



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:	2010.020abV	(to be completed by ICTV officers)
Short title: Renaming of two species within the family Poxviridae (e.g. 6 new species in the genus <i>Zetavirus</i>)		
Modules attached (modules 1 and 9 are required)	1 <input checked="" type="checkbox"/> 2 <input type="checkbox"/> 3 <input type="checkbox"/> 4 <input type="checkbox"/> 5 <input type="checkbox"/> 6 <input type="checkbox"/> 7 <input type="checkbox"/> 8 <input checked="" type="checkbox"/> 9 <input checked="" type="checkbox"/>	

Author(s) with e-mail address(es) of the proposer:

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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
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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 8: **NON-STANDARD**

Template for any proposal not covered by modules 2-7. This includes proposals to change the name of existing taxa (but note that stability of nomenclature is encouraged wherever possible).

non-standard proposal

Code	<i>2010.020aV</i>	(assigned by ICTV officers)
Title of proposal: <i>Rename Squirrel poxvirus to Squirrelpox virus</i>		

Text of proposal:

Squirrel poxvirus was recently created as an unassigned species in the Chordopoxvirinae, renamed from Squirrel parapoxvirus in the Parapoxvirus genus. The proposal does not change the taxonomic structure but the change of name is more consistent with the protocol for naming chordopoxviruses. Where the virus demonstrably causes pox-like disease in an animal, 'pox' should be added as a suffix to the animal name rather than as a prefix to 'virus'. Where pox-like disease is not apparent but a poxvirus is isolated, then 'pox' should be used as a prefix to 'virus'. Particularly in Red Squirrels [Genus Sp], Squirrelpox virus causes clearly demonstrable pox-like lesions, so the proposed amended name is more appropriate.

MODULE 8: **NON-STANDARD**

Template for any proposal not covered by modules 2-7. This includes proposals to change the name of existing taxa (but note that stability of nomenclature is encouraged wherever possible).

non-standard proposal

Code	2010.020bV	(assigned by ICTV officers)
Title of proposal: <i>Rename Deerpox virus W-848-83 to Mule deerpox virus</i>		

Text of proposal:

Deerpox virus W-848-83 was recently created as type species in the new genus *Cervidpoxvirus*. In anticipation that related viruses may be isolated from different species of deer, and following the convention for naming other *Poxviridae* species, we propose that the species name be changed to reflect the nature of the host species (North American free-ranging Mule deer, *Odocoileus hemionus*) and should thus become *Mule deerpox virus*.

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
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Annex:

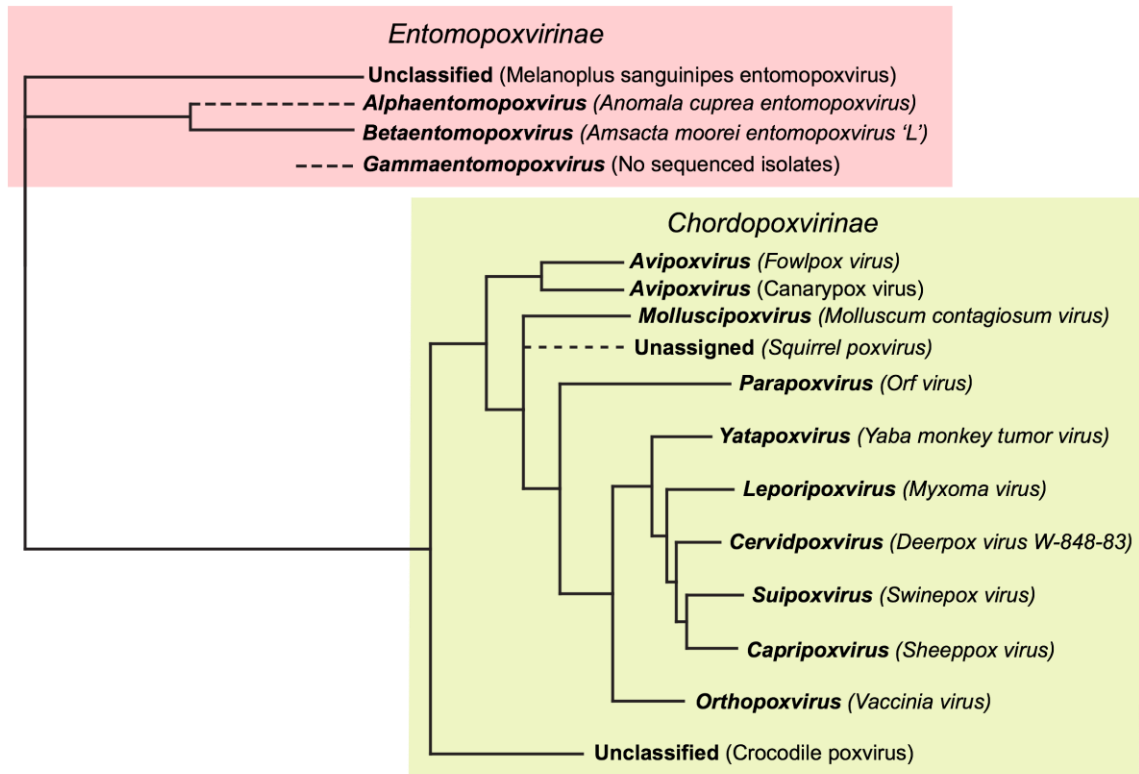
Include as much information as necessary to support the proposal, including diagrams comparing the old and new taxonomic orders. The use of Figures and Tables is strongly recommended but direct pasting of content from publications will require permission from the copyright holder together with appropriate 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

