



MODULE 1: **TITLE, AUTHORS, etc**

Code assigned:	2016.014aD	(to be completed by ICTV officers)
Short title:	1 new species in the genus <i>Alphapolyomavirus</i>	
Modules attached	2 <input checked="" type="checkbox"/> 3 <input type="checkbox"/> 4 <input type="checkbox"/> 5 <input type="checkbox"/> 6 <input type="checkbox"/> 7 <input type="checkbox"/> 8 <input type="checkbox"/> 9 <input type="checkbox"/> 10 <input type="checkbox"/>	

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List the ICTV study group(s) that have seen this proposal:

Polyomaviridae SG

ICTV Study Group comments (if any) and response of the proposer:

Date first submitted to ICTV: June 18, 2016
Date of this revision (if different to above): June 30, 2016

ICTV-EC comments and response of the proposer:

MODULE 2: **NEW SPECIES**

Code	2016.014aD	(assigned by ICTV officers)
To create 1 new species within:		
Genus:	<i>Alphapolyomavirus</i>	
Subfamily:		
Family:	<i>Polyomaviridae</i>	
Order:		
Name of new species:	Representative isolate: (only 1 per species please)	GenBank sequence accession number(s)
<i>Rattus norvegicus polyomavirus 1</i>	Rattus norvegicus polyomavirus 1 (abbr.: RnorPyV1); isolate 3690	KR075943

Reasons to justify the creation and assignment of the new species:
<ol style="list-style-type: none"> 1. Genome of RnorPyV1 is published (Ehlers et al., 2015¹). 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_rev²; Calvignac Spencer et al. 2016³). 2. RnorPyV1 has a genome organization typical for members of the <i>Polyomaviridae</i>. This fulfills number 2 of the species definition criteria. 3. There is sufficient information that RnorPyV1 is naturally hosted by members of the host species <i>Rattus norvegicus</i>: 22/33 individuals from 2 locations in Germany were PCR-positive (sequence confirmed). Six full genomes available (deposited in GenBank under the accession numbers KR065723, KR065724, KR075943–KR075946). This fulfills number 3 of the species definition criteria. 4. Using the MAFFT module in Geneious 9.1.3., the LTA_g CDS of RnorPyV1 was compared pairwise with those of other PyVs. RnorPyV1 (KR075943) LTA_g CDS and LTA_g CDS of hamster polyomavirus isolate Berlin-Buch (species <i>Mesocricetus auratus polyomavirus 1</i>) were most closely related (37 % nucleic acid diversity). This fulfills number 4 of the species definition criteria (>15 % observed genetic distance on basis of LTA_g CDS). 5. RnorPyV1 clusters with members of the genus <i>Alphapolyomavirus</i> (Figure in Appendix).

MODULE 11: **APPENDIX**: supporting material

additional material in support of this proposal

References:

¹ Ehlers, B., Richter, D., Matuschka, F. R., & Ulrich, R. G. (2015). Genome sequences of a rat polyomavirus related to murine polyomavirus, *Rattus norvegicus* polyomavirus 1. *Genome Announcements*, 3(5), e00997-15.

² Calvignac-Spencer, S., Feltkamp, M., Daugherty, M.D., Moens, U., Ramqvist, T., Johne, R., Ehlers, B. (2015). ICTV taxonomic proposal 2015.015a-aaD.A.v2.Polyomaviridae_rev. In the family *Polyomaviridae*, create 4 genera (*Alphapolyomavirus*, *Betapolyomavirus*, *Gammapolyomavirus* and *Deltapolyomavirus*) and reclassify 8 existing species.

http://www.ictvonline.org/proposals-15/2015.015a-aaD.A.v2.Polyomaviridae_rev.pdf

³ Calvignac-Spencer, S., et al. (2016) A taxonomy update for the family *Polyomaviridae*. *Archives of Virology* 161(6), 1739-1750.

Supporting Figure. Maximum likelihood tree based on an alignment of large T sequences (503 amino acid positions). Bayesian analyses supported a very similar topology. Weakly supported branches are grey (approximate likelihood ratio test and/or posterior probability <0.95). Proposed novel species are in enlarged, black font.

