

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

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| **Code assigned:** | ***2023.016D*** |  |
| **Short title:** Creation of a new genus within the *Entomopoxvirinae* subfamily | | |
|  | | |

**Author(s) and email address(es)**

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| --- | --- |
| McInnes CJ, Damon IK, Smith GL, McFadden G, Isaacs SN, Roper RL, Evans DH, Damaso CR, Carulei O, Wise LM, Takatsuka J, Traktman P and Lefkowitz E | colin.mcinnes@moredun.ac.uk; iad7@cdc.gov; geoffrey.smith@path.ox.ac.uk; grantmcf@asu.edu; isaacs@pennmedicine.upenn.edu; roperr@ecu.edu; devans@ualberta.ca; damasoc@biof.ufrj.br; ocarulei@gmail.com; lyn.wise@otago.ac.nz; junsan@affrc.go.jp; traktman@musc.edu; elliotl@uab.edu |

**Author(s) institutional address(es) (optional)**

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**Corresponding author**

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| McInnes CJ |

**List the ICTV Study Group(s) that have seen this proposal**

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| ICTV *Poxviridae* Study Group |

**ICTV Study Group comments and response of proposer**

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| The Study Group was in agreement with the proposal to create a new genus within the *Entomopoxvirinae* subfamily to accommodate the species *Diachasmimorpha longicaudata entomopoxvirus*. If accepted the species would also need to be renamed to the standardised binomial format and would become *Epsilonentomopoxvirus dlongicaudata*. |

**ICTV Study Group votes on proposal**

|  |  |  |  |
| --- | --- | --- | --- |
| **Study Group** | **Number of members** | | |
| **Votes support** | **Votes against** | **No vote** |
| ICTV *Poxviridae* Study Group | 12 | 0 | 1 |

**Authority to use the name of a living person**

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| **Is any taxon name used here derived from that of a living person (Y/N)** | N |

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| **Taxon name** | **Person from whom the name is derived** | **Permission attached (Y/N)** |
| N/A | N/A | N/A |

**Submission dates**

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| --- | --- |
| Date first submitted to SC Chair | June 2023 |
| Date of this revision (if different to above) | 1 Aug 2023 |

**ICTV-EC comments and response of the proposer**

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**Part 2:** **NON-TAXONOMIC PROPOSAL**

**Text of proposal**

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**Part 3:** **TAXONOMIC PROPOSAL**

**Name of accompanying Excel module**

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| --- |
| 2023.016D.N.v3.Poxviridae\_1ng.xlsx |

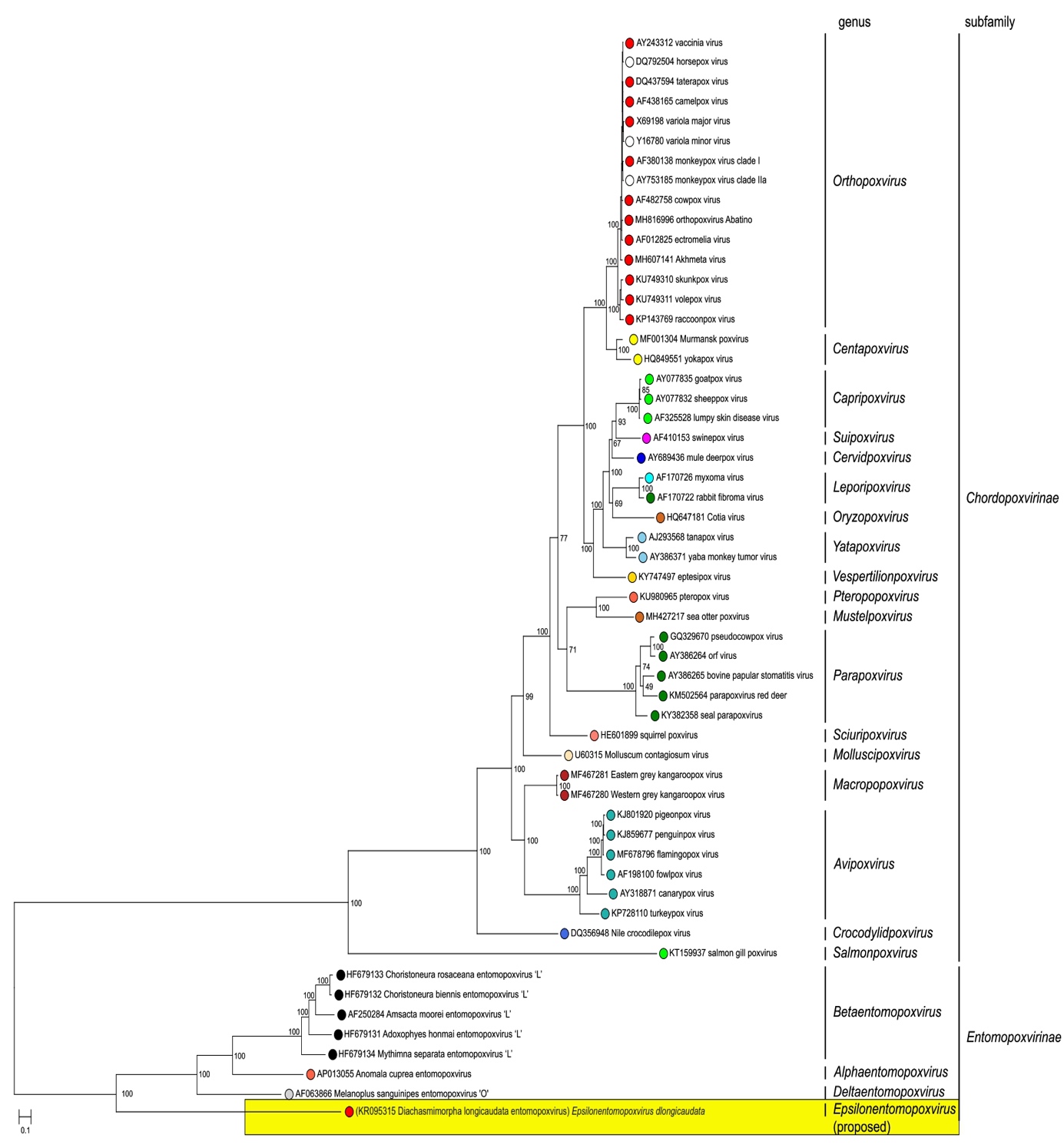
**Abstract**

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| Here we propose to create a new genus within the *Entomopoxvirinae* subfamily of the *Poxviridae* family to accommodate the species *Diachasmimorpha longicaudata entomopoxvirus*. Following past convention within the subfamily the new genus name would be based on the Greek alphabet and would be *Epsilonentomopoxirus*. If accepted, the further proposal would be to rename the *Diachasmimorpha longicaudata entomopoxvirus* species to *Epsilonentomopoxvirus dlongicaudata*. |

**Text of proposal**

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| |  | | --- | | Poxvirus-induced disease and the presence of poxvirions has been reported in host of many different species world-wide, including mammalian, avian, reptilian, piscine and insect species. Traditional poxvirus species demarcation relied on the host spectrum and virus properties such as particle morphology, *in vitro* and *in vivo* growth characteristics*,* cross-neutralisation studies and cross-hybridisation, Restriction fragment length polymorphism (RFLP), and PCR analyses of the DNA genomes. The availability of full genome sequences has added a further dimension to virus species demarcation allowing robust phylogenetic analyses to be used to study the relationship between newly isolated/identified viruses and those of established virus species.  A poxvirus, known as Diachasmimorpha longicaudata entomopoxvirus (DLEV), has been found within the venom glands of a parasitoid wasp (braconid *Diachasmimorpha longicaudata* (Ashmead)) which parasitizes tephritid fruit flies. Uniquely within the *Poxviridae*, it has been reported that this poxvirus exists as a heritable mutualistic symbiont of its wasp host, able to cause pathology in the fruit flies, but also able to complete non-pathogenic replication within the parasitoid wasp.    Complete coding sequence has been obtained (1) from the virus and has revealed a number of characteristics that separate it from all other classified entomopoxviruses sequenced to date. The G+C content is markedly different being 30% in comparison to the 20% normally found among entomopoxviruses; and the coding density of the genome, at 65%, is extremely low in comparison to all other poxviruses in which it is normally around 90%. Annotation of the genome also revealed that 4 of the 49 genes considered to represent the core set present in all poxvirus genomes, are likely missing. Phylogenetic analysis, using the amino acid sequences of 25 genes conserved across all genera of poxviruses (see below), was used to infer the relationship of DLEV with representative viruses from all other established poxvirus species. Bootstrap analysis clearly supported the creation of a new genus within the *Entomopoxvirinae* subfamily to accommodate DLEV.  As a result of the comparative analyses we propose that a new genus is created within the *Entomopoxvirinae*. This would be designated *Epsilonentomopoxvirus* following the previously used convention within the *Entompoxvirinae* of naming genera based on the Greek alphabet. Also following convention, we propose to create a new species, *Epsilonentomopoxvirus dlongicaudata* (following the new standardised binomial format) with DLEV as its exemplar virus. | |  |

**Supporting evidence**



**Phylogenetic relationships in the family *Poxviridae*.** Representative viruses belonging to species in the family *Poxviridae* are shown based on their inferred phylogenetic placement. Individual genera in the subfamilies *Chordopoxvirinae* (vertebrate-infecting viruses) and *Entomopoxvirinae* (invertebrate-infecting viruses) are shown. Each species is represented by an exemplar isolate labeled with the name of the virus isolate and GenBank accession number for the complete genomic nucleotide sequence. Phylogeny was inferred using Maximum Likelihood (ML) phylogenetic inference using an amino acid multiple sequence alignment of 25 genes conserved between poxviruses. 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. The program modeltest-ng (<https://github.com/ddarriba/modeltest>) was used to determine the optimum evolutionary model for phylogenetic reconstruction. Maximum Likelihood (ML) trees were inferred with the program raxml-ng (<https://github.com/amkozlov/raxml-ng>) using the model LG+I+G4+F, and 1,000 bootstrap replicates.

**References**

1. Coffman KA and Burke GR (2020) Genomic analysis reveals an exogenous viral symbiont with dual functionality in parasitoid wasps and their hosts. PLoS Pathog. 16(11):e1009069. doi: 10.1371/journal.ppat.1009069. eCollection 2020 Nov.