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:** | ***2017.002D*** | | | | (to be completed by ICTV officers) |
| **Short title:** 2 new species within the genus *Amdoparvovirus* | | | | | |
| **Modules attached** | | **1**  **2  3  4** | | | |
| **Author(s):** | | | | | |
| Marta Canuti, Emily McDonald, Andrew S. Lang | | | | | |
| **Corresponding author with e-mail address:** | | | | | |
| Marta Canuti: [marta.canuti@gmail.com](mailto:marta.canuti@gmail.com); Andrew Lang: [aslang@mun.ca](mailto:aslang@mun.ca) | | | | | |
| **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:** | | | | | |
| **1) This platform supports your proposal to create a new species taxon for the raccoon dog KJ396347 isolate. The closest link to this isolate is amdoparvovirus KT878839, which is immediately below the raccoon virus in the tree and links at 74% identity. However, KT878839 is the unpublished 2016 red panda isolate from Li, Pesavento and Delwart, which is full length but came from a single infected animal (with no epidemiology to back it up) and thus is not currently being considered for inclusion in the taxonomy.**  We are aware of the existence of this virus, but we did not include it in the proposal, because it is still unpublished.  **2) The RFFAV isolate that you mention in your proposal is not included in ViCtree because the system eliminates partial sequence isolates (since these would not be considered candidates for inclusion in the virus taxonomy). For simplicity, I would strongly suggest you should consider removing any reference to this RFFAV group from your ICTV submission (in the text and the table) because you are not asking the ICTV committee to consider it for inclusion and so it is an unnecessary complication for them (given that they are already swamped with viruses they do need to consider).**  We included this virus in our original proposal as it was discovered chronologically before the skunk virus and didn’t want to exclude any published data. We have however removed it from the current proposal.  **3) The bat virus KJ641663 in the ViCTree  analysis is an unpublished outlier from Wu et al. in China, which only links to the genus at 57% NS1 identity. This same research group has GenBank entries for bat parvoviruses that are distantly linked to several genera, but there is no support data to suggest that the bat is the primary host etc., so they are not currently candidates for inclusion.  However, I would be interested to know whether the gene structure of this isolate looks like an amdoparvovirus to you, given your experience looking at other viruses from the genus.**  We have not included this virus in our current proposal, but it is a very interesting question. We will perform some analyses and will let you know our opinion at a later stage.  **1)   I would like to see details of the alignment procedure,**  We have used Clustal to perform our alignments (as now detailed in the proposal) and we have included the NS1 alignment with the revised submission.  **2)   There is no recognized species called *Carnivore amdoparvovirus* *4*, so the skunk virus should be called Ca4 and not Ca5.**  Our idea was to keep the Ca4 designation for the red fox virus, as it was discovered earlier than the skunk virus. However, we have changed the proposal according to your suggestions.  **3)   Figures. Since this is a submission rather than a paper, the figures should be as simple and clear as possible. The fact that different numbers of isolates are detailed in the two figures suggests that some of the included isolates do not have full length GenBank coding sequences. Is that correct?  If so, I think this adds to complexity but not clarity, and would prefer them to be eliminated. Personally, I would only submit Figure 1 - for the NS protein, as Figure 2 is essentially irrelevant from the taxon demarcation criteria perspective.**  The proposal has been adjusted accordingly. | | | | | |
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| Date first submitted to ICTV: | | | | 19 May 2017 | |
| Date of this revision (if different to above): | | | | 13 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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| **Name of accompanying spreadsheet:** 2017.002D.N.v1.Amdoparvovirus\_2sp |

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

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| **References:** |
| Bodewes R, Ruiz-Gonzalez A, Schapendonk CME, van den Brand JMA, Osterhaus ADME, Smits SL. Viral metagenomic analysis of feces of wild small carnivores. *Virol J* 2014; **11**: 89.  Britton AP, Redford T, Bidulka JJ *et al.* Beyond rabies: are free-ranging skunks (*Mephitis mephitis*) in British Columbia reservoirs of emerging infection? *Transbound Emerg Dis* 2015; **64:** 603–612.  Canuti M, Whitney H, Lang AS. Amdoparvoviruses in small mammals: expanding our understanding of parvovirus diversity, distribution, and pathology. *Front Microbiol* 2015; **6**: 1119.  Canuti M, Doyle HE, Britton A, Lang AS. Full genetic characterization and epidemiology of a novel amdoparvovirus in striped skunk (Mephitis mephitis). *Emerg Microbes Infect* 2017; **6**: e30.  Cotmore SF, Agbandje-McKenna M, Chiorini JA *et al*. The family Parvoviridae. *Arch Virol* 2014; **159(5)**: 1239–1247.  Shao X-Q, Wen Y-J, Ba H-X *et al.* Novel amdoparvovirus infecting farmed raccoon dogs and Arctic foxes. *Emerg Infect Dis* 2014; **20**: 2085–2088. |

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| **Annex:**  The genus *Amdoparvovirus* (family *Parvoviridae*) currently includes 2 members, the Aleutian mink disease virus (AMDV, *Carnivore amdoparvovirus 1*) and the grey fox amdovirus (GFAV, *Carnivore amdoparvovirus 2*). Since the last accepted classification update for this genus in 2014 (Cotmore et al. 2014) several epidemiological studies about amdoparvoviruses have been performed and some of those have led to the identification of previously unrecognized species infecting different furbearing animals (Shao et al. 2014, Bodewes et al. 2014, Canuti et al. 2017).  Specifically:   * an amdoparvovirus infecting raccoon dog and Arctic fox (raccoon dog and fox amdoparvovirus, RFAV) has been identified in several farmed individuals in China. The infected animals showed Aleutian disease-like symptoms and the virus was isolated from various tissues of the affected animals (Shao et al. 2014). * an amdoparvovirus was identified in wild striped skunks from British Columbia, Canada (skunk amdoparvovirus, SKAV). Some of the animals showed Aleutian disease-like symptoms but several animals carried the virus asymptomatically. An in-depth investigation showed that this virus circulated in striped skunks from other distant locations in North America (California and Ontario), that at least 3 different genetic lineages are present and spillover events in mink were detected (Canuti et al. 2017; Britton et al. 2015).   These viruses possess the characteristics for being classified as species within the family *Parvoviridae* (Cotmore et al. 2014). In fact, both RFAV and SKAV have been detected in tissues of unambiguous host origin, they have been identified in multiple individuals in a pattern suggestive of dissemination by infection, and the complete sequence of the viral nonstructural (NS) and capsid (VP) ORFs have been determined and show motifs typical of members of the family *Parvoviridae* and of the genus *Amdoparvovirus* (Shao et al. 2014; Canuti et al. 2017). The genome of both viruses contains the information for coding all 3 NS and 2 VP proteins and putative splicing sites are well supported. The helicase motif is identifiable in NS1, while both viruses lack the phospholipase A2 motif, like of other members of the genus *Amdoparvovirus* (Canuti et al. 2017).  **Taxon demarcation criteria**  These recently discovered viruses possess the requirements to be classified as two separate species within the genus *Amdoparvovirus*. In fact, each group clusters in separate and bootstrap-supported clades (see below) and the NS1 proteins within each group show >85% amino acid sequence identity, while diverging by >15% from viruses in other groups. The table below shows the identities (1 – p-distance) within and between different groups within the genus *Amdoparvovirus* (with pairwise deletion of gaps).  **Table. Average (range) pairwise percentage sequence identity (1 - p distance) within (in bold) and between different amdoparvoviral species for NS1 proteins**   |  |  |  |  |  | | --- | --- | --- | --- | --- | |  | AMDV$ | SKAV$ | RFAV$ | GFAV$ | | AMDV | **87.9 (83.9-99.2)** |  |  |  | | SKAV | 80.1 (77.9-81.4) | **90.4 (85.6-97.3)** |  |  | | RFAV | 74.0 (71.9-75.5) | 73.5 (72.5-75.3) | **95.1 (94.4-96.4)** |  | | GFAV | 67.2 (66.1-68.5) | 66.9 (66.0-67.6) | 65.0 (64.3-65.8) | **NA\*** |   $Sequences used for this analysis and their accession numbers are provided in Figure 1  \*NA: not available as only one member is known for these proposed species  **Phylogenetic tree (next page)**  Phylogenetic analysis presented here is based on the amino acid sequences of the NS1 of viruses currently included (*Carnivore amdoparvovirus 1* and *Carnivore amdoparvovirus 2*) and proposed (Carnivore amdoparvovirus 3 and Carnivore amdoparvovirus 4) in the genus *Amdoparvovirus*. Trees were built on alignment obtained with ClustalX using the maximum likelihood method based on the JTT + Gamma model, determined as the best fitting model for those datasets by the modeltest analysis performed with Mega 7. A bootstrap analysis was performed (1000 replicates) to test the robustness of the clades and the outcome is shown next to the nodes. Branch lengths are proportional to genetic distances as indicated by the scale bar. Viruses included within the two new proposed viral species form two clearly separate clades, characterized by high bootstrap support.  **Conclusions**  For the reasons delineated above, we propose RFAV and SKAV to be included as members within the genus *Amdoparvovirus* and assign to them the species designations of *Carnivore amdoparvovirus 3* and *Carnivore amdoparvovirus 4*, respectively, as indicated in the accompanying spreadsheet and proposed in our recent publications (Canuti et al. 2015 and Canuti et al. 2017).  **Figure. Phylogenetic tree built with amino acid sequences of the NS1 protein of different amdoparvoviral species.** Already accepted species (black): Aleutian mink disease virus (AMDV, *Carnivore amdoparvovirus 1*) and the grey fox amdovirus (GFAV, *Carnivore amdoparvovirus 2*). Proposed species (red): raccoon dog and fox amdoparvovirus (RFAV, Carnivore amdoparvovirus 3) and skunk amdoparvovirus (SKAV, Carnivore amdoparvovirus 5). |