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:	*2016.013aD*	(to be completed by ICTV officers)

Short title: One new species in the subfamily *Chordopoxvirinae*: *Pteropox virus*
(e.g. 6 new species in the genus *Zetavirus*)

Modules attached (modules 1 and 11 are required)	2 ☒ 3 ☐ 4 ☐ 5 ☐
	6 ☐ 7 ☐ 8 ☐ 9 ☐ 10 ☐

Author(s):

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Corresponding author with e-mail address:

Chris Upton, cupton@uvic.ca

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:
Pteropox virus meets the criteria for a new species (and potentially new genus) in the family *Poxviridae*, based on the following demarcation criteria:
1.   Potentially restricted natural host range (*Pteropus scapulatus*).
2.   Phylogenetic analysis. For new virus isolates, levels of clade separation similar to those of existing taxa are suggestive of the necessity of creating a new taxon.
3.   Nucleotide sequence identity. Within the conserved, core region of (at least) orthopoxvirus species, nucleotide sequence identity of >96% is observed between isolates of all non-North American species. Isolates within a species exhibit >98% nucleotide identity. The highest level of similarity of PTPV compared with other poxvirus species is 73.4% (deerpoxvirus).
4.   Gene content comparisons. The variability in the content and conservation of gene sequences between poxvirus isolates can serve as a distinguishing characteristic.
Response: Agreed. These are valuable additional points.

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:

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

MODULE 2: **NEW SPECIES**

Code	*2016.013aD*	(assigned by ICTV officers)

To create 1 new species within:

<table>
<tr><td align="right">Genus:</td><td>Unassigned</td><td rowspan="4">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.</td></tr>
<tr><td align="right">Subfamily:</td><td><i>Chordopoxvirinae</i></td></tr>
<tr><td align="right">Family:</td><td><i>Poxviridae</i></td></tr>
<tr><td align="right">Order:</td><td></td></tr>
</table>

Name of new species:	Representative isolate: (only 1 per species please)	GenBank sequence accession number(s)
Pteropox virus	pteropox virus strain Australia (PTPV-Aus)	KU980965

Reasons to justify the creation and assignment of the new species:
- Explain how the proposed species differ(s) from all existing species.
  - 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

This proposed species differs from all existing as demonstrated by the full genome sequence and phylogenetic analysis outlined in the reference publication (Appendix). While associated with clinical disease in an adult, female, little red flying fox (*Pteropus scapulatus*), the virus genome is unrelated to other poxviruses isolated from bats (Eptesipox virus and Eidolon helvum poxvirus 1). The AT-rich genome encodes 29 novel poxvirus genes and several genes that are commonly known only to the GC-rich poxviruses. Furthermore, these unique genes and the relatively small genome indicate the virus may have undergone extensive host-adaptation, though the specific host remains uncertain.

additional material in support of this proposal

O'Dea MA, Tu SL, Pang S, De Ridder T, Jackson B, Upton C (2016) Genomic characterisation of a novel poxvirus from a flying fox; evidence for a new genus? J Gen Virol. 2016 Jul 7. doi: 10.1099/jgv.0.000538. [Epub ahead of print]

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.

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 JTT matrix-based model. The tree with the highest log likelihood (-17340.5881) 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. The tree is drawn to scale, with branch lengths measured in the number of substitutions per site. The analysis involved 15 amino acid sequences. There were a total of 1280 positions in the final dataset. Amino acid percent identities between pteropox virus and its neighbours are displayed, and were calculated by Base-By-Base. The following viruses were used: cowpox virus (CPXV), raccoonpox virus (RCNV), Yoka poxvirus (YKPV, new), 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), squirrelpox virus (SPXV), pteropox virus (PTPV, new). Evolutionary analyses were conducted in MEGA7.
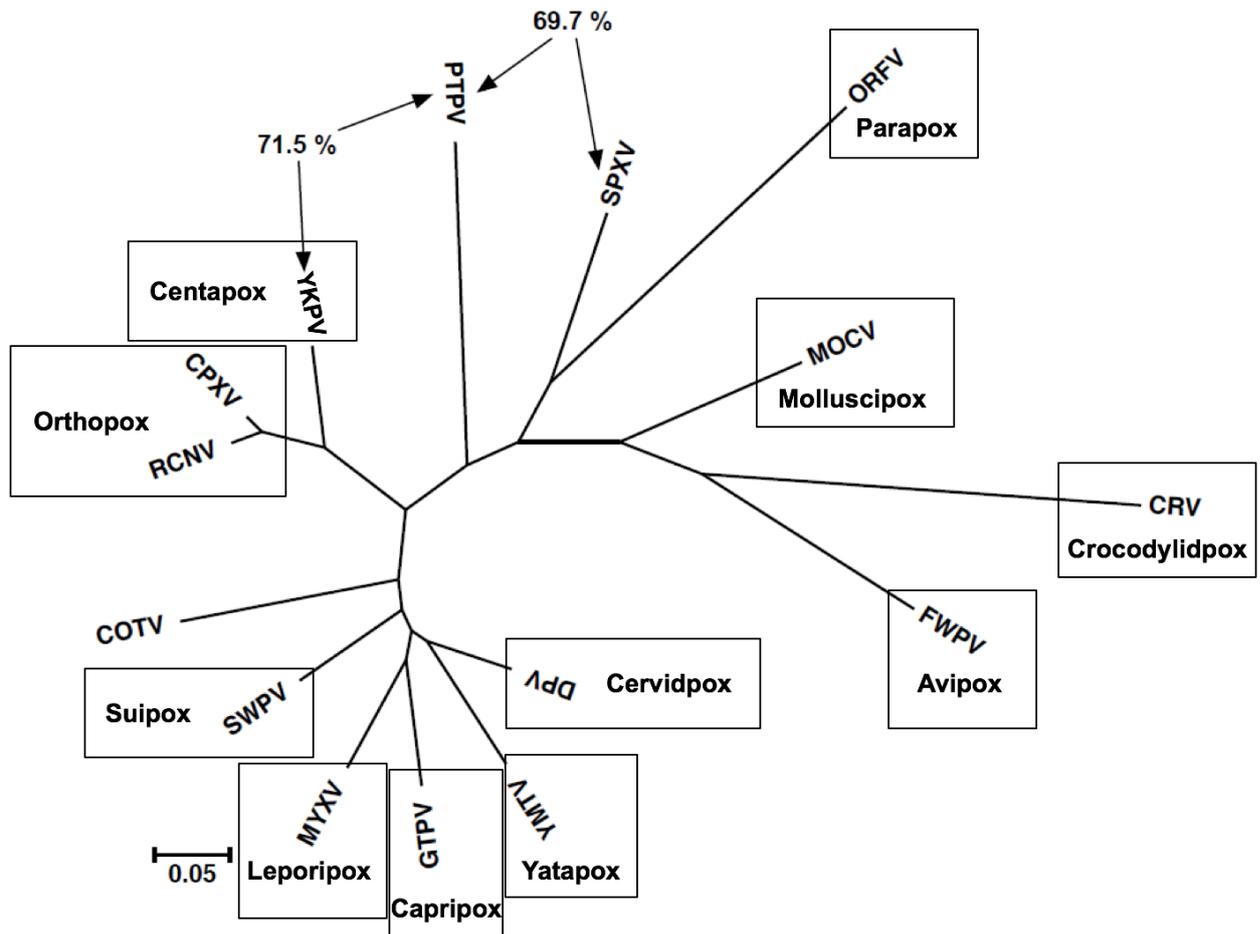
PTPV

71.5 % 69.7 %

YKPV   SPXV

Centapox

CPXV   ORFV
Orthopox   Parapox
RCNV

MOCV
Molluscipox

CRV
Crocodylidpox

COTV

FWPV
Avipox

Suipox   SWPV   DPV   Cervidpox

0.05   Leporipox   MYXV   GTPV   YMTV   Yatapox
Capripox

Table 1. Nucleotide identity when PTPV is compared with other poxvirus

COTV [1]	CPXV [2]	CRV [3]	DPV [4]	FWPV [5]	GTPV [6]	MOCV [7]	MYXV [8]	ORFV [9]	PTPV [10]	RCNV [11]	SPXV [12]	SWPV [13]	YKV [14]	YMTV [15]	
100%	75.47%	62.65%	81.71%	69.21%	78.91%	70.19%	80.16%	64.39%	71.75%	75.16%	72.45%	80.08%	75.29%	79.22%	COTV [1]
75.47%	100%	63.91%	81.70%	71.08%	80.30%	73.29%	81.70%	67.97%	71.08%	96.42%	76.56%	80.14%	88.56%	80.69%	CPXV [2]
62.65%	63.91%	100%	63.55%	66.33%	63.40%	67.44%	63.94%	60.03%	61.98%	64.22%	64.98%	63.01%	64.27%	63.16%	CRV [3]
81.71%	81.70%	63.55%	100%	70.79%	86.23%	73.70%	86.39%	66.59%	73.36%	81.54%	76.50%	86.38%	79.73%	86.46%	DPV [4]
69.21%	71.08%	66.33%	70.79%	100%	69.94%	72.82%	70.56%	61.92%	67.89%	70.46%	67.91%	69.86%	71.14%	69.70%	FWPV [5]
78.91%	80.30%	63.40%	86.23%	69.94%	100%	72.30%	85.53%	65.11%	71.18%	80.37%	73.85%	84.67%	79.35%	84.36%	GTPV [6]
70.19%	73.29%	67.44%	73.70%	72.82%	72.30%	100%	73.23%	67.03%	68.87%	72.98%	74.34%	72.68%	72.64%	71.91%	MOCV [7]
80.16%	81.70%	63.94%	86.39%	70.56%	85.53%	73.23%	100%	67.52%	71.88%	80.61%	75.41%	84.75%	79.66%	84.98%	MYXV [8]
64.39%	67.97%	60.03%	66.59%	61.92%	65.11%	67.03%	67.52%	100%	65.65%	67.26%	70.25%	66.04%	66.93%	65.50%	ORFV [9]
71.75%	71.08%	61.98%	73.36%	67.89%	71.18%	68.87%	71.88%	65.65%	100%	70.93%	69.65%	71.88%	71.45%	72.66%	PTPV [10]
75.16%	96.42%	64.22%	81.54%	70.46%	80.37%	72.98%	80.61%	67.26%	70.93%	100%	76.40%	80.06%	87.86%	80.61%	RCNV [11]
72.45%	76.56%	64.98%	76.50%	67.91%	73.85%	74.34%	75.41%	70.25%	69.65%	76.40%	100%	74.24%	75.53%	75.88%	SPXV [12]
80.08%	80.14%	63.01%	86.38%	69.86%	84.67%	72.68%	84.75%	66.04%	71.88%	80.06%	74.24%	100%	79.58%	83.74%	SWPV [13]
75.29%	88.56%	64.27%	79.73%	71.14%	79.35%	72.64%	79.66%	66.93%	71.45%	87.86%	75.53%	79.58%	100%	79.35%	YKV [14]
79.22%	80.69%	63.16%	86.46%	69.70%	84.36%	71.91%	84.98%	65.50%	72.66%	80.61%	75.88%	83.74%	79.35%	100%	YMTV [15]

Table 2. Genes unique to PTPV

Gene #	ORF position	AA #	Gene function	Orthologs
PTPV-001	1193-447	248	Hypothetical protein (ITR)	Unique to Pteropox
PTPV-002	1700-1272	142	Hypothetical protein	Unique to Pteropox
PTPV-004	2941-2414	175	Hypothetical protein	Unique to Pteropox
PTPV-009	8610-7954	218	Hypothetical protein	Unique to Pteropox
PTPV-010	9180-8665	171	Hypothetical protein	Unique to Pteropox
PTPV-011	10209-9223	328	Hypothetical protein	Unique to Pteropox
PTPV-012	10556-10218	112	Hypothetical protein	Unique to Pteropox
PTPV-013	10893-10588	101	Hypothetical protein	Unique to Pteropox
PTPV-014	11674-11105	189	Hypothetical protein	Unique to Pteropox
PTPV-015	12279-11737	180	Hypothetical protein	Unique to Pteropox
PTPV-022	19411-19220	63	Hypothetical protein	Unique to Pteropox
PTPV-023	19641-19483	52	Hypothetical protein	Unique to Pteropox
PTPV-033	28471-28701	76	Hypothetical protein	Unique to Pteropox
PTPV-034	28754-29074	106	Hypothetical protein	Unique to Pteropox
PTPV-039	33283-33708	141	Hypothetical protein	Unique to Pteropox
PTPV-040	33721-34551	276	TNFSF10-like protein (TRAIL, membrane-associated)	Unique to Pteropox
PTPV-041	34613-35101	162	Hypothetical protein	Unique to Pteropox
PTPV-098	94352-93564	262	Hypothetical protein	Unique to Pteropox
PTPV-128	123536-124072	178	Hypothetical protein	Unique to Pteropox
PTPV-131	125380-125970	196	Hypothetical protein	Unique to Pteropox
PTPV-132	126039-126380	113	Hypothetical protein	Unique to Pteropox
PTPV-133	126452-126709	85	Hypothetical protein	Unique to Pteropox
PTPV-135	127602-127850	82	Hypothetical protein	Unique to Pteropox
PTPV-136	127855-128337	160	Hypothetical protein	Unique to Pteropox
PTPV-138	129158-129694	178	Hypothetical protein	Unique to Pteropox
PTPV-139	129773-130303	176	Hypothetical protein	Unique to Pteropox
PTPV-140	130360-130962	200	Hypothetical protein	Unique to Pteropox
PTPV-141	131034-131531	165	Hypothetical protein	Unique to Pteropox
PTPV-142	131631-132164	177	Hypothetical protein	Unique to Pteropox
PTPV-143	132300-133046	248	Hypothetical protein (ITR)	Unique to Pteropox