This form should be used for all taxonomic proposals. Please complete all those modules that are applicable.

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Please try to keep related proposals within a single document.

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

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| **Code assigned:** | ***2017.003D*** | | | | (to be completed by ICTV officers) |
| **Short title:**  9 new species in genus *Bocaparvovirus* | | | | | |
| **Modules attached**  (Modules 1, 4 and either 2 or 3 are required. | | **1****x 2x  3  4x** | | | |
| **Author(s):** | | | | | |
| Susan F. Cotmore, Mavis Agbandje-McKenna, Marta Canuti, John A. Chiorini. Anna-Maria Eis-Hubinger, Joseph Hughes, Sejal Modha, Mylène Ogliastro, David J. Pintel, Jianming Qiu, Maria Soderlund-Venermo, Peter Tattersall, Peter Tijssen. | | | | | |
| **Corresponding author with e-mail address:** | | | | | |
| Susan F. Cotmore susan.cotmore@yale.edu | | | | | |
| **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 Study Group** | | |
| **ICTV Study Group comments (if any) and response of the proposer:** | | | | | |
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| Date first submitted to ICTV: | | | | 6 June 2017 | |
| Date of this revision (if different to above): | | | | 19 June 2017 | |

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| **ICTV-EC comments and response of the proposer:** |
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**Part 2**: **PROPOSED TAXONOMY**

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| Present the proposed new taxonomy on accompanying spreadsheet |
| **Name of accompanying spreadsheet:** 2017.003D.N.v2.Bocaparvovirus\_9sp |

**Part 4:** **APPENDIX**: supporting material

| additional material in support of this proposal |
| --- |
| **References:** |
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| **Annex:**  Genus *Bocaparvovirus* is one of 8 recognized genera of vertebrate-infecting viruses that make up subfamily *Parvovirinae*, in the family *Parvoviridae*. Its classification has not been updated since it was substantially extended in 2014. Viruses in this genus have been identified predominantly in fecal and/or respiratory samples from both healthy and diseased animals. Epidemiological analysis suggests that they are typically widespread in their respective host populations. Among other characteristics, viruses in the genus share similar genetic strategies, coding patterns, potential classes of small non-structural proteins and protein motifs. Most notably, they all encode a unique type of ancillary protein, NP1, which is not found in viruses from any other genus. Currently there are 12 recognized species, to which we propose adding 9 new species that are broadly distributed throughout the phylogenetic tree. The new viruses infect cats, mink, bats, rabbits or pigs.  **Virus definition:**  Viruses in each of the newly proposed bocaparvovirus species meet the following virus definition, which has been in standard use by the Parvoviridae SG since 2014.  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 unambiguous host origin, supported by evidence of its distribution in multiple individual hosts in a pattern that is compatible with dissemination by infection. 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.  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 or metagenomic data that lack clear host attribution.  **Taxon demarcation criteria**:  Throughout the *Parvovirinae*, viruses within a **genus** are required to be monophyletic and to encode NS1 proteins that are generally at least 30% identical to each other at the amino acid sequence level but less than 30% identical to those of other genera. Viruses within a **species** are generally required to encode NS1 proteins that show at least 85% amino acid sequence identity, while diverging by at least 15% from viruses in other species. Viruses in each of the candidate bocaparvovirus species proposed here meet these criteria.  **Phylogenetic Tree:**  Phylogenetic analyses described here are based on the amino acid sequence of the conserved viral replicase protein, NS1. Taxonomic relationships shown in Figure 1 were determined using the pipeline platform ViCTree, developed by Sejal Modha, Joseph Hughes and Andrew Davison, which automatically selects candidate virus sequences from GenBank, generates pairwise distance matrices and multiple sequence alignments using Clustal-omega and calculates a maximum likelihood phylogenetic tree with bootstrap support using RaxML.  The virus list is updated from GenBank each month, and the processed data is filtered to select a single virus to represent all full-length GenBank protein submissions that share <10% identity. The current *Parvovirinae* tree generated by this procedure can be viewed at the following website: [http://bioinformatics.cvr.ac.uk/victree/#](https://urldefense.proofpoint.com/v2/url?u=http-3A__bioinformatics.cvr.ac.uk_victree_-23&d=CwMF-g&c=-dg2m7zWuuDZ0MUcV7Sdqw&r=uB-YbGLbMS54FSYsLk1W_0zpnKidLBzUoJ6-7dLNXc4&m=MDgCnyxTdgVQGKvrjyXQaRr-cDC4SMsK-RU1f6ukhWE&s=Y3ik9EpYfsU5rV_unJzK7xW45Cp8IMM53EJSo5JcIas&e=)  by 1) selecting *Parvovirinae* under the "example" arrow, 2) the desired labeling system from the "labels" pull down menu, and 3) expanding the tree using the first boxed toggle switch. Pairwise identity scores are obtained using the sliding scale at the top/right. GenBank accession numbers for the rest of the NS1 proteins in each <10% identity cluster are viewed using the "ClusterSequences" tab in the "labels" category.  The exact version of the tree that this TP is based on can be viewed at URL:  https://github.com/josephhughes/ViCTree/blob/d6cc2993a87ac07c1f14a62cf45e09f49b90d69d/txid40119/RAxML\_bipartitions.txid40119  and the alignment file it is based on is at URL:  [https://github.com/josephhughes/ViCTree/blob/d6cc2993a87ac07c1f14a62cf45e09f49b90d69d/txid40119/txid40119\_final\_set\_clustalo\_aln.fa](https://urldefense.proofpoint.com/v2/url?u=https-3A__github.com_josephhughes_ViCTree_blob_d6cc2993a87ac07c1f14a62cf45e09f49b90d69d_txid40119_txid40119-5Ffinal-5Fset-5Fclustalo-5Faln.fa&d=DwMGaQ&c=-dg2m7zWuuDZ0MUcV7Sdqw&r=vu1FD8Y-A24zKnnaDPNiYcYJWmtEKK1Sier6_aslxgI&m=rHJvozXRByKGK5HeZg0b-7S6LJ2PYVr954BX6lQ_am4&s=gkKbnAimcdGCzF2JhoWFSRtofZc14X9_0z1jD0rxQT4&e=)  Candidate new species proposed in this submission were selected by reviewing each cluster of viruses for genomes that accord with our virus definition and taxon demarcation criteria, and have sufficient support data to indicate an infectious aetiology.  The pipeline approach is invaluable in ensuring that databases are scanned effectively for new candidate viruses and renders analysis of large numbers of new and duplicated genomes manageable. However, since the current taxonomy (2014) was based on alignments that included insights from structural biology, the resulting trees do show some disparate branching patterns and bootstrap support values using RaxML.  **Nomenclature:**  Following our standard binomial nomenclature for species in this family, proposed species are named for a host taxon and their genus affiliation, followed by a distinguishing numeral. Species with like names receive numerals that follow on from those of previously recognized species.  **Proposed new species:**  **Table 1: Proposed new species in genus *Bocaparvovirus***   |  |  |  |  |  | | --- | --- | --- | --- | --- | | Proposed new  species | Exemplar isolate | Accession # | Acronym | Ref-  erence | | *Carnivore*  *bocaparvovirus* *4*  *Carnivore*  *bocaparvovirus* *5*  *Carnivore*  *bocaparvovirus* *6*  *Chiropteran*  *bocaparvovirus* *1*  *Chiropteran*  *bocaparvovirus* *2*  *Chiropteran*  *bocaparvovirus* *3*  *Chiropteran*  *bocaparvovirus* 4  *Lagomorph*  *bocaparvovirus* *1*  *Ungulate*  *bocaparvovirus* *6* | feline bocavirus 2  feline bocavirus 3    mink bocavirus    Myotis myotis bocavirus 1  bat bocavirus WM40  bat bocavirus XM30  bat bocaparvovirus Ms-str24  rabbit bocaparvovirus  ungulate bocaparvovirus 6 | KF792837  KM017744  KU950356  JQ814850  KC339251  KC339250  KU321654  KP729195  KU172421 | FBoV2  FBoV3  MiBoV1  BtBoV1  BtBoV WM40  BtBoV XM30  BtBoV Ms  LBoV1  BBoV2 | 1  2  3  4  5  5  6  7  8 |   ***Carnivore bocaparvovirus* *4***  A new species that will accommodate viruses exhibiting >85% NS1 amino acid identity to  feline bocavirus 2 (FBoV2, Genbank KF7922837), which was first reported in fecal samples from cats in Portugal in 2013 (ref 1). This virus requires classification in a new species because the amino acid sequence of its NS1 protein is 66% identical to that of its nearest neighbor in the phylogenetic tree, which is feline bocavirus (GenBank JQ692585) in species *Carnivore bocaparvovirus* *3* (figure 1). Thus FBoV2 is <85% identical to viruses in any recognized species (as required for a new species), while being more than 30% identical, which is required for occupancy of the same genus.  ***Carnivore bocaparvovirus* *5***  To include viruses exhibiting >85% NS1 amino acid identity to feline bocavirus 3 (FBoV3, GenBank KM017744), which was identified in the feces of multiple apparently-healthy cats housed individually in a shelter in Davis, California in 2013 (ref 2). Its NS1 amino acid sequence is around 74% identical to that of its nearest classified neighbor, which is feline bocavirus (GenBank JQ692585) in species *Carnivore bocaparvovirus* *3* (figure 1), and around 66% identical to FBoV2 (GenBank KF799283) in the proposed new species *Carnivore bocaparvovirus* *4.* It therefore qualifies for classification in a different new species.  ***Carnivore bocaparvovirus* *6***  To include viruses clustering with mink bocavirus 1 (MiBoV1, GenBank KU950356), identified in fecal samples from 9/30 domestic mink (30%), including both healthy animals and ones with diarrhea, which were sampled in the Jinzhou economic animal-breeding center, China, in 2016 (ref 3). The NS1 protein of this isolate is around 43% identical to its nearest neighbors in the taxonomy (figure 1), which are a cluster of viruses that infect carnivores, specifically cats (in species *Carnivore bocaparvovirus 3* to *5*), dogs (species *Carnivore bocaparvovirus 1* and *2*), or California sea lions (species *Pinniped bocaparvovirus 1* and *2*).  ***Chiropteran bocaparvovirus* *1***  To include viruses with NS1 proteins exhibiting >85% identity to that of Myotis myotis bocavirus 1 (BtBoV1, GenBank JQ814850), which was identified in pharyngeal and anal swab samples from the insectivorous greater mouse-eared bat, *Myotis myotis*, collected in Hainan, China (ref 4). The sequence of its NS1 protein is around 35% identical to that of its nearest neighbors in the genus, the primate viruses in species *Primate bocaparvoviruses 1* and *2*.  ***Chiropteran bocaparvovirus* *2***  To include viruses clustering with bat bocavirus WM40 (BtBoV WM40, GenBank KC339251), identified in the gut contents of insectivorous bats from species *Miniopterus fuliginosus* collected in the Myanmar county of Wutao (ref 5). The NS1 of this virus is most closely related to that of another bat virus (BtBoV XM3) in the proposed species *Chiropteran bocaparvovirus* *3*, listed immediately below, with which it shares 74% NS1 amino acid identity. Together these two viruses occupy a separate branch of lineage that leads to a fourth bat virus (in proposed species *Chiropteran bocaparvovirus* *4*, with which they share around 37% identity) and a large cluster of new and classified viruses that predominantly infect carnivores (figure 1).  ***Chiropteran bocaparvovirus* *3***  To include viruses clustering with bat bocavirus XM30 (BtBoV XM30, GenBank KC339250), identified in the gut contents of insectivorous bats from species *Miniopterus fuliginosus* collected in the Myanmar county of Sedon (ref 5). As discussed above, the sequence of its NS1 protein shares around 74% identity with BtBoV WM40 from proposed species *Chiropteran bocaparvovirus 2* and, like that virus, it is well separated from its nearest neighbors in recognized and proposed carnivore bocaparvovirus species.  ***Chiropteran bocaparvovirus* *4***  To include viruses clustering with bat bocaparvovirus Miniopterus schreibersii (BtBoV Ms, GenBank KU321654). Viruses from this species were identified in 2.3% (61/2636) of gut samples, 0.15% (4/2636) of respiratory samples and one spleen from bats of six different insectivorous species belonging to three families, Hipposideridae, Rhinolophidae and Vespertilionidae in suborder Microchiroptera*,* collected in Hong Kong and the Guangdong Province of Southern China during an 8 year period between 2006-2013 (ref 6). The NS1 protein of this virus shares around 37% identity with the bat viruses in proposed new species *Chiropteran bocaparvovirus 2* and *3*. A second distinct isolate in this proposed species, called bat bocaparvovirus Rhinolophus sinicus (BtBoV Rs, GenBank KU321655) encodes an NS1 protein that is 87% identical to the exemplar isolate (BtBoV Ms). Epidemiological and genome sequence analysis revealed evidence of the interspecies transmission of both viruses within bat populations.  ***Lagomorph bocaparvovirus* *1***  To include viruses clustering with rabbit bocaparvovirus (LBoV1, GenBank KP729195), detected in the gut contents of laboratory rabbits, both with and without diarrhea, from multiple commercial breeding enterprises in Northern Italy (ref 7). The NS1 protein of this virus shares <36% identity with those of other bocaparvoviruses and occupies a new branch of the tree.  ***Ungulate bocaparvovirus 6***  To include viruses with NS1 proteins exhibiting >85% identity to that of ungulate bocaparvovirus 6 (BBoV2, GenBank KU172421), identified in multiple nasal swabs from feedlot cattle with respiratory disease in both the USA (where a 10% subset of infected animals were detected in 2/4 of the sites tested) and Mexico (where a 15% subset of infected animals were found in 4/6 sites tested) in 2016 (ref 8). The NS1 protein of this virus shows 64% identity to that of its nearest neighbor in the taxonomy, bovine parvovirus 1 (BPV1, GenBank DQ335247), a founder member of the genus, with which it shares an outlying branch of the tree (figure 1).      **Figure 1. Phylogenetic tree proposed for genus *Bocaparvovirus***  Tree based on the amino acid sequence of the viral replicase, NS1. Viruses in proposed new species are labeled in **bold type.** For clarity, a single virus represents each species. Trees are midpoint rooted and branches are labeled with the accession number and name of the exemplar virus, followed by the species name in italic script. Branch lengths are proportional to genetic distances as indicated by arbitrary units in the scale bar. |