



This form should be used for all taxonomic proposals. Please complete all those modules that are applicable (and then delete the unwanted sections). For guidance, see the notes written in blue and the separate document "Help with completing a taxonomic proposal"

Please try to keep related proposals within a single document; you can copy the modules to create more than one genus within a new family, for example.

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

Code assigned:	2016.018a-dD	(to be completed by ICTV officers)
Short title: New species and new genus in <i>Chordopoxvirinae</i> (e.g. 6 new species in the genus <i>Zetavirus</i>)		
Modules attached (modules 1 and 11 are required)	6 <input type="checkbox"/> 7 <input type="checkbox"/> 8 <input type="checkbox"/> 9 <input type="checkbox"/> 10 <input type="checkbox"/>	
2 <input checked="" type="checkbox"/> 3 <input checked="" type="checkbox"/> 4 <input type="checkbox"/> 5 <input type="checkbox"/>		

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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 (fungal, invertebrate, plant, prokaryote or vertebrate viruses)

Poxviridae Study Group

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

SG Comments: It was noted that the three letter abbreviation YKV was not as appropriate and consistent as the alternative YKPV.

Response: Agreed. The abbreviation for the single Yokapox virus isolate has been changed below to YKPV.

Date first submitted to ICTV:

July 18, 2016

Date of this revision (if different to above):

October 28, 2016

ICTV-EC comments and response of the proposer:

Uc. Label tree to show existing genera. [Done]

MODULE 2: **NEW SPECIES**

creating and naming one or more new species.

If more than one, they should be a group of related species belonging to the same genus. All new species must be placed in a higher taxon. This is usually a genus although it is also permissible for species to be “unassigned” within a subfamily or family. Wherever possible, provide sequence accession number(s) for **one** isolate of each new species proposed.

Code	2016.018aD	(assigned by ICTV officers)	
To create 1 new species within:			
Genus:	<i>Centapoxvirus (new)</i>	Fill in all that apply. • If the higher taxon has yet to be created (in a later module, below) write “ (new) ” after its proposed name. • If no genus is specified, enter “ unassigned ” in the genus box.	
Subfamily:	<i>Chordopoxvirinae</i>		
Family:	<i>Poxviridae</i>		
Order:			
Name of new species:	Representative isolate: (only 1 per species please)	GenBank sequence accession number(s)	
<i>Yokapox virus</i>	Yokapox virus (YKPV)	HQ849551	

<p>Reasons to justify the creation and assignment of the new species:</p> <ul style="list-style-type: none"> • Explain how the proposed species differ(s) from all existing species. <ul style="list-style-type: none"> ○ If species demarcation criteria (see module 3) have previously been defined for the genus, explain how the new species meet these criteria. ○ If criteria for demarcating species need to be defined (because there will now be more than one species in the genus), please state the proposed criteria. • Further material in support of this proposal may be presented in the Appendix, Module 11
<p>The original Yokapox virus isolate was isolated from a pool of <i>Aedes simpsoni</i> mosquitoes collected in the Central African Republic in 1972. Structural characteristics, assembly and maturation of the virus particles resemble that of other poxviruses. However, full genome sequence data and molecular phylogenetic analysis have shown the isolate to be unique to <i>Poxviridae</i> (Appendix). A comparison of 35 concatenated amino acid sequences found Yokapox virus to be most closely related to orthopoxviruses, yet clearly distinct at a DNA distance of over 30% when compared to a representative of <i>Orthopoxvirus</i> (VACV-WR), its nearest neighboring genus. In contrast, the genome composition is AT rich at nearly 75%, closer to that of the capri- and suipoxviruses.</p>

MODULE 3: **NEW GENUS**

creating a new genus

Ideally, a genus should be placed within a higher taxon.

Code	2016.018bD	(assigned by ICTV officers)
To create a new genus within:		
Subfamily:	<i>Chordopoxvirinae</i>	Fill in all that apply. • If the higher taxon has yet to be created (in a later module, below) write “(new)” after its proposed name. • If no family is specified, enter “unassigned” in the family box
Family:	<i>Poxviridae</i>	
Order:		

naming a new genus

Code	2016.018cD	(assigned by ICTV officers)
To name the new genus: <i>Centapoxvirus</i>		

Assigning the type species and other species to a new genus

Code	2016.018dD	(assigned by ICTV officers)
To designate the following as the type species of the new genus		
<i>Yokapox virus</i>	Every genus must have a type species. This should be a well characterized species although not necessarily the first to be discovered	
The new genus will also contain any other new species created and assigned to it (Module 2) and any that are being moved from elsewhere (Module 7b). Please enter here the TOTAL number of species (including the type species) that the genus will contain:		
<i>1</i>		

Reasons to justify the creation of a new genus:

Additional material in support of this proposal may be presented in the Appendix, Module 11

The Yokapox virus genome contains unique open reading frames that are not found in other poxviruses. A comparison of 35 concatenated amino acid sequences found Yokapox virus to be most closely related to orthopoxviruses, yet clearly distinct at a DNA distance of over 30% when compared to a representative *Orthopoxvirus* (VACV-WR), its nearest neighboring genus. In contrast, the genome composition is AT rich at nearly 75%, closer to that of the capri- and suipoxviruses. These unique qualities of Yokapox virus among poxviruses justify the creation of a new chordopoxvirus genus.

Origin of the new genus name:

The name is taken from the location from which the type species originated: Central African Republic

Reasons to justify the choice of type species:

It is the first of its kind identified.

Species demarcation criteria in the new genus:

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MODULE 11: **APPENDIX**: supporting material

additional material in support of this proposal

References:

Zhao G, Droit L, Tesh RB, Popov VL, Little NS, Upton C, Virgin HW, Wang D. The genome of_Yoka_poxvirus. J Virol. 2011 85(19):10230-8. doi: 10.1128/JVI.00637-11. <http://www.ncbi.nlm.nih.gov/pmc/articles/PMC3196448/>

Annex:

Include as much information as necessary to support the proposal, including diagrams comparing the old and new taxonomic orders. The use of Figures and Tables is strongly recommended but direct pasting of content from publications will require permission from the copyright holder together with appropriate acknowledgement as this proposal will be placed on a public web site. For phylogenetic analysis, try to provide a tree where branch length is related to genetic distance.

Table 1: Amino acid percent identity matrix of the gene RPO147 from the family Poxviridae.

The protein sequence of RPO147 was retrieved from VOCs and aligned with MAFFT using multiple sequence editor Base-By-Base. The viruses used: cowpox virus (CPXV), raccoonpox virus (RCNV), Yokapox virus (YKPV), Cotia virus (COTV), swinepox virus (SWPV), myxoma virus (MYXV), goatpox virus (GTPV), Yaba monkey tumor virus(YMTV), deerpox virus (DPV), fowlpox virus(FWPV), crocodilepox virus (CRV), Molluscum contagiosum virus (MOCV), Orf virus (ORFV), and squirrelpox virus (SPXV).

COTV [1]	CPXV [2]	CRV [3]	DPV [4]	FWPV [5]	GTPV [6]	MOCV [7]	MYXV [8]	ORFV [9]	RCNV [10]	SPXV [11]	SWPV [12]	YKPV [13]	YMTV [14]	
100%	75.47%	62.57%	81.71%	69.21%	78.91%	70.19%	80.16%	64.46%	75.16%	72.45%	80.08%	75.29%	79.22%	COTV [1]
75.47%	100%	63.83%	81.70%	71.08%	80.30%	73.29%	81.70%	67.89%	96.42%	76.56%	80.14%	88.56%	80.69%	CPXV [2]
62.57%	63.83%	100%	63.47%	66.25%	63.24%	67.37%	63.79%	60.14%	64.07%	64.90%	62.93%	64.20%	63.08%	CRV [3]
81.71%	81.70%	63.47%	100%	70.79%	86.23%	73.70%	86.39%	66.51%	81.54%	76.50%	86.38%	79.73%	86.46%	DPV [4]
69.21%	71.08%	66.25%	70.79%	100%	69.94%	72.82%	70.56%	61.92%	70.46%	67.91%	69.86%	71.14%	69.70%	FWPV [5]
78.91%	80.30%	63.24%	86.23%	69.94%	100%	72.30%	85.53%	65.03%	80.37%	73.85%	84.67%	79.35%	84.36%	GTPV [6]
70.19%	73.29%	67.37%	73.70%	72.82%	72.30%	100%	73.23%	66.95%	72.98%	74.34%	72.68%	72.64%	71.91%	MOCV [7]
80.16%	81.70%	63.79%	86.39%	70.56%	85.53%	73.23%	100%	67.60%	80.61%	75.41%	84.75%	79.66%	84.98%	MYXV [8]
64.46%	67.89%	60.14%	66.51%	61.92%	65.03%	66.95%	67.60%	100%	67.19%	70.25%	66.04%	66.87%	65.50%	ORFV [9]
75.16%	96.42%	64.07%	81.54%	70.46%	80.37%	72.98%	80.61%	67.19%	100%	76.40%	80.06%	87.86%	80.61%	RCNV [10]
72.45%	76.56%	64.90%	76.50%	67.91%	73.85%	74.34%	75.41%	70.25%	76.40%	100%	74.24%	75.53%	75.88%	SPXV [11]
80.08%	80.14%	62.93%	86.38%	69.86%	84.67%	72.68%	84.75%	66.04%	80.06%	74.24%	100%	79.58%	83.74%	SWPV [12]
75.29%	88.56%	64.20%	79.73%	71.14%	79.35%	72.64%	79.66%	66.87%	87.86%	75.53%	79.58%	100%	79.35%	YKPV [13]
79.22%	80.69%	63.08%	86.46%	69.70%	84.36%	71.91%	84.98%	65.50%	80.61%	75.88%	83.74%	79.35%	100%	YMTV [14]

Table 2: Novel genes found in Yokapox virus genome.

ORF name	Length (aa)	Genome location (bp)	% identity (aa)	Homolog	Length (aa)	Description/putative function
YKV157	382	139477–140622	31	Ornithine decarboxylase	445	Similar to host ODCs
YKV173	345	157225–158259	23	MHC class I	362	Similar to host MHC class I proteins

Figure 1. Molecular phylogenetic analysis of the family *Poxviridae* using amino acid sequences of RPO147.

The evolutionary history was inferred by using the Maximum Likelihood method based on the Le_Gascuel_2008 model. The tree with the highest log likelihood (-15239.6017) is shown. Initial tree(s) for the heuristic search were obtained automatically by applying Neighbor-Join and BioNJ algorithms to a matrix of pairwise distances estimated using a JTT model, and then selecting the topology with superior log likelihood value. A discrete Gamma distribution was used to model evolutionary rate differences among sites (5 categories (+G, parameter = 0.4944)). The tree is drawn to scale, with branch lengths measured in the number of substitutions per site. The analysis involved 14 amino acid sequences. All positions with less than 95% site coverage were eliminated. That is, fewer than 5% alignment gaps, missing data, and ambiguous bases were allowed at any position. There were a total of 1281 positions in the final dataset. Amino acid percent identities between Yokapox virus and its neighbours are displayed, and were calculated with Base-By-Base. The viruses used: cowpox virus (CPXV), raccoonpox virus (RCNV), Yokapox virus (YKPV), Cotia virus (COTV), swinepox virus (SWPV), myxoma virus (MYXV), goatpox virus (GTPV), Yaba monkey tumor virus (YMTV), deerpox virus (DPV), fowlpox virus (FWPV), crocodilepox virus (CRV), Molluscum contagiosum virus (MOCV), Orf virus (ORFV), and squirrelpox virus (SPXV). Evolutionary analyses were conducted in MEGA7.

