

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

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| **Code assigned:** | ***2023.015D*** |  |
| **Short title:** Creation of a new genus within the *Entomopoxvirinae* subfamily | | |
|  | | |

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

|  |  |
| --- | --- |
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**Corresponding author**

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| Colin J McInnes |

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

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| Poxviridae Study Group |

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

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| The Study Group discussed the principle of removing species from the ICTV master species list (MSL) where no sequence data was available to support their inclusion as distinct species within the *Poxviridae* family. The study group were in agreement that these virus species should be removed until such time that supporting sequence data became available. |

**ICTV Study Group votes on proposal**

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

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

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

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

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

**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**

|  |
| --- |
| 2023.015D.N.v1.Poxviridae\_ab\_27sp\_1g.xlsx |

**Abstract**

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| Here we propose to abolish 27 poxvirus species due to the lack of sequence data to support their existence as novel species within the *Poxviridae* family. If agreed, this would leave one of the genera within the entomopoxvirinae subfamily without any representative species and therefore our further proposal would be to abolish this genus until such time that data can be produced that would support its re-instatement. |

**Text of proposal**

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| |  | | --- | | Poxvirus-induced disease and the presence of poxvirus virions has been reported in many different host species world-wide, including; mammalian, avian, reptilian, piscine and insect species. Traditional poxvirus species demarcation relied on the host species and virus properties such as morphology, *in vitro* and *in vivo* growth characteristics*,* cross-neutralisation studies and cross-hybridisation, RFLP and PCR analyses of the DNA genomes.  The availability of sequence analyses in the most part supported the original classifications and confirmed that in many cases separate poxvirus species are found in separate host species. However, this is not always the case with, for example, cattle being susceptible to infection with species from at least three different poxvirus genera, the orthopoxviruses, the parapoxviruses and the capripoxviruses. Additionally, some poxvirus species have been reported in more than one host, for example the pseudocowpox species has been reported in cattle, reindeer and camels.  The current *Poxviridae* species listed in the ICTV Master Species List (MSL) include some representing viruses identified in a variety of host species either due to the manifestation of pox-like disease or the presence of poxvirus virions within diseased tissues, as identified by electron microscopy. This is particularly the case within the avipoxvirus genus and the entomopoxvirinae subfamily. Many of these species were identified prior to the ready availability of high throughput sequencing and therefore no sequence data is available to support their classification as separate unique poxvirus species. It is also the case that the original classifications relied on observations at the time and that the viruses in question may not have been isolated or have been subsequently lost. It is therefore considered that sequence data for these species is unlikely to be generated in the short term.  Given the importance of sequence data to the current accurate demarcation of poxvirus species the Poxvirus Study Group propose that poxvirus species in the MSL for which no sequence data has been deposited in the GenBank database should be abolished. This would lead to the abolition of 27 poxvirus species: 5 from the *Avipoxvirus* genus; 1 from the *Leporipoxvirus* genus; 5 from the *Alphaentomopoxvirus* genus; 10 from the  *Betaentomopoxvirus* genus and; 6 from the *Gammaentomopoxvirus* genus.  The *Gammaentomopoxvirus* genus had originally been created due to the distinct virion morphology of the poxviruses found in Dipteran species of insects. However, abolition of the 6 *Gammaentomopoxvirus* species would leave the genus without any representative species and therefore this genus should also be abolished. | |

**Supporting evidence**

**References**