.

Please complete **Part 1** and:

either **Part 3** for proposals to create new taxa or change existing taxa

or **Part 2** for proposals of a general nature.

Submit the completed Word module, together with the accompanying Excel module named in Part 3, to the appropriate ICTV Subcommittee Chair.

The Word module explains and justifies your proposal. The Excel module is a critical document that will be used to implement the proposed taxonomic changes once they are approved and ratified. If proposals presented in the Word module are not presented accurately in the Excel module, the taxonomic changes cannot proceed.

For guidance, see the notes written in blue, below, and the Help Notes in file Taxonomic\_Proposals\_Help\_2019.

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

|  |  |  |  |
| --- | --- | --- | --- |
| **Code assigned:** | ***2019.010D*** | |  |
| **Short title:** Re-organize the family *Parvoviridae* | | | |
|  | | | |
| **Author(s) and email address(es):** | | | |
| List authors in a single line *Archives of Virology* citation format (e.g. Smith AB, Huang C-L) | | Provide email address for each author in a single line separated by semi-colons | |
| Penzes JJ, Soderlund-Venermo M, Canuti M, Eis-Huebinger AM, Hughes J, Cotmore SF | | [Judycash08@gmail.com](mailto:Judycash08@gmail.com); [Maria.Soderlund-Venermo@Helsinki.fi](mailto:Maria.Soderlund-Venermo@Helsinki.fi); [marta.canuti@gmail.com](mailto:marta.canuti@gmail.com); [Anna-Maria.Eis-Huebinger@ukb.uni-bonn.de](mailto:Anna-Maria.Eis-Huebinger@ukb.uni-bonn.de); [Joseph.Hughes@glasgow.ac.uk](mailto:Joseph.Hughes@glasgow.ac.uk); susan.cotmore@yale.edu | |
| **Author(s) institutional address(es) (optional):**   |  | | --- | | Provide institutional addresses, each on a single line followed by author(s) initials (e.g. University of Woolloomooloo [SAB, HCL]) | |  | | | | |
| **Corresponding author** | | | |
| Judit J Penzes | | | |
| **List the ICTV study group(s) that have seen this proposal:** | | | |
| A list of study groups and contacts is provided at <http://www.ictvonline.org/subcommittees.asp> . If in doubt, contact the appropriate subcommittee chair (there are six virus subcommittees: animal DNA and retroviruses, animal ssRNA-, animal ssRNA+, fungal and protist, plant, bacterial and archaeal) | | ***Parvoviridae* SG** | |
| **ICTV Study Group comments (if any) and response of the proposer:** | | | |
|  | | | |
|  | | | |
| Date first submitted to ICTV: | | | 17 June 2019 |
| Date of this revision (if different to above): | | | 2 September 2019 |

|  |
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| **ICTV-EC comments and response of the proposer:** |
| Correct inconsistencies in Excel.  **Response**: Done. |

**Part 3:** **PROPOSED TAXONOMY**

|  |
| --- |
| **Name of accompanying Excel module:** 2019.010D.A.v2.Parvoviridae.xlsx |

The taxonomic changes you are proposing should be presented on an accompanying Excel module, 2019\_TP\_Template\_Excel\_module. Please enter the file name of the completed module in this box.

| additional material in support of this proposal |
| --- |
| Please explain the reasons for the taxonomic changes you are proposing and provide evidence to support them. The following information should be provided, where relevant:   * **Species demarcation criteria**: Explain how new species differ from others in the genus and demonstrate that these differences meet the criteria previously established for demarcating between species. If no criteriahave previously been established, and if there will now be more than one species in the genus, please state the demarcation criteria you are proposing. * **Higher taxa**:   + There is no formal requirement to state demarcation criteria when proposing new genera or other higher taxa. However, a similar concept should apply in pursuit of a rational and consistent virus taxonomy.   + Please indicate the **origin of names** assigned to new taxa at genus level and above.   + For each new genus a **type species** must be designated to represent it. Please explain your choice. * **Supporting evidence**: The use of Figures and Tables is strongly recommended (note that copying from publications will require permission from the copyright holder). For phylogenetic analysis, please provide a tree where branch length is **proportional to genetic** distance, generated using an appropriate algorithm (Neighbour-Joining, Maximum Likelihood, or Bayesian) and provide evidence of the reliability of the branching (e.g., by bootstrapping).   Please refer to the Help Notes file (Taxonomic\_Proposals\_Help\_2019) for more information. |

**Supporting material:**

1. **Modifications from the first version**

This taxonomy proposal (TP) has been modified from its first version (V1). The proposed name of the newly-introduced subfamily has been changed from Epiparvovirinae to Hamaparvovirinae, after the study group (SG) re-discussed the proposal. The reason for the name change is the integrating nature of many members from new subfamily into the genomes of their respective hosts, hence the abbreviation EPV would have collided with the abbreviation for endogenous parvovirus (also EPV). The new name, Hamaparvovirinae, derives from the Latin “together”.

1. **Demarcation criteria, definition of a parvovirus suitable for classification**

Since the last major taxonomy revision of family *Parvoviridae* (Cotmore et al., 2014) the number of novel parvoviruses has substantially increased, initiating the Study Group to decide on the modifications of the current virus definition and demarcation criteria as follows:

I, 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 isolated and sequenced or, failing this, on the basis of having been sequenced in tissues, secretions, or excretions of its possible host and reported in a credible peer-reviewed publication. Insights on its biology, such as genome annotation, transcription strategy, epidemiology, serology, structure, trafficking, replication and evolution are strongly encouraged. The sequence must be in one piece, 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. Furthermore, it must meet the size constraints and motif patterns typical of the family. Upon proposal the Parvoviridae Study Group is obliged to individually verify the integrity of the suggested virus sequence.

II, Demarcation criteria:

*Species:* two parvoviruses can be potentially classified in one species if their NS1 proteins share at least 85% protein sequence identity.

*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 any 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 and genome length and/or transcription strategy, provided the criterion of the well-supported monophyly is still satisfied.

1. **Current problems and challenges of parvovirus taxonomy.**

Since 1993, members of family *Parvoviridae* have been classified into two subfamilies on a basis of their capability to infect either vertebrate or invertebrate hosts (Cotmore et al., 2019). Although NS1-based phylogeny initially conformed with this, the discovery of the first members from current genera *Brevi*-, *Penstyl*- and *Hepandensovirus* revealed a diversity among members of current invertebrate-associated subfamily, *Densovirinae*, which was unmatched with the rather well-conserved nature of the vertebrate-infecting other subfamily, *Parvovirinae*. Members of the latter share NS1 proteins as well as VP proteins of a clearly homologous nature proven by detectable sequence similarity as both proteins align confidently basically throughout their entire length (minus the highly variable N- and C-terminal region of the NS1 as well as the sequences comprising the variable loops of the VP). This is not the case, however, with viruses in *Densovirinae*, as its members are linked together only by a short (approx. 200 aa long) SF3 helicase domain of detectable sequence similarity. The aforementioned domain, however, is highly-conserved throughout the entire family, suggesting that certain members of *Densovirinae*, such as hepandensoviruses, harbor the same amount of similarity to certain densoviruses as they do to members of subfamily *Parvovirinae*.

From 2012 on a novel, divergent lineage, designated Chapparvovirus, have been detected, associated with kidney and liver tissue, as well as with various secretions (such as blood) and excretions (such as feces) of vertebrates (Reuter et al., 2014; Palinski et al., 2016; Yang et al., 2016; Souza et al., 2017; Roedinger et al., 2018; Williams et al., 2018; Fahsbender et al., 2019; Lima et al., 2019). Recent phylogeny evidence, however, has revealed its close relation to current densoviruses, such as members of genera *Hepan*-, *Penstyl*- and *Brevidensovirus* while endogenous sequences, which evidently derive from ancient members of this lineage, have been identified in several arthropod genomes (Mietzsch et al., 2019; Penzes et al., 2019) (Figure 1).

Lastly, in 2014, the mainly transcription strategy-based approach to classify ambisense densoviruses was revised, merging three genera (Densovirus, Pefudensovirus and Cupidensovirus) to establish the large and diverse current genus *Ambidensovirus* (Cotmore et al., 2014). Even at the time the genus did not conform with the then-established genus demarcation criteria, albeit the ambisense genome organization proved to be a strong enough argument to support the existence of *Ambidensovirus*. Since then, however, multiple densoviruses have been described, eventually rendering *Ambidensovirus* paraphyletic (Figure 1 and 2).

Considering the above-mentioned issues, a strong necessity has been risen to revise the current taxonomy of family *Parvoviridae*. In this proposal, we aim to resolve the following:

* Provide a suitable classification for the extensive number of unclassified but characterized parvoviruses, currently dubbed under the umbrella term of Chapparvovirus
* Establish a new subfamily to resolve the issue of the possible polyphyly of the current *Densovirinae* and abandon host affiliation-based classification
* Introduce phylogenetically well-supported, monophyletic genera, which conform with the current genus definition to resolve the paraphyly of the current genus *Ambidensovirus*
* Introduce two new genera into subfamily *Parvovirinae* to accommodate two, hitherto unclassified parvoviruses
* Classify several previously well-characterized but currently unclassified viruses of subfamily *Parvovirinae* into existing genera

1. **Splitting *Densovirinae*; Introducing subfamily Hamaparvovirinae.**

To date, *Densovirinae* has basically served as the melting pot for all invertebrate-infecting parvoviruses. The subfamily, as detailed above, is very heterogenous, moreover, according to phylogenetic inference, novel vertebrate-infecting parvoviruses cluster here as well (Figure 1). Our aim is to split it into two, less heterogenous subfamilies both with better phylogenetic and biological support than the current unified *Densovirinae*. This would be carried out as follows:

I, Current genera *Ambi*- and *Iteradensovirus* to comprise subfamily *Densovirinae*

Despite of ambidensoviruses being distinct for their ambisense genome organization as opposed to the monosense *Iteradensovirus* genome, the two still cluster together as a well-supported monophyletic branch in both NS1-based and helicase domain-based phylogeny (Figure 1 and 2). Furthermore, in pairwise comparison of protein sequences, significant similarity of at least 32% identity can be detected between the NS1 proteins of any itera- or ambidensovirus. In addition, their VP proteins, although only harboring little sequence identity, can still be identified by the aid of a simple BlastP search to have possibly derived from a common ancestral VP protein gene. This is not true in case of the three remaining genera of the current *Densovirinae*, which share no detectable protein sequence similarity to either of the Ambi-Iteradensovirus NS1 or VP, except for the aforementioned helicase domain. Lastly, both ambi- and iteradensoviruses possess a conserved PLA2 domain in their minor capsid protein VP1 N-terminal sequence, similarly to most members of *Parvovirinae* and unlike brevi-, hepan- or penstyldensoviruses (Cotmore et al., 2019, Mietzsch et al., 2019). As Galleria mellonella densovirus, which currently belongs to genus *Ambidensovirus,* was the very first identified member of the *Densovirinae*, we would like to keep the *Densovirinae* designation for this redefined subfamily. Genus *Iteradensovirus* would keep its current name and affiliation. Genus-level changes concerning *Ambidensovirus* will be detailed later.

II, Proposed subfamily Hamaparvovirinae would be comprised of current genera *Hepan*-, *Penstyl*- and *Brevidensovirus*, together with the yet unclassified chapparvoviruses

Although the existence of this subfamily is less well-supported than that of the above-mentioned redefined *Densovirinae*, its members still cluster as a supported monophyletic lineage in helicase-based phylogeny and their NS1 proteins can be aligned at the length of 340 aa, which is on average 30% identical throughout the proposed new subfamily. In contrast, they only share the helicase domain with any other *Parvoviridae* member, with less than 20% identity, limited to the three highly-conserved Walker regions of the domain. Moreover, all members suitable to be classified lack the conserved PLA2 domain from their VP proteins.

This new subfamily would be called Hamaparvovirinae to express their nature of infecting both vertebrate and invertebrate hosts. The following genera, previously members of *Densovirinae*, would be moved here (and renamed according to the new subfamily):

* Genus Hepanhamaparvovirus with one species of Decapod hepanhamaparvovirus 1, which is also the type species of the genus – formerly classified as *Hepandensovirus*
* Genus Penstylhamaparvovirus with one species of Decapod penstylhamaparvovirus 1, also the type species of the genus – formerly classified as genus *Penstyldensovirus*
* Genus Brevihamaparvovirus with two species of Dipteran brevihamaparvovirus 1 and 2, with Dipteran brevihamaparvovirus 1 as the type species – formerly known as genus *Brevidensovirus*

Unclassified parvoviruses, previously known as chapparvoviruses, would also be members of proposed subfamily Hamaparvovirinae. In contrast with the above-mentioned three genera, however, they also harbor NS1 proteins sharing significant percentage of identity at a longer, approx. 500 aa-long stretch, with an average identity of 30-37% between any of these viruses. Their VP-encoding ORFs also share detectable similarity at aa level, suggesting their origin of a single, ancestral chapparvovirus capsid protein (Penzes et al., 2019). Genome organization, phylogeny and identity scores, however, separate these viruses into two potential genera (Figures 1 and 3). These two newly-classified genera would be:

* **Genus Ichthamaparvovirus** with one species, Syngnathid ichthamaparvovirus 1, which would also be the type species. Members share approx. 30% identity with other chapparvoviruses to date at NS1 protein sequence level. The only suggested virus member in this species is:
  + Syngathus scovelli chapparvovirus, derived from homogenized gill, muscle and male brood pouch tissue of the gulf pipefish (*Syngnathus scovelli*), collected for the complete genome sequencing project of this species. It has a closely related (70% identity) NS1 and NP gene spanning an endogenous relative in another syngnathe fish, the tiger seahorse (*Hippocampus comes*) (Penzes et al., 2019).
    - Syngnathus scovelli chapparvovirus has partially sequenced hairpins, based on which the genus is probably heterotelomeric.
* **Genus Chaphamaparvovirus** with eight new species. Members share no less than 37% identity at NS1 protein sequence level, but this number can be up to 55%. It may be a possibility that the detection of new viruses related to this proposed taxon will eventually result in splitting the genus into more. Currently, however, the common node of viruses in these eight proposed species is the only one significantly supported by both Bayesian and maximum likelihood-based inference. Species of this new genus would be:
  + Type species Rodent chaphamaparvovirus 1
    - Two viruses belong to here, which share:
      * Mouse kidney parvovirus: the most well-characterized chapparvovirus to date, with known telomers and solved transcription strategy. Based on this, members of the genus are probably heterotelomeric. Causes chronic kidney infection in immunosuppressed laboratory mice (Roediger et al., 2018).
      * Murine chapparvovirus: a prevalent chapparvovirus in both feces and liver tissue of mice in New York city (Williams et al., 2018).
      * The two, above-mentioned viruses share 98.5% identity at NS1 protein sequence level.
  + Rodent chaphamaparvovirus 2
    - One virus, rat parvovirus 2 comprises the species. Found to be prevalent in the feces of wild rats in China (Yang et al., 2016).
  + Ungulate chaphamaparvovirus 1
    - These viruses appear to harbor an additional, probably non-structural protein encoding ORF compared to other amniote vertebrate-infecting chapparvoviruses (Penzes et al., 2019). At NS1 protein sequence level they share approx. 37% identity with all chapparvoviruses.
    - The only, but abundantly detected virus of this species is porcine parvovirus 7. Partial genome fragments have been derived from feces, rectal swabs and diarrhea of piglets and young pigs on 41 different occasions. There has been one complete coding sequence published to date (Palinski et al., 2016).
  + Chiropteran chaphamaparvovirus 1
    - One virus, Desmodus rotondus chapparvovirus belongs here, derived from kidney tissue of the common vampire bat (*Desmodus rotondus)* (Souza et al., 2017).
  + Carnivore chaphamaparvovirus 1
    - Two, 99% identical chapparvoviruses can be classified here, both derived from dogs with diarrhea, namely cachavirus 1A and cachavirus 1B (Fahsbender et al., 2019).
  + Galliform chaphamaparvovirus 1
    - Turkey parvovirus 2 would be classified into this proposed species, which has been detected along with various circular ssDNA viruses in domestic turkey feces with high prevalence (Reuter et al., 2014).
  + Galliform chaphamaparvovirus 2
    - The only current virus, which belongs here is chicken chapparvovirus 2, derived from the intestines of broiler chickens, where it could not be associated with clinical signs, despite of its high prevalence (Lima et al., 2019).
  + Galliform chaphamaparvovirus 3
    - Chicken chapparvovirus HK and chicken chapparvovirus 1 are members of this species. Chicken chapparvovirus 1 is only available as a partial sequence with a complete NS1. It was derived during the same study as chicken chapparvovirus 2, being 75% identical at NS1 protein sequence level (Lima et al., 2019). Chicken chapparvovirus HK has a fully-determined coding sequence and its NS1 shares 99% identity with that of chicken chapparvovirus 1.

1. **Splitting genus *Ambidensovirus*; resolving the paraphyly**

After investigating phylogenetic relationships in the revised *Densovirinae* subfamily (see above) by both Bayesian and maximum likelihood (ML) tree reconstruction methods we established that there are seven lineages with ambisense genome organization within this proposed subfamily, which not only conform to the current genus demarcation criteria, but are constantly robustly supported, regardless of the phylogeny method (Figure 2). Interestingly, members of some of these newly proposed genera share more NS1 sequence identity with members of genus *Iteradensovirus* than they do with other ambisense invertebrate viruses. Out of the seven proposed genera, six are comprised by members of current *Ambidensovirus*, whereas one is established to accommodate a formerly unclassified ambisense densovirus. To indicate the ambisense nature of these viruses, we are willing to keep the “ambi” prefix even in the new genus names.

I, Genus Miniambidensovirus

* Only one species, Orthopteran miniambidensovirus 1, the type species of the genus, would be classified here.
  + The species comprises only one hitherto known virus, Acheta domestica mini ambidensovirus (AdMDV). AdMDV has the smallest genome in the subfamily (hence its name) and it has been derived from common house crickets (*Acheta domestica*) showing high mortality. AdMDV has a unique, split NS1-encoding ORF, suggesting splicing to be a prominent feature of its yet unresolved transcription strategy (Pham et al., 2013). AdMDV doesn’t display more than 27% identity with any member of proposed subfamily *Densovirinae*.

II, Genus Aquambidensovirus

* Two species are to be classified into this genus, both infecting solely aquatic hosts, which the name reflects. Members of the proposed genus share about 70% identity at NS1 protein sequence level and about 30% with other members of proposed subfamily *Densovirinae*.
  + Decapod aquambidensovirus 1 is the type species of the genus
    - Only one virus can be classified here, Cherax quadricarinatus densovirus (CqDV), derived from the Australian freshwater crayfish (*Cherax quadricarinatus*). CqDV possess one of the largest genome sequences of the family at 6.3 kb (Bochov et al., 2016)
  + Asteroid aquambidensovirus 1
    - Three viruses of echinoderms comprise this species. All of them are highly pathogenic, with sea star-associated densovirus being the only one classified so far (Hewson et al., 2014)

III, Genus Scindoambidensovirus

* Three species comprise this proposed new genus, with viruses sharing 40-43% identity at NS1 protein sequence level, whereas this number is 30% at its highest outside this proposed genus. Apart from phylogeny and sequence identity, the genus is also united by the split VP-encoding ORF, which gives rise to VP1 minor capsid protein via a spliced transcript. This results in not only VP1, but VP2, another minor capsid protein having a unique N-terminal region, which has not been observed in any other parvoviruses to date (Tijssen et al., 2016). The name “Scindo” refers to this split *VP* gene, as it means “split” or “cut” in Latin.
  + Orthopteran scindoambidensovirus 1, the type species
    - One virus, Acheta domestica densovirus (AdDV) belongs here. AdDV is known for causing severe mortality in the common house cricket, reared at large farms both in Europe and North America (Liu et al., 2011)
  + Hymenopteran scindoambidensovirus 1
    - Solenopsis invicta densovirus would be classified here, which is pathogenic in the South African fire ant (*Solenopsis invicta*) (Valles et al., 2013)
  + Hemipteran scindoambidensovirus 1
    - Planococcus citri densovirus, a pathogen of the citrus mealybug comprises this species (Thao et al., 2001)

IV, Genus Protoambidensovirus

* Two species should be classified into this proposed genus. As Galleria mellonella densovirus is the first member of the entire subfamily to be discovered, the genus is designated “Proto” after “first” in Latin. Members of the proposed genus share approx. 50% identity, while not more than 35% with members outside of it.
  + Lepidopteran protoambidensovirus 1, the type species
    - Five densoviruses belong to this species, all infecting important agricultural pests. Galleria mellonella densovirus and Junonia coenia densovirus are two of the few relatively well-characterized invertebrate parvoviruses as far as their structural and trafficking properties are concerned (Simpson et al., 1998; Multaeu et al., 2012)
  + Dipteran protoambidensovirus 1
    - Culex pipiens densovirus, infecting the mosquito species *Culex pipiens pallens* belongs to this genus. This virus is known for its complicated splicing pattern when expressing its NS proteins (Baquerizo-Audiot et al., 2009)

V, Genus Hemiambidensovirus

* This proposed genus includes two species, both pathogens of exclusively hemipteran hosts, namely aphids. The NS1 protein sequence-based identity is 62% within the genus whereas only 35% outside of it. Although members of both species display a split VP ORF, the transcription mechanism with which this is transcribed is currently unknown. Both their phylogenetic positions and the lack of sequence identity suggests that this VP-expression strategy probably evolved independently from that of proposed genus Scindoambidensovirus. Assigned species are:
  + Hemipteran hemiambidensovirus 1, the type species
    - Dysaphis plantaginea densovirus, which infects the rosy aphid (*Dysaphis plantaginea*). This virus is capable of stimulating the aphids to transform into the migratory, winged morph of the species (Ryabov et al., 2009)
  + Hemipteran hemiambidensovirus 2
    - Myzus persicae densovirus comprises this species on its own, infecting the green peach aphid (*Myzus persicae*) (van Munster et al., 2003).

VI, Genus Pefuambidensovirus

* Comprised by only one species namely Blattodean pefuambidensovirus 1 of Periplaneta fuliginosa densovirus, infecting the smoky brown cockroach (*Periplaneta fuliginosa*). The NS1 protein sequence of this virus is maximum 35% identical to any members of its subfamily, hence it should comprise a monotypic genus on its own. Although its genome also displays a split *VP* coding gene, there are two spliced transcripts derived from these, encoding both the VP1 and VP2 minor structural proteins (Guo and Zhang, 2000). The sequence divergence, phylogenetic position and unique splicing pattern of the structural ORFs suggest that Periplaneta fuliginosa densovirus is the first member of a third lineage of ambisense densoviruses possessing a split *VP* gene.

VII, Genus Blattambidensovirus

* A monotypic genus, as its only member, Blattella germanica densovirus 1 of species Blattodean blattambidensovirus 1, derived from the German crockroach (*Blattella germanica*) does not share more than 33% sequence identity with any officially classified densoviral NS1 proteins. Its transcription strategy suggests, however, that genus Blattambidensovirus is a fourth lineage to construct its minor capsid proteins by splicing two VP genes together (Kapelinskaya et al., 2011). Recently, a densovirus-like virus has been derived from great tit (*Parus major*) lung tissue, proven to be infectious even in vertebrate cell lines (Yang et al., 2016). Although its host affiliation has not been clarified yet, this virus still shares 56% identity with the NS1 protein sequence of Blattella germanica densovirus, suggesting it to be a possible second species of the proposed genus.

1. **Introducing two new genera into subfamily *Parvovirinae***

Two parvoviruses have been characterized and detected since 2011, which could not be assigned to any existing genera at the time. Moreover, the former virus definition did not make it possible for one of these two unique vertebrate-infecting parvoviruses to be classified. As a consequence of the new, modified virus definition, however, both are now eligible for classification into new genera of subfamily *Parvovirinae* (Figure 1 and 4).

I, Genus Artiparvovirus

Genus Artiparvovirus would be a monotypic genus of *Parvovirinae*, encompassing one species, Chiropteran artiparvovirus 1. One virus would be classified here, namely Artibeus jamaicensis parvovirus, which was detected in leaf-nosed fruitbats in Panama (Canuti et al., 2011). The complete genome sequence of this parvovirus has been determined and it shares maximum 38% NS1 protein sequence identity with any parvoviral NS1 in the GenBank. This, as well as its divergent phylogeny position (Figure 1 and 4), both indicate this virus to be suitable for classifying in its own monotypic genus.

II, Genus Loriparvovirus

Another proposed monotypic genus of subfamily *Parvovirinae*, comprised by one species, Primate loriparvovirus 1. Slow loris parvovirus, the only parvovirus to be assigned here, has been detected in a slow loris with diffuse histiocytic sarcoma, although despite of its many year-long persistence in the tumor, it is unclear whether or not slow loris parvovirus is an actual oncogenic/oncolytic virus (Canuti et al., 2014). The complete genome of this parvovirus has been sequenced and its NS1 protein sequence is maximum 38% identical to other parvoviral NS1 proteins, being equally similar to three genera of *Parvovirinae*, namely *Copi-, Dependo-* and *Tetraparvovirus*. Both its identity values and its phylogenetic position indicate slow loris parvovirus to be suitable for establishing its separate genus within subfamily *Parvovirinae* (Figure 1 and 4).

1. **Introducing a new species into genus *Amdoparvovirus* of *Parvovirinae***

We would like to assign red panda amdoparvovirus into the new species Carnivore amdoparvovirus 5 of genus *Amdoparvovirus*. This virus has been derived from both tissue and feces samples of the endangered red panda (*Ailurus fulgens*) and clusters into genus *Amdoparvovirus*, similarly to other already established carnivore-infecting parvoviruses (Alex et al., 2018). Red panda amdoparvovirus shares approx. 75% identity with other amdoparvovirus NS1 proteins.

1. **Introducing a new species into genus *Aveparvovirus* of *Parvovirinae***

We would like to assign red-crowned crane parvovirus into the new species Gruiform aveparvovirus 1 of genus *Aveparvovirus* as it robustly clusters with the currently established only species of the genus. Its NS1 protein sequence is 57-58% identical to those already assigned members of *Aveparvovirus*. Red-crowned crane parvovirus has been derived from the fecal virome of highly-endangered red-crowned cranes (*Grus japonensis*) in China (Wang et al., 2019)

1. **Introducing four new species into genus *Bocaparvovirus* of *Parvovirinae***

We would like to assign four parvoviruses into the following four proposed species of genus *Bocaparvovirus* as follows, as they all cluster among already-established bocaparvoviruses:

* Dromedary camel bocaparvovirus 1 to Ungulate bocaparvovirus 7
  + The NS1 of this virus displays 40-60% aa identity to other bocaparvovirus NS1 proteins. The virus was derived from the feces of multiple dromedary camel (*Camelus dromedaries*) individuals in Dubai (Woo et al., 2017).
* Dromedary camel bocaparvovirus 2 to Ungulate bocaparvovirus 8
  + The NS1 protein sequence of this virus is only 41% identical to those of other bocaparvoviruses, including even dromedary camel bocaparvovirus 1. Similarly to dromedary camel bocaparvovirus 1, this virus was also derived from the feces of multiple dromedary camel individuals in Dubai (Woo et al., 2017).
* Rat bocavirus to Rodent bocaparvovirus 1
  + The NS1 protein sequence of this virus is 46-56% identical to those of other bocaparvoviruses. The virus was detected from multiple organs and feces of Norwegian rats (*Rattus norvegicus*) in China (Lau et al., 2016).
* Murine bocavirus to Rodent bocaparvovirus 2
  + The protein sequence of the murine bocavirus NS1 is 48-55% identical to bocaparvoviral NS1 proteins. This virus was detected in house mice of New York City, often simultaneously with murine chapparvovirus (Williams et al., 2018).

1. **Introducing five new species into genus *Copiparvovirus* of *Parvovirinae***

We would like to assign the following parvoviruses into genus *Copiparvovirus*, as they all cluster with the already established two copiparvovirus species as a robustly-supported monophyletic group (Figure 1 and 4).

* Roe deer copiparvovirus to Ungulate copiparvovirus 3.
  + The complete genome of the roe deer copiparvovirus has been sequenced from both ticks (*Ixodes ricinus*) feeding on roe deers and from serum samples of the actual roe deer (*Capreolus capreolus*) individuals as well (Linden et al., 2019). At NS1 protein sequence level it displays 40-48% identity with established copiparvovirus species as well as reliably clusters into the genus.
* Porcine parvovirus 6 to Ungulate copiparvovirus 4.
  + Its complete genome has been characterized and pathology linked to aborted porcine fetuses. It shares 40-58% identity with other copiparvovirus NS1 protein sequences.
* Bosavirus to Ungulate copiparvovirus 5.
  + The NS1 of bosavirus shares 40% identity with other members of genus *Copiparvovirus* and has been detected as an abundant agent of the calf serum virome (Sadeghi et al., 2017).
* Equine parvovirus-hepatitis to Ungulate copiparvovirus 6.
  + The complete genome of equine parvovirus-hepatitis has been characterized and the virus itself is associated with severe pathology in horses (Divers et al., 2018).
  + Although the NS1 protein is only 36-39% identical to the same protein of other copiparvoviruses, we still intend to suggest it as a member of this genus for the following reasons:
    - The genome organization is remarkably copiparvovirus-like, with a genome length of >5k and a *VP* gene capable of encoding a VP1 longer than 900 aa (only true for genus *Copiparvovirus* of *Parvovirinae*).
    - Phylogenetic inference clearly indicates this virus to cluster with other copiparvoviruses, hence assigning it into another genus would mean paraphyly, or splitting the already established two species of this genus apart from each other (Figure 4). It may be a future possibility that in case of more copiparvovirus-like viruses will be characterized this virus will be re-classified into another genus along with sesavirus, although the two are still only 35% identical as far as their NS1 proteins are concerned (see below).
* Sesavirus to Pinniped copiparvovirus 1
  + Sesavirus has been detected only once from a California sea lion pup (*Zalophus californianus*) and its complete coding sequence has been determined (Phan et al., 2015). Although the NS1 protein is only 35% identical to the same protein of other copiparvoviruses, we still intend to suggest it as a member of this genus for the following reasons:
    - The genome organization is remarkably copiparvovirus like, with a genome length of >5k and a VP gene capable of encoding a VP longer than 900 aa (only true for genus *Copiparvovirus* of *Parvovirinae*).
    - It does not show more than 30% NS1 protein sequence identity to any other *Parvovirinae* members outside of *Copiparvovirus*
    - It would be the first non-ungulate copiparvovirus, which may be a reason for the divergence.
    - Phylogenetic inference clearly indicates this virus to cluster with other copiparvoviruses, hence assigning sesavirus into another genus would mean paraphyly, or splitting the already established two species of this genus from each other (Figure 4).

1. **Introducing two new species into genus *Dependoparvovirus* of *Parvovirinae***

Two adeno-associated rodent viruses, namely murine adeno-associated virus 1 and 2, would be assigned to these two new species of *Dependoparvovirus*, Rodent dependoparvovirus 1 and 2, respectively.

The large Rep protein of both viruses is 50-57% identical to dependoparvoviral Rep proteins (equivalent of NS1). These two murine adeno-associated viruses are, however, 75% identical, as far as the same protein sequence is concerned. Our proposal is justified by the phylogenetic position of both viruses and their identity scores suggest that both are divergent enough to comprise a new species on its own. Both viruses were derived from mice living all around New York city, often concordant with murine chapparvovirus and murine bocavirus, described above (Williams et al., 2018).

1. **Introducing a new species into genus *Erythroparvovirus* of *Parvovirinae***

Seal parvovirus was identified in the brain tissue of a stranded harbor seal (*Phoca vitulina*) and its complete coding sequence determined (Bodewes et al., 2013). It shares, however, only 36% identity of its NS1 protein sequence with other erythroparvoviruses, yet this number is only 30% with parvoviruses from other genera. Despite of the low identity, we still decided to submit this parvovirus into genus *Erythroparvovirus*, as Pinniped erythroparvovirus 1. This affiliation is supported by the phylogenetic position of seal parvovirus, as well as by the presence of a small ORF in overlap with the N-terminal coding region of VP1, homologous to the X protein of human parvovirus B19 (Figure 1 and 4).

1. **Introducing two new species into genus *Protoparvovirus* of *Parvovirinae***

We would like to assign two new species into this genus as follows:

* Tusavirus has been detected and characterized in association with an unexplained diarrhea case in Tunisia, concerning a child (Phan et al., 2014). Later anti-Tusavirus antibodies were revealed in the serum of two more patients (Väisänen et al., 2016; Väisänen et al., 2019). The NS1 protein of this virus is 48% identical to that of other members classified as protoparvoviruses and it also clusters with these viruses (Figure 1 and 4). Considering these, we would like to assign it to the species Primate protoparvovirus 4 of genus *Protoparvovirus*.
* Sea otter parvovirus clusters with protoparvoviruses designated as bufaviruses and shares 45-65% identity with the NS1 proteins of protoparvoviruses (Figure 1 and 4). This virus was derived from stranded sea otters (*Enhydra lutris*) in co-infection with various other DNA viruses (Siqueira et al., 2017). We would like to assign this virus to genus *Protoparvovirus* under the new species Carnivore protoparvovirus 2.

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**Figure 1** Bayesian inference of the tripartite helicase domain, the only protein sequence conserved throughout family *Parvoviridae* (167 aa)*.* This calculation was carried out using BEAST v. 1.10.4. Posterior probability support values are indicated as node labels. Viruses and taxa suggested for the first time are indicated in red. The lineages where the new genera, which formerly comprised *Ambidensovirus,* split are shown as colored branches, accordingly.



**Figure 2** Bayesian inference (A) and maximum likelihood calculations (B) of the complete NS1 protein sequence of members of subfamily *Densovirinae* (486 aa). In order to be able to observe relationships in the entire clade, both trees have been rooted to two vertebrate NS1 protein sequences. These calculations were carried out using BEAST v. 1.10.4. and PhyML v3.3, respectively. Posterior probability support values and bootstrap values of 100 iterations are indicated as node labels. Viruses and taxa suggested for the first time are indicated in red. The lineages where the new genera, which formerly comprised *Ambidensovirus,* split are shown as colored branches, accordingly.



**Figure 3** Bayesian inference and maximum likelihood calculations of the NS1 protein sequence of proposed subfamily Hamaparvovirinae (340 aa). As the two topologies were identical, the Bayesian topology is shown. These calculations were carried out using BEAST v. 1.10.4. and PhyML v3.3, respectively. Posterior probability support values and bootstrap values of 100 iterations are indicated as node labels, in the respective order. Viruses and taxa suggested for the first time are indicated in red and are underlined.



**Figure 4** Bayesian inference and maximum likelihood calculations of the complete NS1 protein sequence of subfamily *Parvovirinae* (460 aa). These calculations were carried out using BEAST v. 1.10.4. and PhyML v3.3, respectively. Posterior probability support values and bootstrap values of 100 iterations are indicated as node labels, in the respective order. As the two topologies were identical, only the Bayesian topology is shown. Viruses and taxa suggested for the first time are indicated in red.

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