

The International Committee on Taxonomy of Viruses

Taxonomy Proposal Form, 2024

**Part 1a: Details of taxonomy proposals**

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| **Title:** | Create 4 new species in the genera *Alphapolyomavirus* and *Betapolyomavirus* (*Polyomaviridae*) | |
| **Code assigned:** | 2024.003D.N.v1.Polyomaviridae\_4ns |

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| **Author(s), affiliation and email address(es):** | | | |
| **Name** | **Affiliation** | **Email address** | **Corresponding author(s)** X |
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**Part 1b: Taxonomy Proposal Submission**

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| **ICTV Subcommittee:** | | | |
| Animal DNA Viruses and Retroviruses | **X** | Bacterial viruses |  |
| Animal minus-strand and dsRNA viruses |  | Fungal and protist viruses |  |
| Animal positive-strand RNA viruses |  | Plant viruses |  |
| Archaeal viruses |  | General - |  |

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| **List the ICTV Study Group(s) that have seen or have been involved in creating this proposal:** |
| Polyomaviridae SG  The study group chair supported our proposal. |

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| **Optional – complete only if formally voted on by an ICTV Study Group:** | | | |
| **Study Group** | **Number of members** | | |
| **Votes in support** | **Votes against** | **No vote** |
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| **Submission date:** | 21/06/2024 |

**Part 1c: Feedback from ICTV Executive Committee (EC) meeting**

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| **Executive Committee Meeting Decision code:** | **X** |
| A – Accept |  |
| Ac – Accept subject to revision by relevant subcommittee chair. No further vote required |  |
| U – Accept without revision but with re-evaluation and email vote by the EC |  |
| Uc – Accept subject to revision and re-evaluation and email vote by the EC |  |
| Ud – Deferred to the next EC meeting, with an invitation to revise based on EC comments |  |
| J - Reject |  |
| W - Withdrawn |  |

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| **Comments from the Executive Committee:** |
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**Part 1d: Revised Taxonomy Proposal Submission**

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| **Response of proposer:** |
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| **Revision date:** | DD/MM/YYYY |

**Part 3:** **TAXONOMIC PROPOSAL**

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| **Name of accompanying Excel module:** |
| 2024.003D.N.v1.Polyomaviridae\_4ns.xlsx |

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| **Taxonomic changes proposed:** | | | |
| Establish new taxon | **X** | Split taxon |  |
| Abolish taxon |  | Merge taxon |  |
| Move taxon |  | Promote taxon |  |
| Rename taxon |  | Demote taxon |  |
| Move and rename |  |

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| **Is any taxon name used here derived from that of a living person:** | | **Y/N** |
| **Taxon name** | **Person from whom the name is derived** | **Attached X** |
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| **Abstract of Taxonomy Proposal:** |
| *Taxonomic rank(s) affected*:  Species  *Description of current taxonomy*:  118 species in 8 genera in the family *Polyomaviridae*.  *Proposed* *taxonomic change(s):*  Adding 4 novel species; 3 to genus *Alphapolyomavirus*, 1 to *Betapolyomavirus*  *Justification*:  Novel polyomaviruses have been detected in bat guano and Eurasian beaver kidney tissue samples. Three from the novel bat polyomaviruses and the beaver polyomavirus meet the criteria of establishing a new species. The phylogenetic distance of their LTAg nucleotide sequences is more than 15 percent to members of accepted polyomavirus species and their host species is known, furthermore, they originate from new hosts. |

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| * **Text of Taxonomy proposal:** |
| *Taxonomic rank(s) affected*:  Species  *Description of current taxonomy*:  118 species in 8 genera in the family *Polyomaviridae*.  genus *Alphapolyomavirus*: 51 species  genus *Betapolyomavirus*: 41 species  genus *Gammapolyomavirus*: 10 species  genus *Deltapolyomavirus*: 7 species  genus *Etapolyomavirus*: 1 species  genus *Thetapolyomavirus*: 4 species  genus *Epsilonpolyomavirus*: 3 species  genus *Zetapolyomavirus*: 1 species  *Proposed* *taxonomic change(s)*:  Establish 4 new species (total species number in the family: 122)  genus *Alphapolyomavirus*: 3 new species (total virus species: 54)  genus *Betapolyomavirus*: 1 new species (total virus species: 42)  *Demarcation criteria:*  Phylogenetic distance of the LTAg nucleotide sequence is more than 15 percent to members of accepted polyomavirus species. Known host species.  *Justification*:  In recent years many diverse mammalian polyomaviruses have been detected in bats and rodents (Surján et al., 2023, Surján et al., 2024, Vidovszky et al., 2020). Three from the novel bat polyomaviruses and the beaver polyomavirus meet the criteria of establishing a new species. The phylogenetic distance of their LTAg nucleotide sequences is more than 15 percent to members of accepted polyomavirus species and their host species is known, furthermore, they originate from new hosts.  Precise proposed species names, virus names, host species, GenBank accession numbers, LTAg pairwise identity percentages with most similar polyomaviruses can be seen on Table 1. The inferred Maximum Likelihood phylogenetic tree based on the LTAg nucleotide sequences of approved and the proposed polyomavirus species is shown on Figure 1.  Naming  The ICTV requires the application of a binomial species naming system (Walker et al., 2021). For polyomavirus species we use Latinized species epithets derived by applying different approaches (Postler et al., 2022). We based the names on the abbreviated host species names (*Eptesicus serotinus*, *Myotis daubentonii*) or the epitet of the host species name (*Rhinolophus hipposideros*) or the genus name of the host (*Castor fiber*).  Bioinformatics  Homologous nucleic acid sequences of the LTAg genes of PyVs were aligned using MAFFT 7.49 with the *E*-INS-i algorithm ([Kuraku et al., 2013](https://www.sciencedirect.com/science/article/pii/S1567134824000716?via%3Dihub" \l "bb0110); [Moens et al., 2017](https://www.sciencedirect.com/science/article/pii/S1567134824000716?via%3Dihub" \l "bb0135); [Katoh et al., 2019](https://www.sciencedirect.com/science/article/pii/S1567134824000716?via%3Dihub" \l "bb0095)). The phylogenetic tree reconstruction based on the LTAg nucleotide sequences was performed by PhyML 3.3.1. ([Guindon et al., 2010](https://www.sciencedirect.com/science/article/pii/S1567134824000716?via%3Dihub" \l "bb0065); [Lemoine et al., 2018](https://www.sciencedirect.com/science/article/pii/S1567134824000716?via%3Dihub" \l "bb0120), [Lemoine et al., 2019](https://www.sciencedirect.com/science/article/pii/S1567134824000716?via%3Dihub" \l "bb0125)), using smart model selection (SMS, [Lefort et al., 2017](https://www.sciencedirect.com/science/article/pii/S1567134824000716?via%3Dihub" \l "bb0115)) with BIC as the criterion. The final model was GTR + G + I substitutional model, proportion of invariant sites and the parameter for the gamma model with four categories were estimated. Subtree Pruning and Regraphing (SPR) was applied for tree topology searches. Branch support values were determined using the SH-like aLRT method ([Guindon et al., 2010](https://www.sciencedirect.com/science/article/pii/S1567134824000716?via%3Dihub#bb0065)). |

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| **References:** |
| Calvignac-Spencer, S., Feltkamp, M.C., Daugherty, M.D., Moens, U., Ramqvist, T., Johne, R., Ehlers, B., 2016. A taxonomy update for the family *Polyomaviridae*. Arch. Virol., 161(6), 1739–1750. https://doi.org/10.1007/s00705-016-2794-y  Ehlers, B., Anoh, A.E., Ben Salem, N., Broll, S., Couacy-Hymann, E., Fischer, D., Gedvilaite, A., Ingenhütt, N., Liebmann, S., Martin, M., Mossoun, A., Mugisha, L., Muyembe-Tamfum, J.J., Pauly, M., Pérez de Val, B., Preugschas, H., Richter, D., Schubert, G., Szentiks, C.A., Teichmann, T., Walter, C., Ulrich, R.G., Wiersma, L., Leendertz, F.H., Calvignac-Spencer, S., 2019. Novel polyomaviruses in mammals from multiple orders and reassessment of polyomavirus evolution and taxonomy. Viruses, 11(10), 930. https://doi.org/10.3390/v11100930  Guindon, S., Dufayard, J.F., Lefort, V., Anisimova, M., Hordijk, W., Gascuel, O., 2010. New algorithms and methods to estimate Maximum-Likelihood phylogenies: assessing the performance of PhyML 3.0. Syst. Biol., 59(3), 307–321. https://doi.org/10.1093/sysbio/syq010  Katoh, K., Rozewicki, J., Yamada, K.D., 2019. MAFFT online service: multiple sequence alignment, interactive sequence choice and visualization. Brief Bioinform., 20(4), 1160–1166. https://doi.org/10.1093/bib/bbx108  Kuraku, S., Zmasek, C.M., Nishimura, O., Katoh, K., 2013. aLeaves facilitates on-demand exploration of metazoan gene family trees on MAFFT sequence alignment server with enhanced interactivity. Nucleic Acids Res., 41(W1), W22–W28. https://doi.org/10.1093/nar/gkt389  Lefort, V., Longueville, J.E., Gascuel, O., 2017. SMS: smart model selection in PhyML. Mol. Biol. Evol., 34(9), 2422–2424. https://doi.org/10.1093/molbev/msx149  Lemoine, F., Correia, D., Lefort, V., Doppelt-Azeroual, O., Mareuil, F., Cohen-Boulakia, S., Gascuel, O., 2019. NGPhylogeny.fr: new generation phylogenetic services for non-specialists. Nucleic Acids Res., 47(W1), W260–W265. https://doi.org/10.1093/nar/gkz303  Lemoine, F., Domelevo Entfellner, J.B., Wilkinson, E., Correia, D., Dávila Felipe, M., De Oliveira, T., Gascuel, O., 2018. Renewing Felsenstein’s phylogenetic bootstrap in the era of big data. Nature, 556(7702), 452–456. https://doi.org/10.1038/s41586-018-0043-0  Moens, U., Calvignac-Spencer, S., Lauber, C., Ramqvist, T., Feltkamp, M.C.W., Daugherty, M.D., Verschoor, E.J., Ehlers, B., 2017. ICTV Virus Taxonomy Profile: Polyomaviridae. J. Gen. Virol., 98(6), 1159–1160. https://doi.org/10.1099/jgv.0.000839  Postler, T.S., Rubino, L., Adriaenssens, E.M., Dutilh, B.E., Harrach, B., Junglen, S., Kropinski, A.M., Krupovic, M., Wada, J., Crane, A., Kuhn, J.H., Mushegian, A., Rūmnieks, J., Sabanadzovic, S., Simmonds, P., Varsani, A., Zerbini, F.M., Callanan, J., Draper, L.A., Hill, C., Stockdale, S.R., 2022. Guidance for creating individual and batch latinized binomial virus species names. J. Gen. Virol., 103(12), 001800. https://doi.org/10.1099/jgv.0.001800  Surján, A., Gonzalez, G., Gellért, Á., Boldogh, S., Carr, M.J., Harrach, B., Vidovszky, M.Z., 2023. First detection and genome analysis of simple nosed bat polyomaviruses in Central Europe. Infect. Genet. Evol., 112, 105439. https://doi.org/10.1016/j.meegid.2023.105439  Surján, A., Harrach, B., Vidovszky, M. Z., 2024. Complete genome characterization and phylogenetic analysis of a novel polyomavirus detected in Eurasian beavers (*Castor fiber*). Infect. Genet. Evol., 123, 105620. https://doi.org/10.1016/j.meegid.2024.105620  Vidovszky, M.Z., Tan, Z., Carr, M.J., Boldogh, S., Harrach, B., Gonzalez G., 2020. Bat-borne polyomaviruses in Europe reveal an evolutionary history of intrahost divergence with horseshoe bats distributed across the African and Eurasian continents. J. Gen. Virol., 101(10), 1119–1130. https://doi.org/10.1099/jgv.0.001467  Walker, P.J., Siddell, S.G., Lefkowitz, E.J., Mushegian, A.R., Adriaenssens, E.M., Alfenas-Zerbini, P., Davison, A.J., Dempsey, D.M., Dutilh, B.E., García, M.L., Harrach, B., Harrison, R.L., Hendrickson, R.C., Junglen, S., Knowles, N.J., Krupovic, M., Kuhn, J.H., Lambert, A.J., Łobocka, M., Nibert, M.L., Oksanen H.M., Orton, R.J., Robertson, D.L., Rubino, L., Sabanadzovic, S., Simmonds, P., Smith, D.B., Suzuki, N., Van Dooerslaer, K., Vandamme A., Varsani, A., Zerbini, F.M., 2021. Changes to virus taxonomy and to the International Code of Virus Classification and Nomenclature ratified by the International Committee on Taxonomy of Viruses (2021). Arch. Virol., 166(9), 2633–2648. https://doi.org/10.1007/s00705-021-05156-1 |

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| **Tables, Figures:** |

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**Table 1. Pairwise sequence identity analysis of the proposed new polyomavirus species based on the LTAg nucleotide sequences**

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| **Proposed new species** | | **Most similar PyVs (GenBank accession number)** | **Pairwise**  **LTAg nucleotide sequence identity (%; <85)** |
| **Virus name, GenBank accession number (host species)** | **Proposed species name** |
| Castor fiber polyomavirus 1, OR735477.2 (*Castor fiber*) | *Alphapolyomavirus castoris* | *Alphapolyomavirus quintipanos* (Pan troglodytes polyomavirus 5, JX159981) | 66 |
| Eptesicus serotinus polyomavirus 1, OK428546.1  (*Eptesicus serotinus*) | *Alphapolyomavirus epserotini* | Scotophilus kuhlii polyomavirus 2  (LC426707) | 58 |
| Myotis daubentonii polyomavirus 2, OK300052.1  (*Myotis daubentonii*) | *Alphapolyomavirus myodaubentonii* | Rhinolophus sinicus polyomavirus 2  (LC426697) | 73 |
| Rhinolophus hipposideros polyomavirus 1, MT276890.1  (*Rhinolophus hipposideros*) | *Betapolyomavirus hipposideri* | Rhinolophus simulator PyV-4 (LC269981) | 78 |

100

***Gammapolyomavirus***

***Deltapolyomavirus***

***Deltapolyomavirus***

*Alphapolyomavirus tubelangeri* Tupaia belangeri polyomavirus 1 MK443498

*Alphapolyomavirus septipanos* Pan troglodytes polyomavirus 7 JX159983

*Alphapolyomavirus nonihominis* Human polyomavirus 9 HQ696595

*Alphapolyomavirus sextipanos* Pan troglodytes polyomavirus 6 JX159982

*Alphapolyomavirus macacae* Macaca fascicularis polyomavirus 1 JX159986

*Alphapolyomavirus tertichlopygerythrus* Chlorocebus pygerythrus polyomavirus 3 AB767297

*Alphapolyomavirus pacynocephalus* Papio cynocephalus polyomavirus 1 AB767294

*Alphapolyomavirus dobsoniae* Dobsonia moluccensis polyomavirus 1 AB972945

*Alphapolyomavirus ptevampyrus* Pteropus vampyrus polyomavirus 1 AB972944

*Alphapolyomavirus acelebensis* Acerodon celebensis polyomavirus 1 AB972940

*Alphapolyomavirus apaniscus* Ateles paniscus polyomavirus 1 JX159987

*Alphapolyomavirus octihominis* Human polyomavirus 8 GU989205

*Alphapolyomavirus ponpygmaeus* Pongo pygmaeus polyomavirus 1 FN356900

***Alphapolyomavirus castoris* Castor fiber polyomavirus 1 OR735477**

*Alphapolyomavirus quintipanos* Pan troglodytes polyomavirus 5 JX159981

*Alphapolyomavirus ponabelii* Pongo abelii polyomavirus 1 FN356901

*Alphapolyomavirus quartipanos* Pan troglodytes polyomavirus 4 JX159980

*Alphapolyomavirus mischreibersii* Miniopterus schreibersii polyomavirus 1 LC185213

*Alphapolyomavirus secumischreibersii* Miniopterus schreibersii polyomavirus 2 LC185216

*Alphapolyomavirus molossi* Molossus molossus polyomavirus 1 JQ958893

*Alphapolyomavirus secomartiensseni* Otomops martiensseni polyomavirus 2 JX520658

*Alphapolyomavirus sturnirae* Sturnira lilium polyomavirus 1 JQ958888

*Alphapolyomavirus secarplanirostris* Artibeus planirostris polyomavirus 2 JQ958886

*Alphapolyomavirus chlopygerythrus* Chlorocebus pygerythrus polyomavirus 1 AB767298

*Alphapolyomavirus pibadius* Piliocolobus badius polyomavirus 1 KX509984

*Alphapolyomavirus pirufomitratus* Piliocolobus rufomitratus polyomavirus 1 JX159984

*Alphapolyomavirus terdecihominis* Human polyomavirus 13 KF954417

*Alphapolyomavirus panos* Pan troglodytes polyomavirus 1 FR692334

*Alphapolyomavirus philantombae* Philantomba monticola polyomavirus 1 MG654482

*Alphapolyomavirus callosciuri* Callosciurus erythraeus polyomavirus 1 MK671087

*Alphapolyomavirus tuglis* Tupaia glis polyomavirus 1 MG721015

*Alphapolyomavirus quardecihominis* Human polyomavirus 14 KY404016

*Alphapolyomavirus procyonis* Procyon lotor polyomavirus 1 JQ178241

*Alphapolyomavirus suis* Sus scrofa polyomavirus 1 KR065722

*Alphapolyomavirus secupanos* Pan troglodytes polyomavirus 2 HQ385746

*Alphapolyomavirus quintihominis* Human polyomavirus 5 HM011556

*Alphapolyomavirus gorillae* Gorilla gorilla polyomavirus 1 HQ385752

*Alphapolyomavirus tertipanos* Pan troglodytes polyomavirus 3 HQ385748

*Alphapolyomavirus eidoli* Eidolon helvum polyomavirus 1 JX520660

***Alphapolyomavirus epserotini* Eptesicus serotinus polyomavirus 1 OK428546**

*Alphapolyomavirus cardiodermae* Cardioderma cor polyomavirus 1 JX520659

***Alphapolyomavirus myodaubentonii* Myotis daubentonii polyomavirus 1 OK300052**

*Alphapolyomavirus omartiensseni* Otomops martiensseni polyomavirus 1 JX520664

*Alphapolyomavirus carolliae* Carollia perspicillata polyomavirus 1 JQ958889

*Alphapolyomavirus tertarplanisrostris* Artibeus planirostris polyomavirus 3 JQ958887

*Alphapolyomavirus sominutus* Sorex minutus polyomavirus 1 MF401583

*Alphapolyomavirus socoronatus* Sorex coronatus polyomavirus 1 MF374999

*Alphapolyomavirus saraneus* Sorex araneus polyomavirus 1 MF374997

Human polyomavirus 12 JX308829

*Alphapolyomavirus muris* Mus musculus polyomavirus 1 AF442959

*Alphapolyomavirus tertimastomysis* Mastomys natalensis polyomavirus 3 MN417229

*Alphapolyomavirus ranorvegicus* Rattus norvegicus polyomavirus 1 KR075943

*Alphapolyomavirus aflavicollis* Apodemus flavicollis polyomavirus 1 MG654476

*Alphapolyomavirus mauratus* Mesocricetus auratus polyomavirus 1 JX036360

*Alphapolyomavirus secumastomysis* Mastomys natalensis polyomavirus 2 MG701350

***Alphapolyomavirus***

***Zetapolyomavirus***

*Zetapolyomavirus delphini* KC594077

***Epsilonpolyomavirus***

*Betapolyomavirus meletis* Meles meles polyomavirus 1 KP644238

*Betapolyomavirus lepweddellii* Leptonychotes weddellii polyomavirus 1 KX533457

*Betapolyomavirus zacalifornianus* Zalophus californianus polyomavirus 1 GQ331138

*Betapolyomavirus callosciuri* Callosciurus prevostii polyomavirus 1 MK883808

*Betapolyomavirus leporis* Lepus granatensis polyomavirus 1 MN994868

*Betapolyomavirus gliris* Glis glis polyomavirus 1 MG701352

*Betapolyomavirus sciuri* Sciurus carolinensis polyomavirus 1 MK671101

*Betapolyomavirus canis* Canis familiaris polyomavirus 1 KY341899

*Betapolyomavirus vicugnae* Vicugna pacos polyomavirus 1 KU879245

*Betapolyomavirus quartihominis* Human polyomavirus 4 EF444549

*Betapolyomavirus tertihominis* Human polyomavirus 3 EF127906

*Betapolyomavirus marvalis* Microtus arvalis polyomavirus 1 KR612373

*Betapolyomavirus myoglareolus* Myodes glareolus polyomavirus 1 KR612368

*Betapolyomavirus tertimuris* Mus musculus polyomavirus 3 MF175082

*Betapolyomavirus securanorvegicus* Rattus norvegicus polyomavirus 2 KX574453

*Betapolyomavirus equi* Equus caballus polyomavirus 1 JQ412134

*Betapolyomavirus enhydrae* Enhydra lutris polyomavirus 1 KM282376

*Betapolyomavirus macacae* Macaca mulatta polyomavirus 1 J02400

*Betapolyomavirus secuhominis* Human polyomavirus 2 J02226

*Betapolyomavirus octipanos* Pan troglodytes polyomavirus 8 KT884050

*Betapolyomavirus hominis* Human polyomavirus 1 V01108

*Betapolyomavirus secuchlopygerythrus* Chlorocebus pygerythrus polyomavirus 2 AB767299

*Betapolyomavirus secupacynocephalus* Papio cynocephalus polyomavirus 2 AB767295

*Betapolyomavirus cercopitheci* Cercopithecus erythrotis polyomavirus 1 JX159985

*Betapolyomavirus desrotundus* Desmodus rotundus polyomavirus 1 JQ958892

*Betapolyomavirus arplanirostris* Artibeus planirostris polyomavirus 1 JQ958890

*Betapolyomavirus ptedavyi* Pteronotus davyi polyomavirus 1 JX520662

*Betapolyomavirus pteparnellii* Pteronotus parnellii polyomavirus 1 JQ958891

*Betapolyomavirus elephanti* Loxodonta africana polyomavirus 1 KF147833

*Betapolyomavirus mafricanus* Miniopterus africanus polyomavirus 1 JX520661

*Betapolyomavirus calbifrons* Cebus albifrons polyomavirus 1 JX159988

*Betapolyomavirus saboliviensis* Saimiri boliviensis polyomavirus 1 AM748741

*Betapolyomavirus sasciureus* Saimiri sciureus polyomavirus 1 JX159989

*Betapolyomavirus tertidobsoniae* Dobsonia moluccensis polyomavirus 3 AB972946

*Betapolyomavirus secacelebensis* Acerodon celebensis polyomavirus 2 AB972941

*Betapolyomavirus raegyptiacus* Rousettus aegyptiacus polyomavirus 1 LC185218

*Betapolyomavirus secudobsoniae* Dobsonia moluccensis polyomavirus 2 AB972947

***Betapolyomavirus hipposideri* Rhinolophus hipposideros PyV-1 MT276890**

*Betapolyomavirus secumuris* Mus musculus polyomavirus 2 M55904

*Betapolyomavirus mastomysis* Mastomys natalensis polyomavirus 1 AB588640

*Betapolyomavirus myolucifugus* Myotis lucifugus polyomavirus 1 FJ188392

*Betapolyomavirus pantherae* Panthera leo polyomavirus 1 MG701353

***Betapolyomavirus***

***Etapolyomavirus***

*Etapolyomavirus rhyndjiddensis* KP264963

***Thetapolyomavirus***

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**Fig. 1. Phylogenetic tree of all accepted and proposed polyomavirus species based on the LTAg nucleotide sequences.** Proposed species are emphasized in bold type and red or blue letters.