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.

For guidance, see the notes written in blue, below, and the help notes in file Taxonomic\_Proposals\_Help\_2018.

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

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| **Code assigned:** | ***2018.008D*** | (to be completed by ICTV officers) |
| **Short title: 10 new species and 1 renamed species in the family *Polyomaviridae*** |
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| **Author(s):** |
| Sébastien Calvignac-Spencer, Michael Carr, Matthew D. Daugherty, Mariet C.W. Feltkamp, Chris Lauber, Ugo Moens, Ernst J. Verschoor, Bernhard Ehlers |
| **Corresponding author with e-mail address:** |
| Bernhard Ehlers ehlersb@rki.de |
| **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) | Polyomaviridae SG |
| **ICTV Study Group comments (if any) and response of the proposer:** |
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| Date first submitted to ICTV: | 9 May 2018 |
| Date of this revision (if different to above): | 14 June 2018 |

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| **ICTV-EC comments and response of the proposer:** |
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**Part 3:** **PROPOSED TAXONOMY**

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| **Name of accompanying Excel module:** 2018.008D.N.v1.Polyomaviridae\_10sp |

**Supporting material:**

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| **Reasons to justify the creation and assignment of the new species:** |
| 1. The complete genomes of the giant panda polyomavirus, Canis familiaris polyomavirus 1, raccoon-associated polyomavirus 2, Sorex coronatus polyomavirus 1, Sorex minutus polyomavirus 1, Miniopterus schreibersii polyomavirus 1, Miniopterus schreibersii polyomavirus 2, Rousettus aegyptiacus polyomavirus 1 (all from mammalian hosts) and those of Sparus aurata polyomavirus 1, Emerald notothen polyomavirus 1 (both from fish) are published1-7. This fulfills number 1 of the species definition criteria published in 2016 by the Polyomaviridae Study Group and ratified by ICTV in May 2016 (2015.015a-aaD.A.v2.Polyomaviridae\_rev8; Calvignac Spencer et al. 20169).
2. The above listed 8 mammalian polyomaviruses have a genome organization typical for members of the *Polyomaviridae*. The genomes of the 2 fish viruses display large T, VP1 and VP2 coding sequences, but appear to lack small T coding sequence, a common feature of members of fish polyomavirus species. This fulfills number 2 of the species definition criteria.
3. There is sufficient information about the natural host of the above listed viruses1-7. Full genomes are available (deposited in GenBank under the accession numbers KY612371, KY341899, KY549442, MF374999, MF401583, KX643371, MG800627, LC185213, LC185216, LC185218). This fulfills number 3 of the species definition criteria.
4. Using the MAFFT module in Geneious 10.0.5., the LTAg CDS of the above listed 10 polyomaviruses display >15 % observed genetic distance to LTAg CDS of members of existing polyomavirus species. Thus number 4 of the species definition criteria is fulfilled.
5. In a phylogenetic analysis of LTAg sequences of members of existing polyomavirus species, the members of *Sorex coronatus polyomavirus 1*, *Sorex minutus polyomavirus 1*, *Miniopterus schreibersii polyomavirus 1*, and *Miniopterus schreibersii polyomavirus 2* cluster with other members of the genus *Alphapolyomavirus*, and the members of *Canis familiaris polyomavirus 1* and *Rousettus aegyptiacus polyomavirus 1* cluster with other members of the genus *Betapolyomavirus*. The members of *Ailuropoda melanoleuca polyomavirus 1* and *Procyon lotor polyomavirus 2* do not firmly cluster with members of any currently defined genus. These and the 2 fish polyomaviruses (Sparus aurata polyomavirus 1 and emerald notothen polyomavirus 1) were defined as belonging to floating species (i.e. not assigned to a genus) within the family (Fig. 1).
6. Renaming of species *Human polyomavirus 12* to *Sorex araneus polyomavirus 1*: Recently, three sorex polyomaviruses (Sorex araneus polyomavirus 1, Sorex coronatus polyomavirus 1, Sorex minutus polyomavirus) were discovered. Phylogenetic relationships with their hosts suggest virus-host co-divergence4. The complete genome of one of them, Sorex araneus polyomavirus 1, is nearly identical (99%) to that of human polyomavirus 12 (species *Human polyomavirus 12*), their 1 % difference located in the NCCR4. As Sorex araneus PyV1 is 99% identical to human polyomavirus 12, it violates the species definition criterion C4: “The observed genetic distance to members of the most closely related species is >15 % for the large T antigen coding sequence”. Therefore only one of them can constitute a species. Of note, in the paper of Gedvilaite et al.4 it is discussed whether HPyV12 (i) is a *bona fide* human virus that was recently transmitted from S. araneus, or (ii) was identified by PCR in human samples as a lab artefact (please see the detailed discussion of this issue therein). Taken together, this justifies renaming of species *Human polyomavirus 12* to *Sorex araneus polyomavirus 1*. Included in this species is the Sorex araneus isolate GER\_#4608\_MU/06/0215/MV and the human polyomavirus 12 isolate hu1403.
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| **References:** |
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| 1 Qi, Dunwu, et al. "A novel polyomavirus from the nasal cavity of a giant panda (*Ailuropoda melanoleuca*)." *Virology Journal* 14.1 (2017): 207.2 Delwart, Eric, et al. "Genome sequence of canine polyomavirus in respiratory secretions of dogs with pneumonia of unknown etiology." *Genome Announcements* 5.29 (2017): e00615-17.3 Geoghegan, Eileen M., et al. "Identification of a second raccoon-associated polyomavirus." *Genome Announcements* 5.26 (2017): e00548-17.4 Gedvilaite, Alma, et al. "Novel polyomaviruses in shrews (Soricidae) with close similarity to human polyomavirus 12." *Journal of General Virology* 98 (2017) 3060-3067.5 Carr, Michael, et al. "Discovery of African bat polyomaviruses and infrequent recombination in the large T antigen in the *Polyomaviridae*." *Journal of General Virology* 98.4 (2017): 726-738.6 López-Bueno, Alberto, et al. "Concurrence of iridovirus, polyomavirus, and a unique member of a new group of fish papillomaviruses in lymphocystis disease-affected gilthead sea bream." *Journal of Virology* 90.19 (2016): 8768-8779. 7 Van Doorslaer, Koenraad, et al. "Fish polyomaviruses belong to two distinct evolutionary lineages." *Journal of General Virology* 99.4 (2018): 567-573.8 Calvignac-Spencer, S., Feltkamp, M., Daugherty, M.D., Moens, U., Ramqvist, T., Johne, R., Ehlers, B. ICTV taxonomic proposal 2015.015a-aaD.A.v2.Polyomaviridae\_rev (2015).9 Calvignac-Spencer, S., et al. “A taxonomy update for the family *Polyomaviridae*.” Archives of Virology 161.6 (2016): 1739-1750.  |

**Figure 1**. Maximum likelihood tree based on an alignment of large T amino acid sequences (479 amino acid positions) reconstructed with PhyML v3.1. Model of aa substitution (determined with Prottest v3.2): LG+I+G+F. Branch support values: Shimodaira-Hasegawa-like approximate likelihood ratio tests (SH-like aLRT), grey branches: <0.95 SH-like aLRT. Proposed novel species are in enlarged, black font.

