

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

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| **Code assigned:** | **2021.014M** |  |
| **Short title:** Create eight new species in genus *Jeilongvirus* (*Mononegavirales*: *Paramyxoviridae*) | | |
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**Author(s) and email address(es)**

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

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| ICTV *Paramyxoviridae* Study Group |

**ICTV study group comments and response of proposer**

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| None. |

**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 |

**Submission dates**

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| Date first submitted to SC Chair | May 28, 2021 |
| Date of this revision (if different to above) | September 13, 2021 |

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

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| * do I understand correctly that <70% nucleotide identity in PASC analysis is the demarcation criterion used for this genus? If so, this could be explicitly stated.   Response: The 70% only serves to indicate that they are clearly distinct entities.   * Please note that both files have the extension \_2nsp instead of \_8nsp. Not important, but why not?   Response: Filenames were changed accordingly.   * Read the EC-distributed guidance on species naming document, confirm that proposed species names adhere to the guidance, and confirm that you would like to keep the proposed species names as originally proposed.   Response: Read, confirmed, and confirmed. |

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

**Name of accompanying Excel module**

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| 2021.014M.R.Jeilongvirus\_2nsp |

**Abstract**

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| We propose here the creation of eight new species within orthoparamyxovirin genus *Jeilongvirus* (*Mononegavirales*: *Paramyxoviridae*). The viruses representing these species were discovered in bats, eulipotyphla, and rodents, and (near-) complete genome sequences are available for all of them. Bayesian phylogenetic analysis based on the deduced amino acid sequence of the six major paramyxovirus proteins shows clear clustering of these eight sequences as individual species. |

**Text of proposal**

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| |  | | --- | | We recently described the discovery and genome characterization of belerina virus and ruloma virus [[1](#_ENREF_1), [2](#_ENREF_2)]. Belerina virus was found in West European hedgehogs (*Erinaceus europaeus* Linnaeus, 1758) from Belgium, whereas ruloma virus was detected in a Machangu’s brush-furred rat (*Lophuromys machangui* Verheyen, Hulselmans, Dierckx, Mulungu, Leirs, Corti & Verheyen, 2007) from Tanzania. Phylogenetic analysis based on the deduced amino acid sequences of the N, P, M, F, G, and L open reading frames showed belerina virus and ruloma virus clustering as outliers within genus *Jeilongvirus*, (subfamily *Orthoparamyxovirinae*, family *Paramyxoviridae*). In our analyses, we also included (near-) complete genome sequences of yet unclassified paramyxoviruses. Three of these, rodent paramyxovirus isolate RtAp-ParaV/NX2015, bat paramyxovirus strain Bat-PV-17770 and bat paramyxovirus strain Bat-PV-16797, are labeled in GenBank as ‘complete genomes’. Rodent paramyxovirus was found in a Korean field mouse (*Apodemus peninsulae* (Thomas, 1907)) in China, whereas both bat paramyxoviruses were discovered in *Miniopterus griveaudi* (Harrison, 1959) bats from Madagascar and the Comoros, respectively [[3](#_ENREF_3)]. Three others, feline paramyxovirus 163, Miniopterus schreibersii paramyxovirus isolate Bat Ms-ParaV/Anhui2011 and bat paramyxovirus isolate BtMl-ParaV/QH2013, are not associated with complete genome sequences, but there is sufficient sequence information available to confidently classify them into separate species. Feline paramyxovirus was found in domestic cats (*Felis catus* Linnaeus, 1758) from Japan, whereas the two bat paramyxoviruses were found in China in a common long-fingered bats (*Miniopterus schreibersii* (Kuhl, 1817)) and a greater tube-nosed bat (*Murina leucogaster* (Milne-Edwards, 1872)), respectively [[4](#_ENREF_4), [5](#_ENREF_5)].  All eight of the aforementioned viruses represent individual, novel species. Pairwise sequence comparison using PASC (<https://www.ncbi.nlm.nih.gov/sutils/pasc/viridty.cgi>) shows that each of them shares <70% nucleotide identity with their closest related species (see Table 1). Moreover, Bayesian phylogenetic analysis using the deduced amino acid sequence of the six major paramyxovirus open reading frames (N-P-M-F-G-L) of all 34 currently classified orthoparamyxoviruses and these eight novel sequences shows each of them clustering as a separate branch of sufficient length to warrant the establishment of a separate species (although the current paramyxovirus taxonomy is based on the sequence of only the L protein, trees made using all six major ORFs are usually more informative and better supported [[6](#_ENREF_6)]).  In line with the recently approved proposal 2018.001G to move towards a binomial nomenclature for virus taxa, we propose the following species names, referring either to the geographical location where the viruses were first discovered (*Jeilongvirus rungweense*, *Jeilongvirus comorosense*, *Jeilongvirus madagascarense*, *Jeilongvirus anhuiense*) or the host (genus name) in which they were found *(Jeilongvirus apodemi*, *Jeilongvirus felis*, *Jeilongvirus erinacei*, *Jeilongvirus murinae*) (Table 1). Ruloma virus (*Jeilongvirus rungweense*) was found in a lophuromys from Rungwe district in Tanzania. Bat paramyxovirus strain Bat-PV-16797 (*Jeilongvirus comorosense*) and Bat paramyxovirus strain Bat-PV-17770 (*Jeilongvirus madagascarense*) were found in bats from Comoros and Madagascar, respectively, whereas Miniopterus schreibersii paramyxovirus isolate Bat Ms-ParaV/Anhui2011 (*Jeilongvirus anhuiense*) was discovered in a bat from Anhui Province, China. | |

**Supporting evidence**

**Table 1: Proposed species names for the eight putative species and their % identity to the closest related species as determined by PASC.**

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| **Proposed species name** | **Virus sequence** | **Closest related sequence** | **% identity** |
| *Jeilongvirus rungweense* | MW579602.1 ruloma virus isolate TA502 | LC431581.1 feline paramyxovirus 163 | 41.68 |
| *Jeilongvirus apodemi* | KY370098.1 rodent paramyxovirus isolate RtAp-ParaV/NX2015 | MT085491.1 Beilong virus strain Rbeiv/GD2017 | 55.72 |
| *Jeilongvirus comorosense* | MG203877.1 bat paramyxovirus strain Bat-PV-16797 | MG203878.1 bat paramyxovirus strain Bat-PV-17770 | 68.49 |
| *Jeilongvirus madagascarense* | MG203878.1 bat paramyxovirus strain Bat-PV-17770 | MG203877.1 bat paramyxovirus strain Bat-PV-16797 | 68.49 |
| *Jeilongvirus felis* | LC431581.1 feline paramyxovirus 163 | NC\_043539.1 Mount Mabu Lophuromys virus 1 | 48.82 |
| *Jeilongvirus anhuiense* | KC154054.1 Miniopterus schreibersii paramyxovirus isolate Bat Ms-ParaV/Anhui2011 | MG203877.1 bat paramyxovirus strain Bat-PV-16797 | 59.86 |
| *Jeilongvirus erinacei* | MN561699.1 belerina virus isolate HH114 | KJ641657.1 bat paramyxovirus isolate BtMl-ParaV/QH2013 | 49.57 |
| *Jeilongvirus murinae* | KJ641657.1 bat paramyxovirus isolate BtMl-ParaV/QH2013 | MN561699.1 belerina virus isolate HH114 | 49.57 |

Afbeelding met tekst

Beschrijving is gegenereerd met zeer hoge betrouwbaarheid

**Figure 1:** Bayesian phylogenetic tree of subfamily *Orthoparamyxovirinae*. Separate alignments were made for the deduced amino acid sequences of each of the six major paramyxovirus open reading frames (N-P-M-F-G-L) using Mafft v7.310, L-INS-I method. The resulting alignments were trimmed using TrimAl v1.4.rev15, gappyout setting, and subsequently concatenated. Following model selection using IQ-TREE, the resulting alignment was used for phylogenetic analysis with Beast v1.10.4, employing an LG+G4+I model to describe the amino acid substitution process and a Yule process for tree priors. Posterior support values are shown at each node. The eight viruses representing proposed putative species are marked in red. Used GenBank accession numbers are shown at each branch.

**References**

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