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

For guidance, see the notes written in blue and the separate document “Help with completing a taxonomic proposal”

Please try to keep related proposals within a single document.

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

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| --- | --- | --- | --- | --- | --- |
| **Code assigned:** | ***2017.004D*** | | | | (to be completed by ICTV officers) |
| **Short title:** 6 new species in the genus *Protoparvovirus* | | | | | |
| **Modules attached**  (Modules 1, 4 and either 2 or 3 are required. | | **1****x 2 x 3  4 x** | | | |
| **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: | | | | 4 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: 2017.004D.N.v2.Protoparvovirus\_6sp** |

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

| additional material in support of this proposal |
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| **References:** |
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Virol., 2016](https://recommendations.springernature.com/v1272/redirect/lp1qxDpozhFnVawMltYFf44_rEjHUJFbXxA6U-2Bkfvqbq3Sd5zB2eqB1CFNDAt6_gq9VriUzsC1hcAyfd6cksUO60H5tSk0Vz-VK3p8Q_vL1eWC7lH2nVIEM6QDth7wQFxqBoRXEURwrXl5OJOUsGOiB6tGsfkIhbLW3AG89jEVLZBrWNlLONQaOfCor89ZHXmAyXEcEnLfdvgRtDq0otgKIuIm5dx8JMFmnGfxCOlH5J_3z4JwQCR_bXSUzit5vGHVvF-HyRj8qr8lkm-pJIpGGUX-YPY9nTiaLLlgCVUpvEVyZuzMaw7uNprpdAbMvruNj4hXEpnPyiKVM2_7BiepeymOMaK-b6Ama-QzpxU_iLry3ryLT63vxzn5rpuDP-IL_H9JixJB6qy2o8zWnZeDsD-eS95q-dFSMwUBG1FiG3e6cpvgAJ-sF3q6SHBbOLeOu9emgLpf800doMrIcJdKhAhF9ZtpUN1-zm7HYBbu4s24F4ejo7-8tCULq4WMe495UKVob_6spfkH3KiyyEIVVQlgGkEFXSozVQzW-_R4tCRhW-2iVoA0_0x7QE6YAl0UksOKnBYbrsDFri7uIyWUS9tcKX7DAlgtWkhfgaeaQhO5UeFzAHafvJvClNvdjCKiBJRm2cwwR8T-a5Z8QGbkRuyOxuTr45WMhTn9oNvnQSVXzWROOI2upz-ifV1wklgUMH55ywegwLzWTL9OCwCLnjNgrnaFBzF9V4W3fLVlHWLvErrMpiUYy4qO-xze2__sBXCMGNi_Z5qBhQZREtuKlBZmJLT_aEkMj7VxG3k4fvlDc8pV3p5C-u_QRScLnnibDz1EQEOsM4cmCXMsFmyZOOyA78WtFi1TZXamuADKFPhMRp4USl61hqOGuaM5YtWt4eQpWAjSGTkaEk7wXNhiyN8COGv9PwBsK9TUabuO3bs4dvFr_dbwdEVxKvfw2KPwnXKT8OCX78VhZUbZPbQMIP5x38fkl_keyEg4Jns9zY4Xt9UNn2Kmx1hjwkiD9EVJKmxCr_kPAIft293xdoX3dgqT4NBvn4llgaQ7APez6SsU-9g-dWbRkfm2ZhfKo823EGp1TVZeKpExsEVccanN2uS4OL-iwmKbGigiAnkREhFj87RpruR-Q9Tf2mVJqTcIFoJvKMppS6yd_T15-ndnbCSKJ-NbDp-E45ULTBkJsn-Q-TeCvRzfb4skytwORyQ5k4cfJqbA4gA-dUgz8d6OXzG0J88yfsIO9YShR_dyY19aGWQQjtqV-tjpCHdtzXITUmeAxVe4KcWbj6DNy_WAO-YSCDkPG2kDRiK8o4e7GkCQfL9PGuGJ4U0dZOoY3Ckw4jRzrzcLC4ysFgkG8uXuytI5jwGRa-BP7VGsouXFj5HR5AC5PSsoGQIznKX0xmTk0VCatTbNbcewlTVAGe4L87UKgp_HOGvuVUQ9VcUi9M6i0WNucxve5_7vLJXca_pA8Kt8qwSDf5IEbhHsGIwL5ZNMAQTvGAHg8_Du7UQtVoSpELFPNKR4lA6IyfknwzMnH7QR14mt7vwhR4t_RQ0AZNVYxFf_rWWkJPucX4MnZ8wutJOJlHGU6KXYQ7djZrmh9mPCM3YPnxgd_2qgJLV-XlbbcgKqU95-2xW2wXJw7ykUiaTDF5SDEk2SRgPl7-KVE-zxSlbpVDuOskSXYxvzPo6unBzumZ-k38rwLg8nDzQtOXcFsX0SxfdKOcsMe7mY5ofp-MS1NlB3Jk9Wv9iUZe20G74OtY6H9BGDUbZe_smkNpDa2Tri7c70U60S9xlDd63sAOTKeC3OrMOirS3ruV05UpxJfPhLsP7ZWGib3livweFdwSXpFFyRXk-AJtKmpIErck5fyohfiRiB9Q%3D%3D). **97**:](https://recommendations.springernature.com/v1272/redirect/lp1qxDpozhFnVawMltYFf44_rEjHUJFbXxA6U-2Bkfvqbq3Sd5zB2eqB1CFNDAt6_gq9VriUzsC1hcAyfd6cksUO60H5tSk0Vz-VK3p8Q_vL1eWC7lH2nVIEM6QDth7wQFxqBoRXEURwrXl5OJOUsGOiB6tGsfkIhbLW3AG89jEVLZBrWNlLONQaOfCor89ZHXmAyXEcEnLfdvgRtDq0otgKIuIm5dx8JMFmnGfxCOlH5J_3z4JwQCR_bXSUzit5vGHVvF-HyRj8qr8lkm-pJIpGGUX-YPY9nTiaLLlgCVUpvEVyZuzMaw7uNprpdAbMvruNj4hXEpnPyiKVM2_7BiepeymOMaK-b6Ama-QzpxU_iLry3ryLT63vxzn5rpuDP-IL_H9JixJB6qy2o8zWnZeDsD-eS95q-dFSMwUBG1FiG3e6cpvgAJ-sF3q6SHBbOLeOu9emgLpf800doMrIcJdKhAhF9ZtpUN1-zm7HYBbu4s24F4ejo7-8tCULq4WMe495UKVob_6spfkH3KiyyEIVVQlgGkEFXSozVQzW-_R4tCRhW-2iVoA0_0x7QE6YAl0UksOKnBYbrsDFri7uIyWUS9tcKX7DAlgtWkhfgaeaQhO5UeFzAHafvJvClNvdjCKiBJRm2cwwR8T-a5Z8QGbkRuyOxuTr45WMhTn9oNvnQSVXzWROOI2upz-ifV1wklgUMH55ywegwLzWTL9OCwCLnjNgrnaFBzF9V4W3fLVlHWLvErrMpiUYy4qO-xze2__sBXCMGNi_Z5qBhQZREtuKlBZmJLT_aEkMj7VxG3k4fvlDc8pV3p5C-u_QRScLnnibDz1EQEOsM4cmCXMsFmyZOOyA78WtFi1TZXamuADKFPhMRp4USl61hqOGuaM5YtWt4eQpWAjSGTkaEk7wXNhiyN8COGv9PwBsK9TUabuO3bs4dvFr_dbwdEVxKvfw2KPwnXKT8OCX78VhZUbZPbQMIP5x38fkl_keyEg4Jns9zY4Xt9UNn2Kmx1hjwkiD9EVJKmxCr_kPAIft293xdoX3dgqT4NBvn4llgaQ7APez6SsU-9g-dWbRkfm2ZhfKo823EGp1TVZeKpExsEVccanN2uS4OL-iwmKbGigiAnkREhFj87RpruR-Q9Tf2mVJqTcIFoJvKMppS6yd_T15-ndnbCSKJ-NbDp-E45ULTBkJsn-Q-TeCvRzfb4skytwORyQ5k4cfJqbA4gA-dUgz8d6OXzG0J88yfsIO9YShR_dyY19aGWQQjtqV-tjpCHdtzXITUmeAxVe4KcWbj6DNy_WAO-YSCDkPG2kDRiK8o4e7GkCQfL9PGuGJ4U0dZOoY3Ckw4jRzrzcLC4ysFgkG8uXuytI5jwGRa-BP7VGsouXFj5HR5AC5PSsoGQIznKX0xmTk0VCatTbNbcewlTVAGe4L87UKgp_HOGvuVUQ9VcUi9M6i0WNucxve5_7vLJXca_pA8Kt8qwSDf5IEbhHsGIwL5ZNMAQTvGAHg8_Du7UQtVoSpELFPNKR4lA6IyfknwzMnH7QR14mt7vwhR4t_RQ0AZNVYxFf_rWWkJPucX4MnZ8wutJOJlHGU6KXYQ7djZrmh9mPCM3YPnxgd_2qgJLV-XlbbcgKqU95-2xW2wXJw7ykUiaTDF5SDEk2SRgPl7-KVE-zxSlbpVDuOskSXYxvzPo6unBzumZ-k38rwLg8nDzQtOXcFsX0SxfdKOcsMe7mY5ofp-MS1NlB3Jk9Wv9iUZe20G74OtY6H9BGDUbZe_smkNpDa2Tri7c70U60S9xlDd63sAOTKeC3OrMOirS3ruV05UpxJfPhLsP7ZWGib3livweFdwSXpFFyRXk-AJtKmpIErck5fyohfiRiB9Q%3D%3D)1592-1596. |

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| **Annex:**  Genus *Protoparvovirus* 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 rationalized and extended in 2014. Among other characteristics, viruses in this genus share similar genetic strategies, coding patterns, reiterated NS1-binding sites, potential classes of small non-structural proteins and protein motifs. Currently there are 5 recognized species, to which we propose adding 6 new species that share an existing branch of the phylogenetic tree with human bufaviruses 1-3 (species *Primate protoparvovirus* *1*). The new viruses infect bats, shrews, primates, rodents or pigs.  **Virus definition:**  Viruses in each of the newly proposed protoparvovirus 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 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 more than 15% from viruses in other species. Viruses in each of the candidate parvovirus 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 were determined using a pipeline platform called 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 genome to represent all full-length GenBank protein submissions that share <10% identity. The resulting *Parvovirinae* tree 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 selecting 1) *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. Candidate new species proposed in this submission were selected by reviewing each cluster of viruses in the tree for genomes that accord with our virus definition and taxon demarcation criteria, and have sufficient support data to indicate an infectious aetiology.  This pipeline approach ensures 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 the standard nomenclature for species in this family, proposed species are named for a host taxon (generally order) and their genus affiliation, followed by a distinguishing numeral. Species with like names receive numbers that follow those of previously recognized species, to be assigned at the time of recognition according to the date of their GenBank citation.  **Proposed new species:**  Viruses in the species proposed here are often named “bufavirus” (a siglum for Burkina Faso) because they resemble and share a branch of the phylogenetic tree with human bufaviruses from recognized species *Primate protoparvovirus 1*, which were first reported in samples from that locale.  **Table 1: Proposed new species in genus *Protoparvovirus*.**   |  |  |  |  |  | | --- | --- | --- | --- | --- | | Proposed new  species | Exemplar isolate | Accession # | Acronym | Ref-  erence | | *Chiropteran*  *protoparvovirus* *1*  *Eulipotyphla*  *protoparvovirus* *1* *Primate*  *protoparvovirus* *2*  *Primate*  *protoparvovirus* *3*  *Rodent*  *protoparvovirus* *3*  *Ungulate*  *protoparvovirus* *2* | megabat bufavirus 1  Mpulungu bufavirus  Wuharv parvovirus 1  cutavirus  rat bufavirus SY-2015  protoparvovirus Zsana/2013/HUN | LC085675  AB937988  JX627576  KT868811  KT716186  KT965075 | BtBuV1  ShBuV1  RhBuV1  HCutaV1  RatBuV  PBuV1 | 1  2  3  4 & 5  6  7 & 8 |   ***Chiropteran protoparvovirus*** *1*  To include viruses encoding NS1 proteins with >85% identity to that of megabat bufavirus 1 (BtBuV1, GenBank LC085675), which was identified in spleen (2%) and fecal (9%) samples from frugivorous "flying fox" bats (most notably from species *Pteropus vampyrus*, suborder Megachiroptera)*,* collected at eight regions in Indonesia during the period 2010-2014 (ref 1). This species occupies a deep branch in the bufavirus group (see tree in figure 1). The NS1 amino acid sequence of the virus is around 52% identical to those encoded by its nearest neighbors in the tree, which include all viruses in the new species proposed here plus the human bufaviruses in the previously recognized species *Primate protoparvovirus* *1*.  ***Eulipotyphla protoparvovirus* *1***  To include viruses clustering withMpulungu bufavirus (ShBuV1, GenBank AB937988), which was identified in 22% (5/23) of intestinal content samples, and in the spleens and livers, of wild shrews from genus *Crocidura* that weresampled at Mpulungu, Zambia, in 2012 (ref 2). The sequence of its NS1 protein is around 76% identical to that encoded by its nearest neighbor, rat bufavirus SY-2015 (KT716186) in proposed species *Rodent protoparvovirus* *3*. As seen in figure 1, its nearest neighbors in a recognized species are human bufavirus strains in species *Primate protoparvovirus* *1*, which encode NS1 proteins that share around 52% identity.  ***Primate protoparvovirus* *2***  To include viruses with NS1 proteins exhibiting >85% identity to that of rhesus monkey parvovirus Wuharv 1 (RhBuV1, GenBank JX627576), which was identified in the enteric contents and blood of rhesus monkeys suffering from AIDs following infection with pathogenic simian immunodeficiency virus (SIV, ref 3). Control monkeys that were not infected with SIV did not show appreciable levels of this virus or viruses from several other families, indicating that SIV infection was associated with a significant expansion of the enteric virome, which the authors suggest likely contributes to AIDS enteropathy and disease progression. The amino acid sequence of the NS1 protein from RhBuV1 is around 60% identical to that of the human bufaviruses in species *Primate protoparvovirus* *1* (Figure 1).  ***Primate protoparvovirus 3***  To include viruses clustering with human cutavirus (for cutaneous T-cell lymphoma associated parvovirus) strain BR-337 (HCutaV1, GenBank KT868811), which was 1 of 3 complete cds reported in fecal samples from children with diarrhea collected in Brazil between 2007-2008 (ref 4). The amino acid sequence of its NS1 protein is ~76% identical to that of its nearest neighbors in the genus, which are the human bufaviruses in species *Primate protoparvovirus* *1*. In the original study (Ref 4), HCutaV1 DNA was found in 1.6% (4/245) and 1% (1/100) of diarrhea samples from Brazil and Botswana respectively, and was also detected in a number of skin biopsies from patients with epidermotropic cutaneous T-cell lymphoma. A subsequent study (ref 5), identified a very similar virus in a Danish clinical sample of cutaneous malignant melanoma (strain CGG5-268, GenBank KX685945).  ***Rodent protoparvovirus*** *3*  To include viruses encoding NS1 proteins with >85% identity to that encoded by rat bufavirus SY-2015 (RatBuV1, GenBank KT716186), which was identified in the intestinal contents of apparently-healthy wild adult rats captured by the Chinese Center for Disease Control and Prevention in Taizhou City, China in 2004 (Ref 6). In the examined rat cohort, 12.5% (5/40) of the rats carried the virus. Its NS1 amino acid sequence is around 76% identical to that of its nearest neighbor, which is Mpulungu bufavirus in the proposed species *Eulipotyphla protoparvovirus* *1*, while the nearest recognized species is *Primate protoparvovirus* *1*, containing human bufavirus strains with which it shares around 52% NS1 identity.  ***Ungulate protoparvovirus* *2***  To include viruses clustering with protoparvovirus Zsana/2013/HUN (PBuV1, KT965075), identified in fecal samples from domestic pigs collected from commercial swine herds in Hungary between January and September 2013 (ref 7). PBuV1 was observed in samples from 66% (24/36) of the pigs tested, and is thus highly prevalent in the area. Its NS1 protein shares around 61% identity with those of its nearest neighbors in the phylogenetic tree, which are the rat and Mpulungu bufaviruses in the proposed new species *Rodent protoparvovirus* *3* and *Eulipotyphla protoparvovirus* *1*, respectively. As seen in the figure, its nearest neighbors in a recognized species are, once again, the human bufavirus strains in species *Primate protoparvovirus* *1*, with which it shares around 60% identity. A second virus (ref 8, Porcine bufavirus strain 61, KU867071), which shares an NS1 amino acid identity of around 93% with the exemplar strain and thus belongs to the same species, was identified in 2016 in Austrian farms, where it was detected in 13.3% (8/60) of samples, suggesting a relatively lower prevalence.  **Figure 1. Proposed phylogenetic organization of genus *Protoparvovirus***  Tree based on the amino acid sequence of the viral replicase, NS1. Viruses in proposed new species are labeled in **bold type.** For clarity, all species are represented by a single exemplar virus. Trees are midpoint rooted and branches labeled with the accession numbers and names of exemplar viruses, followed by the binomial species name in italic script. Branch lengths are proportional to genetic distances as indicated by arbitrary units in the scale bar. |