

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

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| **Code assigned:** | **2020.011D** |  |
| **Short title:** Create three new genera and 19 new species (*Piccovirales*: *Parvoviridae*) | | |
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**List the ICTV Study Group(s) that have seen this proposal**

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| *Parvoviridae* SG |

**ICTV study group comments and response of proposer**

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

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| **Taxon name** | **Person from whom the name is derived** | **Permission attached (Y/N)** |
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**ICTV-EC comments and response of the proposer**

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

**Name of accompanying Excel module**

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| 2020.011.R.Parvoviridae\_3ngen\_20nsp |

**Abstract**

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| We propose the creation of three new genera in the subfamily *Densovirinae* and the creation of 18 new species in the family *Parvoviridae.* We would like to correct the name of one species, which got accepted under the wrong name due to an unnoticed mistake in the proposal of 2019**.** |

**Text of proposal**

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| |  | | --- | | **1. Demarcation criteria, definition of a parvovirus suitable for classification**  As a result of our previous taxonomy proposal (2019.010D) the virus definition and taxon demarcation criteria of family *Parvoviridae* have been established 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. The sequence must be in one piece, contain all the nonstructural (NS) and virus particle (VP) coding regions, and meet the size constraints and motif patterns typical of the family. Host assignments require evidence of distribution in multiple individuals. This definition is designed to allow the inclusion of viruses identified by virus discovery approaches, which typically lack reliable sequences from the telomeric hairpins, while avoiding viral sequence fragments integrated into host genomes as well as environmental samples lacking associations with a particular animal species.  II, Demarcation criteria:  *Species:* two parvoviruses can be potentially classified in one species if their NS1 proteins share at least 90% 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 at least 40% protein sequence identity and display a coverage of at least 80% between any two members of the genus in question concerned. Failing the latter criterion, common genus affiliation can also be justified by similar genome organization and/or transcription strategy, provided the phylogenetic criterion is still satisfied.  **2. Objectives and aims of the current proposal**  As a result of the modification of the definitions and demarcation criteria above, several novel parvoviruses have become eligible for classification. The vast majority of these, including 18 new parvoviruses, have been deposited to the GenBank during the past two years, indicating the importance of timely parvovirus classification. Further two parvoviruses, though introduced to the GenBank several years ago, have become eligible for classification as well, either due to the above-mentioned relaxation of the definition or by managing to meet classification criteria only by present times. With this taxonomy proposal we aim to:   * Establish three new genera within subfamily *Densovirinae*, each comprising one new species * Introduce a new species to genus *Aquambidensovirus* of subfamily *Densovirinae* * Establish eight new species within genus *Chaphamaparvovirus* of subfamily *Hamaparvovirinae* * Introduce a new species to genus *Aveparvovirus* of subfamily *Parvovirinae* * Introduce three new species to genus *Bocaparvovirus* of subfamily *Parvovirinae* * Introduce a new species to genus *Dependoparvovirus* of subfamily *Parvovirinae* * Introduce two new species to genus *Protoparvovirus* of subfamily *Parvovirinae* * Correct a nomenclature error in genus *Protoparvovirus* of subfamily *Parvovirinae*   **3. Establishing three new monotypic genera within subfamily *Densovirinae***  I, Genus *Tetuambidensovirus*  We would like to classify a recently detected densovirus of the red spider mite, *Tetranychus urticae*, into this new genus. Tetranychus urticae-associated ambidensovirus (TuDV) robustly clusters with members of subfamily *Densovirinae* and harbors an ambisense genome, similarly to the majority of members already classified to this subfamily (Francois et al. 2019) (Figures 1 and 2). Based on its large non-structural protein (NS1) deduced protein sequence, however, it displays only 26-35% identity and 40-77% coverage with any other member of the *Densovirinae*, which justifies TuDV to be classified as a single species of a monotypic genus on its own. Despite including two potential NS and one structural (VP) protein-encoding open reading frames (ORFs), the known coding sequence of TuDV is only 3.4 kb, making it the smallest potential member of family *Parvoviridae*. TuDV appears to be the only hitherto member of subfamily *Densovirinae*, which lacks the canonical phospholipase A2 (PLA2) domain. We would like to classify TuDV into genus *Tetuambidensovirus* as the type member of the species *Trombiditiform tetuambidensovirus 1*. The proposed name is derived from the initials and first syllables of the Latin name of the TuDV host, ***Tet****ranychus* ***u****rticae*, and the -ambi prefix, referring to its ambisense genome organization.  II, Genus *Diciambidensovirus*  Diaphorina citri densovirus (DcDV) persistently infects the Asian citrus psyllid (*Diaphorina citri*) and has been shown to be transmitted vertically to all the offspring of a single female (Nigg and Falk 2020). DcDV harbors an ambisense genome, which exhibits characteristics of the monosense genus, *Iteradensovirus*, as well as the ambisense genus, *Hemiambidensoivirus,* both of subfamily *Densovirinae*. Based on its NS1 protein sequence, DcDV clusters among members of the *Densovirinae* (Figure 1) yet comprises a separate lineage within the subfamily (Figures 1 and 2). At the protein sequence level of its NS1, DcDV displays identity of 30-36% and coverage at least 60% with each member of the *Densovirinae*. Based on these criteria, we would like to classify DcDV as the exemplar of its own species and the type species *Hemipteran diciambidensovirus 1* of genus *Diciambidensovirus*. The proposed name of the genus is derived from the first syllables of the Latin name of the DcDV host, ***Di****aphorina* ***ci****tri*, and the -ambi prefix, referring to its ambisense genome organization.  III, Genus *Muscodensovirus*  Hematobia irritans densovirus (HiDV) has been recently detected by next generation sequencing when analyzing the virome of the salivary glands of the bloodsucking dipteran species, the horn fly (*Hematobia irritans*) (Ribeiro et al. 2019). HiDV shares 43% NS1 protein sequence identity and 77% coverage with Linvill Road densovirus, detected from the sialome of another muscomorph fly, *Drosophila melanogaster*. HiDV clusters within subfamily *Densovirinae*, yet only displays 26-30% identity with any of its members (Figures 1 and 2). Interestingly, both HiDV and Linvill Road densovirus harbor monosense genomes, comprising the second independent lineage of subfamily *Densovirinae*, which has evolved a monosense genome expression strategy, with the first being genus *Iteradensovirus*. As Linvill Road densovirus is not eligible for classification, we would like to introduce HiDV into its proposed monotypic genus, *Muscodensovirus* as the type species *Diptheran muscodensovirus 1*. The name of the suggested genus derives from the Latin word *musca*, which means fly.  **4. Introducing a new species to genus *Aquambidensovirus* of subfamily *Densovirinae***  Recently two novel densoviruses have been derived by next generation sequencing from the Suminoe oyster (*Crassostrea ariakensis*), designated Crassostrea ariakensis densovirus 1 and 2 (CaaDV1 and 2) (Kang et al. 2017). The complete coding sequence, however, could only be assembled in case of CaaDV1, while the CaaDV2 genome lacks the N-terminal coding region of its hypothetical VP gene. They both, however, cluster with members of genus *Aquambidensovirus* (Figures 1 and 2), with CaaDV1 displaying 61 and 62% NS1 protein sequence identity with members of both hitherto classified *Aquambidensovirus* species, respectively. Consequently, we would like to assign CaaDV1 into the species *Ostreid aquambidensovirus 1* of genus *Aquambidensovirus,* within subfamily *Densovirinae*. CaaDV1 and 2 are the first parvoviruses to have been derived from a species from the vast protostome invertebrate phylum, Mollusca.  **5. Establishing eight new species within genus *Chaphamaparvovirus* of subfamily *Hamaparvovirinae***  I, We would like to assign three new chapparvoviruses, identified during the same study, to genus *Chaphamaparvovirus*, to three separate species. Tasmanian devil-associated chapparvovirus (TdChPV) 1, 2 and 6 were all derived during the metagenomic characterization of the Tasmanian devil fecal virome, together with three further, only partially sequenced chapparvoviruses (Chong et al. 2019). Based on their NS1 genes, all three viruses cluster with members of genus *Chaphamaparvovirus*, with a robust support (Figures 1 and 3).   * TdChPV1 to be assigned to species *Dasyurid chaphamaparvovirus 1*, displaying 33-40% identity and at least 90% coverage at NS1 protein sequence level with any member of genus *Chaphamaparvovirus* * TdChPV2 to species *Dasyurid chaphamaparvovirus 2*, displaying 45-70% identity and at least 90% coverage at NS1 protein sequence level with any member of genus *Chaphamaparvovirus* * TdChPV6 to species *Dasyurid chaphamaparvovirus 3*, displaying 40-62% identity and at least 97% coverage at NS1 protein sequence level with any member of genus *Chaphamaparvovirus*   II, We would like to introduce two novel peafowl chapparvoviruses, derived from deceased domesticated peafowls in China, to genus *Chaphamaparvovirus* (Liu et al. 2020). Both peafowl parvovirus 1 and 2 (PePV1 and 2), based on their NS1 derived protein sequences, cluster with members of genus *Chaphamaparvovirus* with a significant support (Figures 1 and 3). They are eligible for comprising separate species, sharing only 50% NS1 protein sequence identity between each other. They would be classified as the following:   * PePV1 to species *Galliform chaphamaparvovirus 4*, displaying 46-51% identity and at least 95% coverage at the NS1 protein sequence level with any member of genus *Chaphamaparvovirus* * PePV2 to species *Galliform chaphamaparvovirus 5*, displaying 45-52% identity and at least 95% coverage at the NS1 protein sequence level with any member of genus *Chaphamaparvovirus*   III, We are to classify Psittacara leucophthalmus chapparvovirus (PlChPV) to the species *Psittacine chaphamaparvovirus 1*. PlChPV was detected from the fecal virome of Cerrado birds (*Psittacara leucophthalmus*) during a metagenomic analysis in Brazil (Duarte et al. 2019). Its deduced NS1 protein sequence clusters with other avian members of genus *Chaphamaparvovirus* (Figures 1 and 3), with a significant support. It also displays 47-59% identity and at least 97% coverage with any member of the genus, also at the NS1 protein sequence level.  IV, We would like to assign fechavirus (FeChPV), a feline chapparvovirus, to the species *Carnivore chaphamaparvovirus 2*. Fechavirus was detected from the fecal virome of shelter cats during an enteritis outbreak of unknown origin at three Canadian stray pet shelters (Li et al. 2020). Fechavirus clusters with members of genus *Chaphamaparvovirus* (Figures 1 and 3) and its NS1 protein sequence displays 100% coverage and 65% identity with that of its closest relative, catchavirus of species *Carnivore chaphamaparvovirus 1*.  V, We are to classify Capuchin kidney parvovirus (CKPV) to the species *Primate chaphamaparvovirus 1*. CKPV has been verified to replicate in the kidney tissue of Capuchin monkeys, similarly to mouse kidney parvovirus (Lee et al. 2020). Its derived NS1 protein sequence clusters among members of genus *Chaphamaparvovirus,* with significant support (Figures 1 and 3). The same protein sequence displays 48% identity and 90% coverage with its closest relative, porcine parvovirus 7 of *Ungulate chaphamaparvovirus 1*.  **6. Establishing a new species within genus *Aveparvovirus* of subfamily *Parvovirinae***  We would like to assign pigeon parvovirus 1 (PiPV1) into the new species *Columbid aveparvovirus 1* of genus *Aveparvovirus* as its derived NS1 protein sequence robustly clusters with the currently established two species of the genus (Figures 1 and 4). Furthermore, its NS1 is 45-46% identical to those already assigned members of *Aveparvovirus,* at the aa level. PiPV1 has been derived from the pooled sample of several pigeon (*Columba livia f. domestica*) droppings, collected in Hungary and Hong Kong (Phan et al. 2013). Unlike other aveparvoviruses, its genome sequence contains a 477-aa-long potential protein-encoding ORF of unknown function.  **7. Introducing three new species into genus *Bocaparvovirus* of *Parvovirinae***  We would like to assign three new parvoviruses into the following three proposed species of genus *Bocaparvovirus* as follows, as they all robustly cluster among already-established members of the genus, based on their NS1 protein sequences (Figures 1 and 4):  I, Vicugna pacos bocaparvovirus (VpBoV) to *Ungulate bocaparvovirus 9*, as   * + The NS1 of this virus displays 69% aa identity and 98% coverage to its closest relative, Dromedary camel bocaparvovirus 1 of *Ungulate bocaparvovirus 7*. VpBoV was detected from the fecal virome of an alpaca (*Vicugna pacos*) with recurring diarrhea and signs of respiratory infection (Kumar et al. 2019).   II, Macaca mulatta bocaparvovirus to *Primate bocaparvovirus 3*   * + The NS1 protein sequence of this virus is 69% identical to that of its closest relative, gorilla bocaparvovirus. This virus was detected in feces of Rhesus macaques in China (Ao and Duan 2020).   III. Rousettus leschenaultii bocaparvovirus 1 to *Chiropteran bocaparvovirus 5*   * + The protein sequence of the Rousettus leschenaultii bocaparvovirus 1 NS1 is 44-49% identical to any bocaparvoviral NS1 protein. This virus was detected during the PCR screening of several bat species in Hong Kong (Lau et al. 2017).   **8. Introducing a new species to genus *Dependoparvovirus* of *Parvovirinae***  Feline dependoparvovirus (FdPV) was detected during the same Canadian shelter enteritis outbreak as Fechavirus (Li et al. 2020). The FdPV Rep deduced protein sequence clusters robustly with members of genus *Dependoparvovirus* and displays 45-47% identity with that of various dependoparvoviruses, making it eligible for being assigned to species *Carnivore dependoparvovirus 1* (Figures 1 and 4).  **9. Introducing two new species into genus *Protoparvovirus* of *Parvovirinae***  We would like to assign two new species into this genus as follows, as they both clusters robustly among members of genus *Protoparvovirus*, based on their NS1 protein sequences (Figures 1 and 4):   * + Canine bufavirus (CBuV) to the species *Carnivore protoparvovirus 3*. The NS1 protein of this virus is 67% identical to that of porcine bufavirus, yet only 40.6% with canine parvovirus, both members of *Protoparvovirus*. Although canine parvovirus is extremely virulent in puppies, CBuV appears to be a common agent of both the canine nasal and fecal virome (Martella et al. 2018).   + Fox parvovirus was detected during the metagenomic screening of the fecal virome of 13 European red foxes (*Vulpes vulpes*) (Bodewes et al. 2013). Its NS1 protein is 58-60% identical to those of its closest relatives among members of genus *Protoparvovirus*, making it eligible to be assigned to the new species *Carnivore protoparvovirus 4*.   **9. Correction of the species name of *Carnivore protoparvovirus*** Here, we would like to correct an error made in the proposal of 2019 (2019.010D) and re-name *Carnivore protoparvovirus* to *Carnivore protoparvovirus 2*, as sea otter parvovirus was the second carnivore parvovirus classified to genus *Protoparvovirus*. | |

**Supporting evidence**

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**Figure 1** Bayesian inference of the tripartite helicase domain, the only protein sequence conserved throughout family *Parvoviridae* (168 aa)*.* This calculation was carried out using BEAST v. 1.10.4. Posterior probability support values are indicated as node labels, if significant (>0.7). Viruses and taxa suggested for the first time are indicated in red.

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**Figure 2** Bayesian inference of the complete NS1 protein sequence of subfamily *Densovirinae* (550 aa). These calculations were carried out using BEAST v. 1.10.4. Posterior probability support values are indicated as node labels, if significant (>0.7). Viruses and taxa suggested for the first time are indicated in red.

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**Figure 3** Bayesian inference (A) and maximum likelihood calculations (B) of the NS1 protein sequence of proposed subfamily *Hamaparvovirinae* (337 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. Viruses and taxa suggested for the first time are indicated in red.

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**Figure 4** Bayesian inference of the complete NS1 protein sequence of subfamily *Parvovirinae* (460 aa). These calculations were carried out using BEAST v. 1.10.4. Posterior probability support values, if significant (>0.7), are indicated as node labels. Viruses and taxa suggested for the first time are indicated in red.

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