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:	***2010.019a-eV***	(to be completed by ICTV officers)

Short title: Create genus named Crocodylidpoxvirus (type species Nile crocodilepox virus), and a species in the genus Orthopoxvirus, in the family Poxviridae
(e.g. 6 new species in the genus *Zetavirus*)

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

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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)	Poxvirus

ICTV-EC or Study Group comments and response of the proposer:

Date first submitted to ICTV:
Date of this revision (if different to above):

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	***2010.019aV***	(assigned by ICTV officers)

To create 1 new species within:

Genus:	***Orthopoxvirus***
Subfamily:	***Chordopoxvirinae***
Family:	***Poxviridae***
Order:	

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.

And name the new species:	**GenBank sequence accession number(s) of reference isolate:**
Skunkpox virus	FJ807755-63

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 9

Phylogenetic analysis (see Appendix Fig. 1) of the recent genomic DNA sequence data (Emerson et al. 2009 PLoS One 4: e7666) indicates Skunkpox virus [FJ807755-63] forms a distinct species within a clade of closely related North American viruses (including Racoonpox virus [FJ807746-54] and Volepox virus [FJ807737-45]). It should therefore be raised from tentative to definitive species within the genus.

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	***2010.019bV***	(assigned by ICTV officers)

To create 1 new species within:

Genus:	***Crocodylidpoxvirus* (new)**
Subfamily:	***Chordopoxvirinae***
Family:	***Poxviridae***
Order:	

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.

And name the new species:	**GenBank sequence accession number(s) of reference isolate:**
Nile crocodilepox virus	*NC_008030*

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 9

Previously an unassigned virus in the family, determination of the complete genome sequence (Afonso et al. 2006 J Virol. 80:4978-91) of a virus isolated from Nile crocodiles (*Crocodylus niloticus*) has allowed its placement in the taxonomic structure of the family to be ascertained. It represents the only fully characterized virus not only from Crocodylids but even from Reptilia. CRV is a highly divergent Chordopoxvirus (ChPV). Even genes within the central conserved region share a low level of amino acid identity with ChPV homologues (some less than 34% with VACV homologues). There are also novel gene arrangements at specific loci within the central conserved region. Phylogenetic analysis indicates a long, discrete branch distinct from all mammalian poxviruses as well as from Avipoxviruses (see Appendix Fig. 1). Modification to the name previously used for the unassigned virus in the family reflects the pathological presentation of the disease which includes the presence of “nodular skin lesions”.

MODULE 3: **NEW GENUS**

creating a new genus

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

Code	***2010.019cV***	(assigned by ICTV officers)

To create a new genus within:

Subfamily:	***Chordopoxvirinae***
Family:	***Poxviridae***
Order:	

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

naming a new genus

Code	***2010.019dV***	(assigned by ICTV officers)

To name the new genus: *Crocodylidpoxvirus*

Assigning the type species and other species to a new genus

Code	***2010.019eV***	(assigned by ICTV officers)

To designate the following as the type species of the new genus

Nile crocodilepox virus
(accession number NC_008030)

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:**

1

Reasons to justify the creation of a new genus:

Additional material in support of this proposal may be presented in the Appendix, Module 9

CRV is a highly divergent Chordopoxvirus (ChPV). Even genes within the central conserved region share a low level of amino acid identity with ChPV homologues (some less than 34% with VACV homologues). There are also novel gene arrangements at specific loci within the central conserved region. Phylogenetic analysis indicates a long, discrete branch distinct from all mammalian poxviruses as well as from Avipoxviruses (see Fig. 5, Afonso et al. 2006 J Virol. 80:4978-91).

Origin of the new genus name:

Crocodylidae - represents the taxonomic family name of the host species, following the naming convention of other Poxviridae genera

Reasons to justify the choice of type species:

Sole sequenced representative

Species demarcation criteria in the new genus:

If there will be more than one species in the new genus, list the criteria being used for species demarcation and explain how the proposed members meet these criteria.

MODULE 9: **APPENDIX**: supporting material

additional material in support of this proposal

References:

Afonso et al. 2006 J Virol. 80: 4978-91
Emerson et al. 2009 PLoS One 4: e7666

Annex:

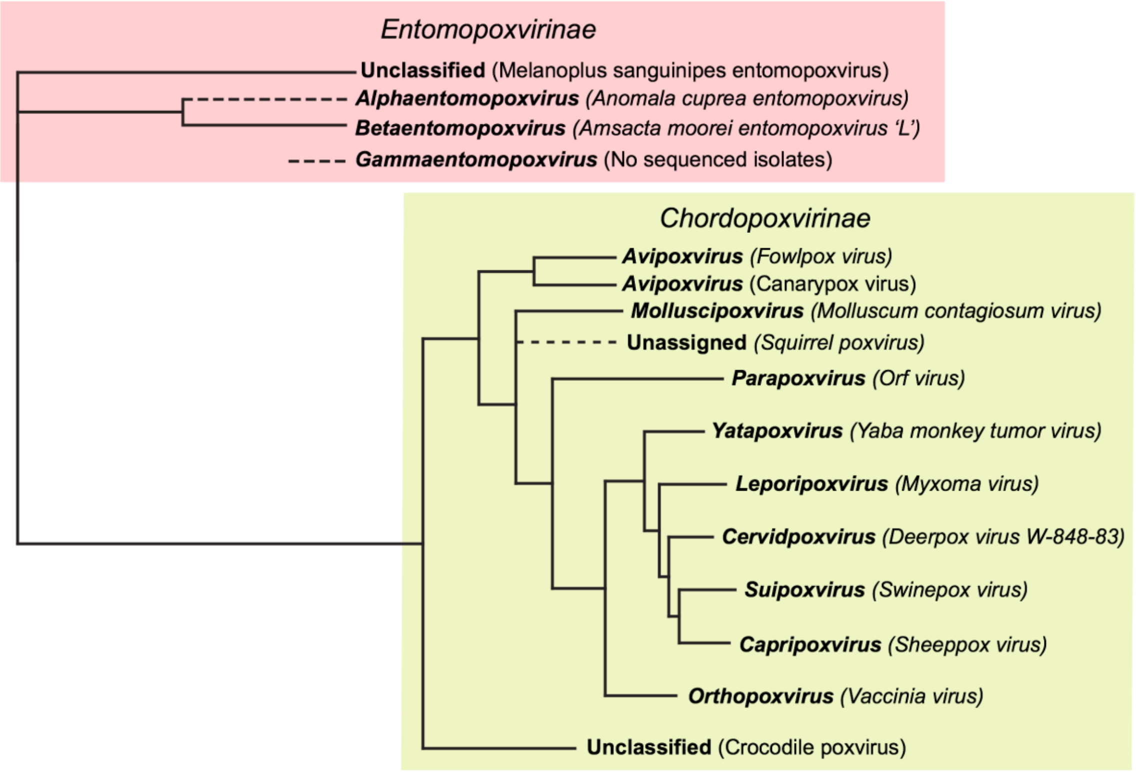
Include as much information as necessary to support the proposal, including diagrams comparing the old and new taxonomic orders. The use of Figures and Tables is strongly recommended but direct pasting of content from publications will require permission from the copyright holder together with appropriate 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. Currently accepted phylogenetic structures within the Family Poxviridae (E. Lefkowitz) Unclassified viruses have not yet been assigned to a taxon and are the subject of this proposal.

Panel A: Phylogenetic relationships in the family Poxviridae. Phylogenetic predictions are based upon codon-aligned nucleic acid sequences from 20 conserved genes of virus isolates from representative species of each genus. Genera are indicated by bold, italic text, while species are represented in italic text. Branches with dotted lines indicate virus isolates for which limited sequence information is available and therefore their placement on the tree is not definitive. The species Squirrel poxvirus has not yet been assigned to a genus. There are no sequenced isolates within the genus Gammaentomopoxvirus.

Panel B: Phylogenetic relationships in the genus Orthopoxvirus. Phylogenetic predictions are based upon codon-aligned nucleic acid sequences from 9 conserved genes of isolates from each species. Two strains of cowpox virus were included in the analysis to demonstrate the discordant placement of different isolates of this species on the genus tree. Tree topologies for both analyses were inferred using Bayesian analysis as implemented by the program MrBayes.

A. Poxviridae



B. Orthopoxvirus