

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

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| **Code assigned:** | **2020.019D** |  |
| **Short title:** Create two new genera and 15 new species (*Sepolyvirales*: *Polyomaviridae*) | | |
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**List the ICTV Study Group(s) that have seen this proposal**

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| *Polyomaviridae* Study Group |

**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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**Submission dates**

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| Date first submitted to SC Chair | August 4, 2020 |
| Date of this revision (if different to above) | November 24, 2020 |

**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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| 2020.019D.R.Polyomaviridae\_2ngen\_15nsp.xlsx |

A**bstract**

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| 15 novel polyomavirus (PyV) species are proposed that accommodate 15 PyVs of mammals. Four existing PyV species are incorporated into genera. Two novel genera are defined (*Epsilonpolyomavirus*, *Zetapolyomavirus*). |

**Text of proposal**

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| |  | | --- | | Create 15 novel species *Apodemus flavicollis polyomavirus 1, Callosciurus erythraeus polyomavirus 1, Callosciurus prevostii polyomavirus 1, Canis lupus polyomavirus 1, Capra aegragus polyomavirus 1, Glis glis polyomavirus 1, Lepus granatensis polyomavirus 1, Mastomys natalensis polyomavirus 2, Mastomys natalensis polyomavirus 3, Panthera leo polyomavirus 1, Potamochoerus porcus polyomavirus 1, Philantomba monticola polyomavirus 1, Sciurus carolinensis polyomavirus 1, Sus scrofa polyomavirus 1, Tupaia glis polyomavirus 1 for* polyomaviruses Apodemus flavicollis polyomavirus 1, Callosciurus erythraeus polyomavirus 1, Callosciurus prevostii polyomavirus 1, Canis lupus polyomavirus 1, Capra aegragus polyomavirus 1, Glis glis polyomavirus 1, Lepus granatensis polyomavirus 1, Mastomys natalensis polyomavirus 2, Mastomys natalensis polyomavirus 3, Panthera leo polyomavirus 1, Potamochoerus porcus polyomavirus 1, Philantomba monticola polyomavirus 1, Sciurus carolinensis polyomavirus 1, Sus scrofa polyomavirus 1, Tupaia glis polyomavirus 1.  Justifiction:   1. The complete genomes of the 15 novel polyomaviruses are published [1, 3-5]:   MG654476, MG654477, MG654478 Apodemus flavicollis polyomavirus 1  MK671087, MK671088, MK671089 Callosciurus erythraeus polyomavirus 1  MK883808, MK883809, MK883810 Callosciurus prevostii polyomavirus 1  MG701355, MG701356 Canis lupus polyomavirus 1  MG654479, MG654480 Capra aegragus polyomavirus 1  MG701352 Glis glis polyomavirus 1  MN994868; MN994869 Lepus granatensis polyomavirus 1  MG701350, MG701351 Mastomys natalensis polyomavirus 2  MN417229 Mastomys natalensis polyomavirus 3  MG701353, MG701354 Panthera leo polyomavirus 1  MG654481 Potamochoerus porcus polyomavirus 1  MG654482 Philantomba monticola polyomavirus 1  MK671101, MK671096, MK671097 Sciurus carolinensis polyomavirus 1  KR065722 Sus scrofa polyomavirus 1  MG721015, MG721016, MG721017 Tupaia glis polyomavirus 1.  This fulfills number 1 of the species definition criteria published in 2016 by the *Polyomaviridae* Study Group [2] and ratified by ICTV in May 2016 (2015.015a-aaD.A.v2.Polyomaviridae\_rev).   1. The above listed 15 mammalian polyomaviruses have a genome organization typical for members of the *Polyomaviridae*. This fulfills number 2 of the species definition criteria. There is sufficient information about the natural host of the above listed viruses[1, 3-5]. This fulfills number 3 of the species definition criteria. 2. Using the MAFFT module in Geneious 11.1.5., the LTAg CDSs of the above listed 15 polyomaviruses were aligned with members of existing polyomavirus species. All 15 LTAg CDSs display >15 % observed genetic distance to those of members of existing polyomavirus species and among each other. Thus number 4 of the species definition criteria is fulfilled. 3. In a phylogenetic analysis of LTAg amino acid sequences with members of existing polyomavirus species (Fig. 1), the members of *Apodemus flavicollis polyomavirus 1, Mastomys natalensis polyomavirus 2, Mastomys natalensis polyomavirus 3, Sus scrofa polyomavirus 1, Philantomba monticola polyomavirus 1, Callosciurus erythraeus polyomavirus 1*, and *Tupaia glis polyomavirus 1* cluster with members of the genus *Alphapolyomavirus*. These novel species are therefore assigned to genus *Alphapolyomavirus*. 4. In the same analysis, the members of *Panthera leo polyomavirus 1*, *Glis glis polyomavirus 1, Lepus granatensis polyomavirus 1, Sciurus carolinensis polyomavirus 1,* and *Callosciurus prevostii* *polyomavirus 1* cluster with members of the genus *Betapolyomavirus* (Fig. 1). These novel species are therefore assigned to genus *Betapolyomavirus*. 5. The members of *Canis lupus polyomavirus 1, Procyon lotor polyomavirus 2* and *Ailuropoda melanoleuca polyomavirus 1* (the latter 2 already established as species, but currently not assigned to a genus) cluster with members of genus *Deltapolyomavirus* (Fig. 1). The three are therefore assigned to genus *Deltapolyomavirus*. 6. The members of the 2 novel species *Capra aegragus polyomavirus 1* and *Potamochoerus porcus polyomavirus 1* cluster with that of the established species *Bos taurus polyomavirus 1* as a deep branching lineage*.* As *Bos taurus polyomavirus 1* is currently not assigned to a genus, the three species are now proposed to be assigned to the newly created genus *Epsilonpolyomavirus* (Fig. 1), with B*os taurus polyomavirus 1* as type species. This novel genus is also supported by the fact that the LTAg CDS of the three member viruses contains 2 introns (instead of one) [4]. 7. We also identified another deep branching lineage with the member of the established species *Delphinus delphis polyomavirus 1* (currently not assigned to a genus). This is now proposed to be assigned as type species to the novel genus *Zetapolyomavirus* (Fig. 1), which is based on tree topology (Figure 1; [2]) and on analysis of pairwise genetic distances (Fig. 2). The latter shows that the smallest dolphin polyomavirus distance (to its closest relative in the data set) is (slightly) larger than the smallest inter-genus distance involving established genera. In addition to the deep branching of the dolphin polyomavirus (Fig. 1;[2]) this supports the notion that the dolphin PyV (*Delphinus delphis polyomavirus 1*) prototypes a separate genus. | |

**Supporting evidence**

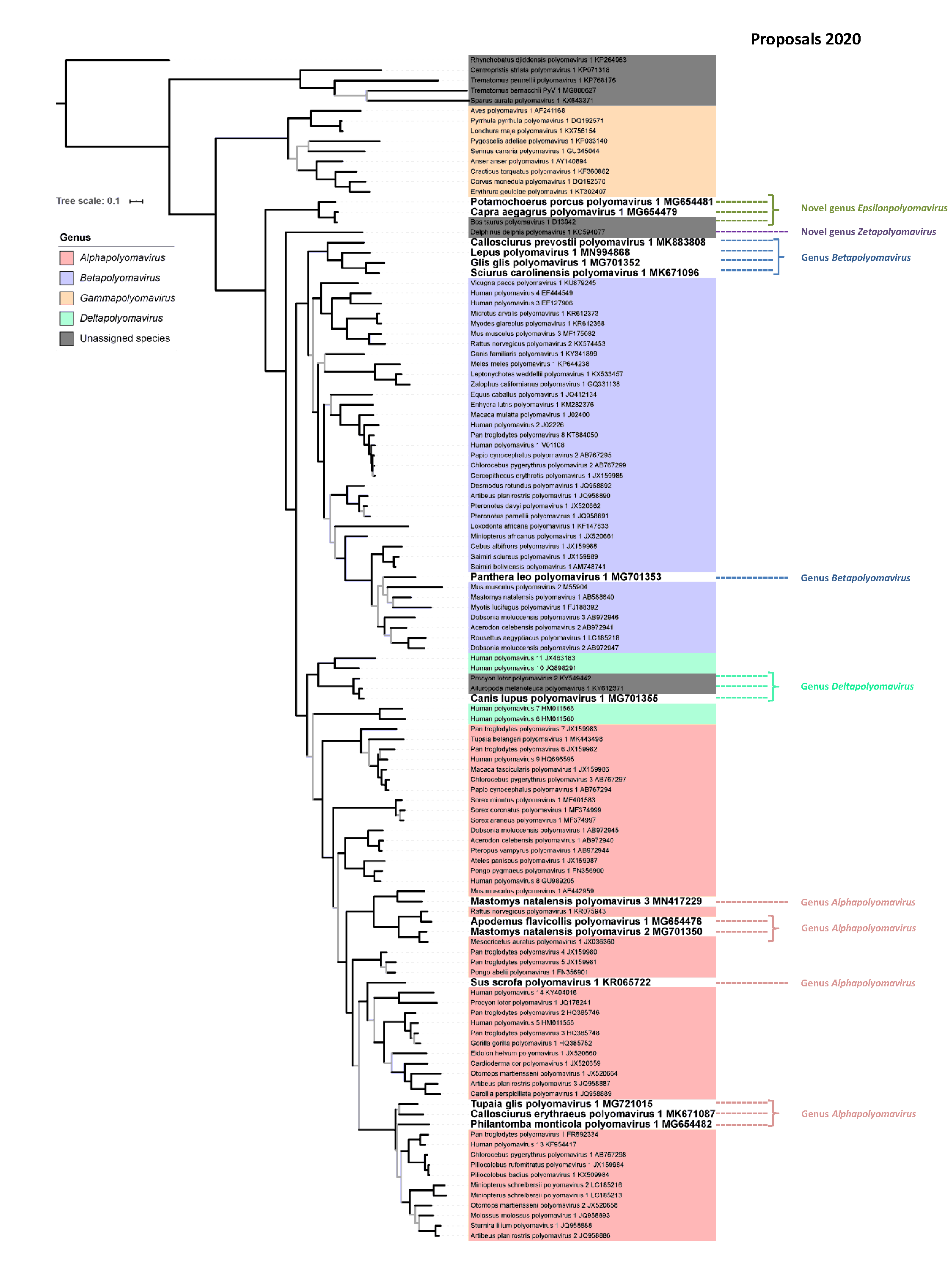


Figure 1. Maximum likelihood tree based on an alignment of large T amino acid sequences reconstructed with PhyML v3.1. Model of amino acid substitution (determined with smart model selection): LG+I+G+F. Branch support values: Shimodaira-Hasegawa-like approximate likelihood ratio tests (SH-like aLRT), grey branches: <0.9 SH-like aLRT. Proposed novel species are in enlarged, bold font. Existing species currently assigned to a genus are marked with yellow, blue, green or red color (see color code explanation within the figure). Existing species so far not assigned to a genus are marked with grey color.

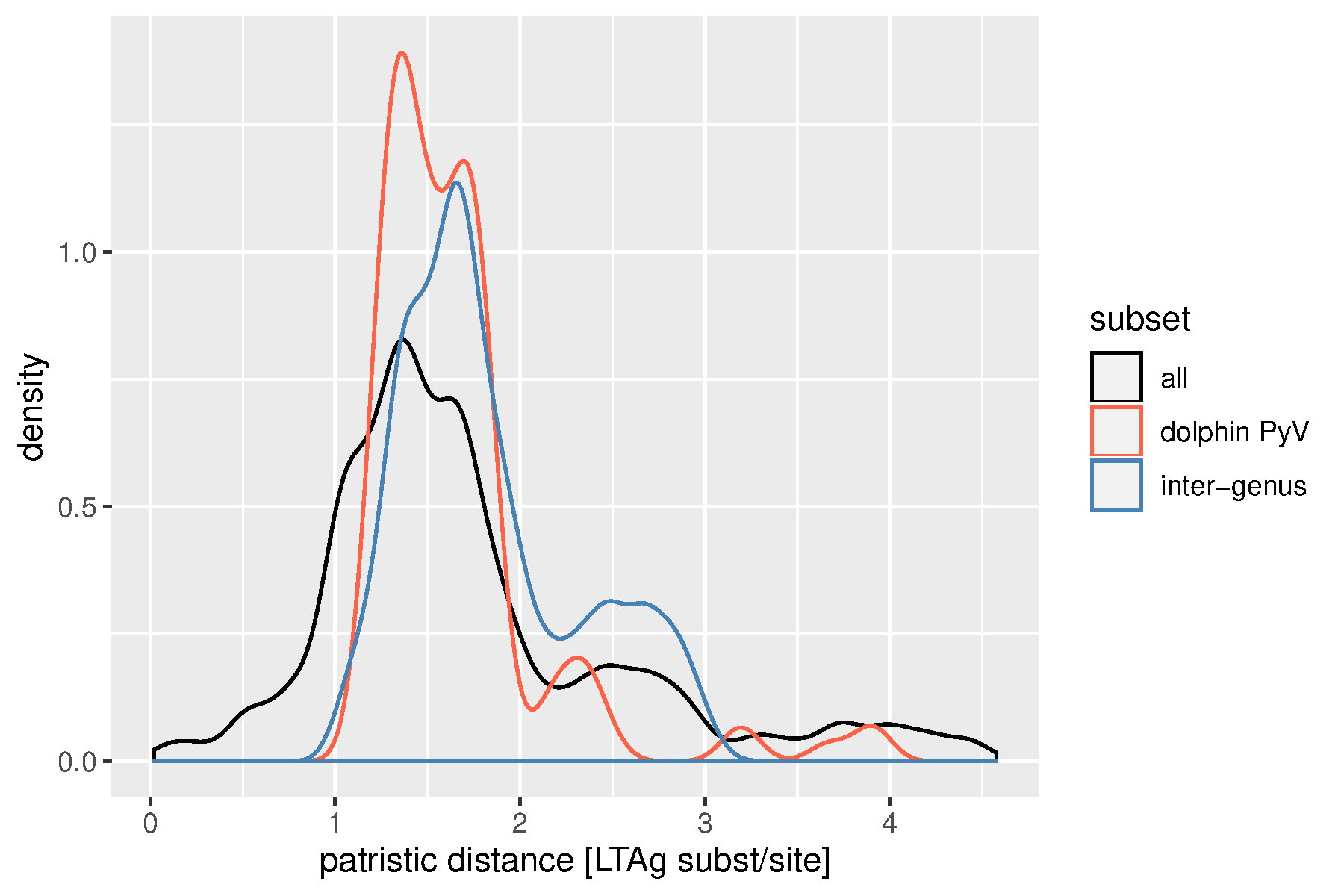
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Figure 2. The plot shows pairwise LTAg distance distributions for different subsets of polyomaviruses. The distance values have been extracted from the alignment used for tree reconstruction in Figure 1. The blue curve shows the distribution of all distances involving two viruses from different established polyomavirus genera (included re alpha, beta, gamma, delta and epsilon). The red curve shows the distribution of all distances the dolphin PyV is involved in.

**References**

1. Águeda-Pinto A, Kraberger S, Lund MC, Gortázar C, McFadden G, Varsani A, Esteves PJ (2020) Coinfections of novel polyomavirus, anelloviruses and a recombinant strain of nyxoma virus-MYXV-Tol identified in Iberian hares. Viruses 12:340  
PMID: 32244962; PMCID: PMC7150814; DOI: [10.3390/v12030340](https://doi.org/10.3390/v12030340)

2. Calvignac-Spencer S, Feltkamp MC, Daugherty MD, Moens U, Ramqvist T, Johne R, Ehlers B (2016) A taxonomy update for the family Polyomaviridae. Archives of Virology 161:1739-1750  
PMID: 26923930; DOI: [10.1007/s00705-016-2794-y](https://doi.org/10.1007/s00705-016-2794-y)

3. Calvignac-Spencer S, Kouadio L, Couacy-Hymann E, Sogoba N, Rosenke K, Davison AJ, Leendertz FH, Jarvis MA, Feldmann H, Ehlers B (2020) Multiple DNA viruses identified in multimammate mouse (Mastomys natalensis) populations from across regions of sub-Saharan Africa. Arch Virol 165:2291-2299  
PMID: 32754877 DOI: [10.1007/s00705-020-04738-9](https://doi.org/10.1007/s00705-020-04738-9)

4. Ehlers B, Anoh AE, Ben Salem N, Broll S, Couacy-Hymann E, Fischer D, Gedvilaite A, Ingenhütt N, Liebmann S, Martin M, Mossoune A, Mugisha L, Muyembe-Tamfum J-J, Pauly M, Pérez de Val B, Preugschas H, Richter D, Schubert G, Szentiks CA, Teichmann T, Walter C, Ulrich RG, Wiersma L, Leendertz FH, Calvignac-Spencer S (2019) Novel polyomaviruses in mammals from multiple orders and reassessment of polyomavirus evolution and taxonomy. Viruses 11:930  
PMID: 31658738; PMCID: PMC6833039; DOI: [10.3390/v11100930](https://doi.org/10.3390/v11100930)

5. Schulze V, Lurz PW, Ferrari N, Romeo C, Steele MA, Marino S, Mazzamuto MV, Calvignac-Spencer S, Schlottau K, Beer M (2020) Search for polyoma-, herpes-, and bornaviruses in squirrels of the family Sciuridae. Virology Journal 17:42  
PMID: 32220234; PMCID: PMC7099801; DOI: [10.1186/s12985-020-01310-4](https://doi.org/10.1186/s12985-020-01310-4)