This Word module should be used for all taxonomic proposals.

Please complete **Part 1** and:

either **Part 3** for proposals to create new taxa or change existing taxa

or **Part 2** for proposals of a general nature.

Submit the completed Word module, together with the accompanying Excel module named in Part 3, to the appropriate ICTV Subcommittee Chair.

The Word module explains and justifies your proposal. The Excel module is a critical document that will be used to implement the proposed taxonomic changes once they are approved and ratified. If proposals presented in the Word module are not presented accurately in the Excel module, the taxonomic changes cannot proceed.

For guidance, see the notes written in blue, below, and the Help Notes in file Taxonomic\_Proposals\_Help\_2019.

**Part 1:** **TITLE, AUTHORS, etc**

|  |  |  |
| --- | --- | --- |
| **Code assigned:** | ***2019.005D*** |  |
| **Short title:** Create eight new genera and twelve new species within the family *Poxviridae* andrename one species and move three species |
|  |
| **Author(s) and email address(es):**  |
| List authors in a single line *Archives of Virology* citation format (e.g. Smith AB, Huang C-L, Santos, F) | Provide email address for each author in a single line separated by semi-colons |
| Lefkowitz EJ, Li Y, Mauldin M, McInnes C, Mercer A, Meyer H, Smith GL, Tu, C, Upton C | elliotl@uab.edu; lay4@cdc.gov; mmauldin@cdc.gov ; Colin.McInnes@moredun.ac.uk; andy.mercer@otago.ac.nz; Hermann1Meyer@Bundeswehr.org; gls37@cam.ac.uk; cindytu@uvic.ca; cupton@uvic.ca |
| **Author(s) institutional address(es) (optional):**

|  |
| --- |
| Provide institutional addresses, each on a single line followed by author(s) initials (e.g. University of Woolloomooloo [SAB, HCL]) |
| University of Alabama at Birmingham, Birmingham AL, USA [EJL]Center for Disease Control, Atlanta GA, USA [YL, MM]Moredun Research Institute, Midlothian, UK [CM]University of Otago, Dunedin, New Zealand [AM]Bundeswehr Institute of Microbiology, Munich, Germany [HM]University of Cambridge, Cambridge, UK [GLS]University of Victoria, Canada [CT, CU] |

 |
| **Corresponding author** |
| Elliot J. Lefkowitz, elliotl@uab.eduGeoffrey L. Smith, gls37@cam.ac.uk |
| **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 (there are six virus subcommittees: animal DNA and retroviruses, animal ssRNA-, animal ssRNA+, fungal and protist, plant, bacterial and archaeal) | Poxviridae SG |
| **ICTV Study Group comments (if any) and response of the proposer:** |
| Approved unanimously by the Poxviridae Study Group |
|  |
| Date first submitted to ICTV: | 13 June 2019 |
| Date of this revision (if different to above): | 22 July 2019 |

|  |
| --- |
| **ICTV-EC comments and response of the proposer:** |
| Removed the creation of the species *Turkeypox virus* since it already exists. |

**Part 3:** **PROPOSED TAXONOMY**

|  |
| --- |
| **Name of accompanying Excel module:** 2019.005D.A.v1.8newgen\_Poxviridae.xlsx |

The taxonomic changes you are proposing should be presented on an accompanying Excel module, 2019\_TP\_Template\_Excel\_module. Please enter the file name of the completed module in this box.

**Supporting material:**

| additional material in support of this proposal |
| --- |
| Please explain the reasons for the taxonomic changes you are proposing and provide evidence to support them. The following information should be provided, where relevant:* **Species demarcation criteria**: Explain how new species differ from others in the genus and demonstrate that these differences meet the criteria previously established for demarcating between species. If no criteriahave previously been established, and if there will now be more than one species in the genus, please state the demarcation criteria you are proposing.
* **Higher taxa**:
	+ There is no formal requirement to state demarcation criteria when proposing new genera or other higher taxa. However, a similar concept should apply in pursuit of a rational and consistent virus taxonomy.
	+ Please indicate the **origin of names** assigned to new taxa at genus level and above.
	+ For each new genus a **type species** must be designated to represent it. Please explain your choice.
* **Supporting evidence**: The use of Figures and Tables is strongly recommended (note that copying from publications will require permission from the copyright holder). For phylogenetic analysis, please provide a tree where branch length is **proportional to genetic** distance, generated using an appropriate algorithm (Neighbour-Joining, Maximum Likelihood, or Bayesian) and provide evidence of the reliability of the branching (e.g., by bootstrapping).

Please refer to the Help Notes file (Taxonomic\_Proposals\_Help\_2019) for more information. |

**Proposal:**

This represents a catchall proposal to bring *Poxviridae* taxonomy (mostly) up-to-date. Since the last proposal submitted by the Poxviridae Study Group, there have been a number of new viruses isolated and sequenced that, based on the family’s demarcation criteria, represent new species, and in some cases new genera. In addition, we are also taking this opportunity to assign several species not previously assigned to genera, to newly created genera. Finally, one awkwardly-named species, *Parapoxvirus of red deer in New Zealan*d, is being renamed.

**Taxon demarcation criteria for the family *Poxviridae*:**

The following criteria are used as a guideline to establish taxonomic status of species, genera, and subfamilies within the *Poxviridae* family. Phylogenetic distance and natural host are the primary criteria used by this proposal for the creation of new species and genera.

1. Natural host range. In some cases, host range may be very narrow, and in others very broad, but in most cases, the delineation of the natural host(s) is a defining characteristic.
2. Phylogenetic analysis. Taxonomic groupings can in most cases be readily inferred from the evolutionary clades observed following phylogenetic inference. 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 orthopoxvirus genome, nucleotide sequence identity of >96% is observed between isolates of all non-North American species. Isolates within a species exhibit >98% nucleotide identity. These levels of identity are sufficiently high that it is frequently difficult to obtain the resolution necessary to use the shared core region of poxvirus genomes as a definitive demarcation criterion. Outside the conserved core region, genome and gene alignments become much more difficult and subjective.
4. Amino acid or nucleotide sequence identity between specific, commonly shared genes. Sequence polymorphisms within genes such as the hemagglutinin or A-type inclusion protein can frequently exhibit high levels of variation that provide the resolving power necessary to make demarcation decisions.
5. Gene content comparisons. The variability in the content and conservation of gene sequences between poxvirus isolates can serve as a distinguishing characteristic.
6. Organization of the genome. Syntenic relationships between genes may in some cases serve to distinguish taxa. But similar to nucleotide sequence identity, conservation of gene synteny can frequently be so high that the resolving power is not available to distinguish between taxa.
7. Growth characteristics and host range in cell culture. Characteristics of in vitro growth such as the production and morphology of pocks produced on the chorioallantoic membranes of embryonated chicken eggs or plaque characteristics on cell monolayers may distinguish between taxa.
8. Disease characteristics. The morbidity, mortality and other distinguishing features of the disease resulting from poxvirus infection can be used to support taxonomic decisions.
9. Serological criteria, including plaque neutralization tests and cross-protection in animals, may help to identify new, unique isolates and serve as a criterion for taxonomic demarcation.

**Supporting Evidence:**

Genomes utilized for the analysis (Names of proposed new genera and species are indicated with ‘\*’; all new/moved/renamed taxa are highlighted in grey.):

|  |  |  |  |  |
| --- | --- | --- | --- | --- |
| **Acc** | **Subfamily** | **Genus** | **Species** | **Isolate** |
| AY318871 | *Chordopoxvirinae* | *Avipoxvirus* | *Canarypox virus* | canarypox virus ATCC VR-111 |
| MF678796 | *Chordopoxvirinae* | *Avipoxvirus* | *Flamingopox virus\** | flamingopox virus FGPVKD09 |
| AF198100 | *Chordopoxvirinae* | *Avipoxvirus* | *Fowlpox virus* | fowlpox virus |
| KJ859677 | *Chordopoxvirinae* | *Avipoxvirus* | *Penguinpox virus\** | penguinpox virus PSan92 |
| KJ801920 | *Chordopoxvirinae* | *Avipoxvirus* | *Pigeonpox virus* | pigeonpox virus FeP2 |
| KP728110 | *Chordopoxvirinae* | *Avipoxvirus* | *Turkeypox virus* | turkeypox virus TKPV-HU1124/2011 |
| AY077835 | *Chordopoxvirinae* | *Capripoxvirus* | *Goatpox virus* | goatpox virus Pellor |
| AF325528 | *Chordopoxvirinae* | *Capripoxvirus* | *Lumpy skin disease virus* | lumpy skin disease virus NI-2490 |
| AY077832 | *Chordopoxvirinae* | *Capripoxvirus* | *Sheeppox virus* | sheeppox virus 10700-99 |
| MF001304 | *Chordopoxvirinae* | *Centapoxvirus* | *Murmansk microtuspox virus\** | Murmansk poxvirus LEIV-11411 |
| HQ849551 | *Chordopoxvirinae* | *Centapoxvirus* | *Yokapox virus* | Yoka poxvirus DakArB 4268 |
| AY689436 | *Chordopoxvirinae* | *Cervidpoxvirus* | *Mule deerpox virus* | deerpox virus W-848-83 |
| DQ356948 | *Chordopoxvirinae* | *Crocodylidpoxvirus* | *Nile crocodilepox virus* | Nile crocodilepox virus |
| JX565564 | *Chordopoxvirinae* | *Leporipoxvirus* | *Myxoma virus* | myxoma virus BRK 897 |
| AF170726 | *Chordopoxvirinae* | *Leporipoxvirus* | *Myxoma virus* | myxoma virus Lausanne |
| AF170722 | *Chordopoxvirinae* | *Leporipoxvirus* | *Rabbit fibroma virus* | rabbit fibroma virus |
| MF467281 | *Chordopoxvirinae* | *Macropopoxvirus\** | *Eastern kangaroopox virus\** | Eastern grey kangaroopox virus Sunshine Coast |
| MF467280 | *Chordopoxvirinae* | *Macropopoxvirus\** | *Western kangaroopox virus\** | Western grey kangaroopox virus Western Australia |
| U60315 | *Chordopoxvirinae* | *Molluscipoxvirus* | *Molluscum contagiosum virus* | molluscum contagiosum virus subtype 1 |
| MH427217 | *Chordopoxvirinae* | *Mustelpoxvirus\** | *Sea otterpox virus\** | sea otter poxvirus ELK |
| MH816996 | *Chordopoxvirinae* | *Orthopoxvirus* | *Abatino macacapox virus\** | orthopoxvirus Abatino |
| MH607141 | *Chordopoxvirinae* | *Orthopoxvirus* | *Akhmeta virus\** | Akhmeta virus Akhmeta\_2013-88 |
| AY009089 | *Chordopoxvirinae* | *Orthopoxvirus* | *Camelpox virus* | camelpox virus CMS |
| AF438165 | *Chordopoxvirinae* | *Orthopoxvirus* | *Camelpox virus* | camelpox virus M-96 |
| AF482758 | *Chordopoxvirinae* | *Orthopoxvirus* | *Cowpox virus* | cowpox virus Brighton Red |
| JQ410350 | *Chordopoxvirinae* | *Orthopoxvirus* | *Ectromelia virus* | ectromelia virus ERPV |
| AF012825 | *Chordopoxvirinae* | *Orthopoxvirus* | *Ectromelia virus* | ectromelia virus Moscow |
| DQ792504 | *Chordopoxvirinae* | *Orthopoxvirus* | *Horsepox virus* | horsepox virus MNR-76 |
| AY753185 | *Chordopoxvirinae* | *Orthopoxvirus* | *Monkeypox virus* | monkeypox virus COP-58 |
| AF380138 | *Chordopoxvirinae* | *Orthopoxvirus* | *Monkeypox virus* | monkeypox virus Zaire-96-I-16 |
| KP143769 | *Chordopoxvirinae* | *Orthopoxvirus* | *Raccoonpox virus* | raccoonpox virus |
| KU749310 | *Chordopoxvirinae* | *Orthopoxvirus* | *Skunkpox virus* | skunkpox virus WA |
| DQ437594 | *Chordopoxvirinae* | *Orthopoxvirus* | *Taterapox virus* | taterapox virus Dahomey 1968 |
| AY243312 | *Chordopoxvirinae* | *Orthopoxvirus* | *Vaccinia virus* | vaccinia virus WR |
| X69198 | *Chordopoxvirinae* | *Orthopoxvirus* | *Variola virus* | variola virus major India-1967 |
| Y16780 | *Chordopoxvirinae* | *Orthopoxvirus* | *Variola virus* | variola virus minor Garcia-1966 |
| KU749311 | *Chordopoxvirinae* | *Orthopoxvirus* | *Volepox virus* | volepox virus CA |
| HQ647181 | *Chordopoxvirinae* | *Oryzopoxvirus\** | *Cotia virus\** | Cotia virus SPAn232 |
| AY386265 | *Chordopoxvirinae* | *Parapoxvirus* | *Bovine papular stomatitis virus* | bovine papular stomatitis virus BV-AR02 |
| KY382358 | *Chordopoxvirinae* | *Parapoxvirus* | *Grey sealpox virus\** | seal parapoxvirus AFK76s1 |
| DQ184476 | *Chordopoxvirinae* | *Parapoxvirus* | *Orf virus* | orf virus NZ2 |
| AY386264 | *Chordopoxvirinae* | *Parapoxvirus* | *Orf virus* | orf virus OV-SA00 |
| GQ329670 | *Chordopoxvirinae* | *Parapoxvirus* | *Pseudocowpox virus* | pseudocowpox virus VR634 |
| KM502564 | *Chordopoxvirinae* | *Parapoxvirus* | *Red deerpox virus* (Renamed from Parapoxvirus of red deer in New Zealand) | parapoxvirus red deer/HL953 |
| KU980965 | *Chordopoxvirinae* | *Pteropopoxvirus\** | *Pteropox virus* | pteropox virus Australia |
| KT159937 | *Chordopoxvirinae* | *Salmonpoxvirus\** | *Salmon gillpox virus\** | salmon gill poxvirus |
| HE601899 | *Chordopoxvirinae* | *Sciuripoxvirus\** | *Squirrelpox virus* | squirrel poxvirus Red squirrel UK |
| AF410153 | *Chordopoxvirinae* | *Suipoxvirus* | *Swinepox virus* | swinepox virus 17077-99 |
| KY747497 | *Chordopoxvirinae* | *Vespertilionpoxvirus\** | *Eptesipox virus\** | Eptesipox virus Washington |
| AJ293568 | *Chordopoxvirinae* | *Yatapoxvirus* | *Tanapox virus* | Yaba-like disease virus |
| AY386371 | *Chordopoxvirinae* | *Yatapoxvirus* | *Yaba monkey tumor virus* | Yaba monkey tumor virus |
| AP013055 | *Entomopoxvirinae* | *Alphaentomopoxvirus* | *Anomala cuprea entomopoxvirus* | Anomala cuprea entomopoxvirus CV6M |
| HF679131 | *Entomopoxvirinae* | *Betaentomopoxvirus* | *Adoxophyes honmai entomopoxvirus* | Adoxophyes honmai enomopoxvirus 'L' |
| AF250284 | *Entomopoxvirinae* | *Betaentomopoxvirus* | *Amsacta moorei entomopoxvirus* | Amsacta moorei entomopoxvirus |
| HF679132 | *Entomopoxvirinae* | *Betaentomopoxvirus* | *Choristoneura biennis entomopoxvirus* | Choristoneura biennis entomopoxvirus 'L' |
| HF679133 | *Entomopoxvirinae* | *Betaentomopoxvirus* | *Choristoneura rosaceana entomopoxvirus* | Choristoneura rosaceana entomopoxvirus 'L' |
| HF679134 | *Entomopoxvirinae* | *Betaentomopoxvirus* | *Mythimna separata entomopoxvirus* | Mythimna separata entomopoxvirus 'L' |
| AF063866 | *Entomopoxvirinae* | *Deltaentomopoxvirus\** | *Melanoplus sanguinipes entomopoxvirus* | Melanoplus sanguinipes entomopoxvirus 'O' Tucson |

**Isolate abbreviations in Figures:**

Isolates in the phylogenetic trees are labelled as below using the indicated abbreviations followed by the GenBank genome nucleotide sequence accession number in parentheses.

|  |  |
| --- | --- |
| **Isolate** | **Abbreviation** |
| Abatino macacapox virus | ABMPV |
| Adoxophyes honmai enomopoxvirus 'L' | AHEV |
| Akhmeta virus Akhmeta\_2013-88 | AKHV |
| Amsacta moorei entomopoxvirus | AMEV |
| Anomala cuprea entomopoxvirus CV6M | ACEV |
| bovine papular stomatitis virus BV-AR02 | BPSV |
| camelpox virus CMS | CMPV-c |
| camelpox virus M-96 | CMPV-m |
| canarypox virus ATCC VR-111 | CNPV |
| Choristoneura biennis entomopoxvirus 'L' | CBEV |
| Choristoneura rosaceana entomopoxvirus 'L' | CREV |
| Cotia virus SPAn232 | COTV |
| cowpox virus Brighton Red | CPV |
| deerpox virus W-848-83 | DPV |
| Eastern grey kangaroopox virus Sunshine Coast | EKPV |
| Ectromelia virus ERPV | ECTV-e |
| Ectromelia virus Moscow | ECTV-m |
| eptesipox virus Washington | EPTPV |
| flamingopox virus FGPVKD09 | FLMPV |
| fowlpox virus | FWPV |
| goatpox virus Pellor | GTPV |
| horsepox virus MNR-76 | HSPV |
| lumpy skin disease virus NI-2490 | LSDV |
| Melanoplus sanguinipes entomopoxvirus 'O' Tucson | MSEV |
| molluscum contagiosum virus subtype 1 | MCV |
| monkeypox virus COP-58 | MPV-c |
| monkeypox virus Zaire-96-I-16 | MPV-z |
| Murmansk microtuspox virus LEIV-11411 | MMPV |
| Mythimna separata entomopoxvirus 'L' | MYSEV |
| myxoma virus BRK 897 | MYXV-b |
| myxoma virus Lausanne | MYXV-l |
| Nile crocodilepox virus | NCPV |
| orf virus NZ2 | ORFV-n |
| orf virus OV-SA00 | ORFV-o |
| parapoxvirus red deer/HL953 | RDPV |
| penguinpox virus PSan92 | PNGPV |
| pigeonpox virus FeP2 | PGNPV |
| pseudocowpox virus VR634 | PCPV |
| pteropox virus Australia | PTPV |
| rabbit fibroma virus | RFV |
| raccoonpox virus | RACPV |
| salmon gill poxvirus | SMGPV |
| sea otter poxvirus ELK | SOPV |
| seal parapoxvirus AFK76s1 (Grey sealpox virus) | GSEPV |
| sheeppox virus 10700-99 | SHPV |
| skunkpox virus WA | SKPV |
| squirrel poxvirus Red squirrel UK | SQPV |
| swinepox virus 17077-99 | SWPV |
| taterapox virus Dahomey 1968 | TATPV |
| turkeypox virus TKPV-HU1124/2011 | TKPV |
| vaccinia virus WR | VACV |
| variola virus major India-1967 | VARV-ma |
| variola virus minor Garcia-1966 | VARV-mi |
| volepox virus CA | VOPV |
| Western grey kangaroopox virus Western Australia | WKPV |
| Yaba monkey tumor virus | YMTV |
| Yaba-like disease virus | YLDV |
| Yoka poxvirus DakArB 4268 | YKPV |

**Phylogenetic Inference:**

To construct the phylogenetic trees, the amino acid sequences of 25 genes conserved throughout the *Poxviridae* family were extracted from 58 genomes representing each existing and proposed species, as well as a few additional clades to represent the degree of variation between clades, species, genera, and subfamilies. Amino acid sequences were used since the large variation in GC content across the family will greatly skew the resulting phylogeny if the trees were inferred on the basis of nucleotide sequences.

Genes utilized for the analysis (Vaccinia-Cop designation - protein name):

A18-DNA helicase

A2-VLTF-3

A22-holliday junction resolvase

A23-VITF-3

A24-RPO132

A28-IMV-MP

A3-P4b

A32-ATPase DNA packaging protein

A7-VETF-L

D1-large capping enzyme

D11-NPH-I

D12-small capping enzyme

D5-NTPase

D6-VETF-S

E1-polyA polymerase large

E10-sulfhydryl oxidase

E9-DNA-polymerase

G5-FEN1

H2-IMV entry-fusion

H4-RAP94

H6-DNA topoisomerase

I8-NPH-II

J3-polyA polymerase small

J6-RPO147

L1-IMV membrane protein

**Alignments:**

The amino acid sequences for each gene were aligned using MUSCLE, and then the aligned sequences were concatenated into a single sequence for each isolate prior to phylogenetic inference.

**Trees:**

Phylogeny was inferred using the Maximum Likelihood method based on the LG matrix-based model (Le and Gascuel, 2008). The log likelihood of the tree is (-435387.036). A discrete Gamma distribution was used to model evolutionary rate differences among sites (5 categories (+G, parameter = 0.783)). The rate variation model allowed for some sites to be evolutionarily invariable ([+I], 1.1% sites). The tree is drawn to scale, with branch lengths measured in the number of substitutions per site. The analysis involved 58 genomes and 25 genes that are conserved throughout the family. 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 12283 positions in the final dataset. Evolutionary analyses were conducted in MEGA10 (Kumar et al., 2018).

Figure 1. *Poxviridae* tree. Maximum Likelihood phylogenetic inference was based on the poxvirus 25-gene amino acid alignment described above. Bootstrap values on each node, represented as a percentage of all replicates, were derived from a separate Neighbor-Joining analysis using 1,000 bootstrap replicates. (Due to space limitations, bootstrap values on most orthopoxvirus nodes are not shown. They are displayed in figure 2.) Proposed new genera and species are highlighted in grey.



Figure 2. *Orthopoxvirus* tree. Maximum Likelihood phylogenetic inference was based on the poxvirus 25-gene amino acid alignment described above. Bootstrap values on each node, represented as a percentage of all replicates, were derived from a separate Neighbor-Joining analysis using 1,000 bootstrap replicates. Proposed new species are highlighted in grey.

Figure 3. *Avipoxvirus* tree. Maximum Likelihood phylogenetic inference was based on the poxvirus 25-gene amino acid alignment described above. Bootstrap values on each node, represented as a percentage of all replicates, were derived from a separate Neighbor-Joining analysis using 1,000 bootstrap replicates. Proposed new species are highlighted in grey.

|  |
| --- |
| **References:** |
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