



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

<b>Code assigned:</b>	<b>2016.016aD</b>	(to be completed by ICTV officers)
<b>Short title:</b>	2 new species in the genus <i>Betapolyomavirus</i>	
<b>Modules attached</b>	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	<b>2016.016aD</b>	(assigned by ICTV officers)
<b>To create 3 new species within:</b>		
Genus:	<b><i>Betapolyomavirus</i></b>	
Subfamily:		
Family:	<b><i>Polyomaviridae</i></b>	
Order:		
<b>Name of new species:</b>	<b>Representative isolate: (only 1 per species please)</b>	<b>GenBank sequence accession number(s)</b>
<i>Myodes glareolus polyomavirus</i> <i>1</i>	Myodes glareolus polyomavirus 1 (abbr.: MglPyV1); isolate KS/14/281	KR612368
<i>Microtus arvalis polyomavirus</i> <i>1</i>	Microtus arvalis polyomavirus 1 (abbr.: MarvPyV1); isolate KS13/0947	KR612373

<b>Reasons to justify the creation and assignment of the new species:</b>
<ol style="list-style-type: none"> <li>1. Genomes of MglPyV1 and MarvPyV1 are published (Nainys et al., 2015<sup>1</sup>). 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_rev<sup>2</sup>; Calvignac Spencer et al. 2016<sup>3</sup>).</li> <li>2. MglPyV1 and MarvPyV1 have a genome organization typical for members of the <i>Polyomaviridae</i>. This fulfills number 2 of the species definition criteria.</li> <li>3. There is sufficient information that MglPyV1 and MarvPyV1 are naturally hosted by members of the host species <i>Myodes glareolus</i> and <i>Microtus arvalis</i> accordingly: <ol style="list-style-type: none"> <li>a) 62/172 individuals of <i>Myodes glareolus</i> from 9 locations in Germany were PCR-positive (sequence confirmed) and other 11 individuals were seropositive with MglPyV1 VP1 VLPs. Five full genomes are available (deposited in GenBank under the accession numbers KR612368, KR612369, KR612370–KR612372).</li> <li>b) 11/85 individuals of <i>Microtus arvalis</i> from 7 locations in Germany were PCR-positive (sequence confirmed) and other 4 individuals were seropositive with MarvPyV1 VP1 VLPs. Two full genomes are available (deposited in GenBank under the accession numbers KR612373, KR612374). This fulfills number 3 of the species definition criteria.</li> </ol> </li> <li>4. Using the MAFFT module in Geneious 9.1.3., the LTA<sub>g</sub> CDS of MglPyV1 and MarvPyV1 were compared pairwise with those of other PyVs. Both were most closely related with WuPyV (species <i>Human polyomavirus 4</i>) (40 % and 39 % nucleic acid diversity, respectively). Among each other, they revealed 19 % diversity of LTA<sub>g</sub> CDS. This fulfills number 4 of the species definition criteria (&gt;15 % observed genetic distance on basis of LTA<sub>g</sub> CDS).</li> <li>5. MglPyV1 and MarvPyV1 cluster with members of the genus <i>Betapolyomavirus</i> (Figure in Appendix).</li> </ol>

MODULE 11: **APPENDIX**: supporting material

additional material in support of this proposal

**References:**

<sup>1</sup> Nainys J, Timinskas A, Schneider J, Ulrich RG, Gedvilaite A (2015) Identification of two novel members of the tentative genus Wukipolyomavirus in wild rodents. PLoS One 10 (10), e0140916.

<sup>2</sup> Calvignac-Spencer S, Feltkamp M, Daugherty MD, 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](http://www.ictvonline.org/proposals-15/2015.015a-aaD.A.v2.Polyomaviridae_rev.pdf)

<sup>3</sup> 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.

